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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                             Score
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Match Length
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.bA1:
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.bA1:
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.bAT:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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(SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*
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               Factor-VIII heavy
Factor-VIII heavy
Human Factor-VIII/
Human Factor-VIII
Human Factor-VIII
                                                                                                                                                                                                                                     Description
                                                                                                                                          Human factor VIII
Human Factor-VIII
                                                                                                                                                                                          Anti-FIX/FIXa anti
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45	44	43	42	41	40	9	38	37	36	ü	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
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Homo sapiens modif	Human factor VIII.	Procoagulant-activ	Procoagulant-activ	Procoagulant-activ	Procoagulant-activ	Procoagulant-activ	n Factor	VIII:c	VIII:c	VIII:c		<	OD.			factor	factor	Human factor VIII			Human factor VIII	SArg B-domain-dele	œ.		B-domain deleted f	Modified factor VI	Human mature B-dom	Mutant mature huma		Modified factor VI	Procoagulant-activ	Procoagulant-activ	Procoagulant-activ		Factor-VIII heavy

## ALIGNMENTS

RESULT 1 AAB20445

New factor IX/factor IXa antibodies and their derivatives useful for WFI; 2001-290358/30. Factor IX, FIX, Factor IXa; FIXa; antibody; procoagulant; Factor VIII coffactor; blood coagulation disorder; haemophilia A; haemorrhagic diathesis; haemostatic; anidolytic; therapy; mouse; complementarity determining region; CDR. Scheiflinger F, Kerschbaumer R, 21-JUN-2001 (first entry) 14-SEP-1999; 13-SEP-2000; 2000WO-EP08936. 22-MAR-2001. WO200119992-A2 Mus musculus. Anti-FIX/FIXa antibody CDR3. AAB20445; AAB20445 standard; Peptide; 16 AA (BAXT ) BAXTER AG. 99AT-0001576 Falkner F, Dorner

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RESULT 2
AAG79422
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Best Local :
The sequences given in AAG79422-23 represent regions 2 and 3 of human factors VIII and IX. Region 2 comprises the interaction between N346 of factor IXa and E455 and K570 of factor VIIIa, and the interaction between R403 of factor IXa and E633 of factor VIIIa. Region 3 comprises the interaction between K293 of factor IXa and D712 of factor VIIIa, and the interaction between K293 of factor IXa and D712 of factor VIIIa, and Fragments of these polypeptides inhibit the interaction of blood
                                                                                                                                                                  New polypeptide inhibits interaction of blood coagulation factor VIIIa with factor IXa precluding activation of factor X, useful for preventing or treating coagulation disorders, such as thrombosis, atherosclerosis and restenosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activating activity. Administration of the antibodies or their derivatives leads to an increase in the procoagulant activity of FIXA, even in the presence of FVIIIa inhibitors. This allows for rapid blood coagulation even in the absence of FVIII or FVIIIA, ar in the case of FVIII inhibitor patients. The antibodies or their derivatives are used in a claimed pharmaceutical composition for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic diathesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 region 3 (CDR3) of an antibody having anti-Factor IX (FIX) or anti-activated Factor IX (FIXa) activity. Such antibodies and their derivatives (including those that comprise the present CDR3 peptide) have Factor VIIIa (FVIIIa) cofactor activity or FIXa
                                                                                                                                      Claim
                                                                                                                                                                                                                                                     WPI; 2002-599771/64.
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                                                                                                                                                                                                                                                                                                                                                    23~JAN-2001; 2001US-263431P
                                                                                                                                                                                                                                                                                                                                                                                   23-JAN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Factor VIII;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG79422 standard; protein; 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      increasing amidolytic coagulation disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Page 74; 138pp; English
                                                                                                                                    2; Fig 7A; 61pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factor VIII region 2/3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRNRGMTALLKVSSCD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor IX; coagulation; blood; cardiovascular
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                                                                                                                                    English.
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Pred. No.
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Matches 16
                                                                                                                                                                                           This is a fragment corresponding to internal AAs 373-740 of human Factor-VIII which may be crosslinked resulting in increased stability and retention of high activity over extended periods of time after activation by thrombin. The polypeptide is used to prevent or treat diseases caused by the absence or deficit of Factor-VIII in a subject such as haemophilia. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crosslinked Factor VIII polypeptide which is stable - is prepd. using bis(sulphosuccinimydyl) suberate or disuccinimydyl suberate in the presence of polysorbate 80 to produce a coagulant with long lasting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coagulation factor VIIIa with blood coagulation factor IXa. They als inhibit the activation of blood coagulation factor X, or inhibit blo coagulation. These peptide fragments are useful in preventing and/or treating coagulation disorders, in particular cardiovascular disorde such as thrombosis, atherosclerosis and restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-194038/25
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21-NOV-1995
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llarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 82;
Pred. No.
                                                                           Score 82;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ζ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 23;
                                                                           3.8e-07;
                                                                                                  BB
                                                                                                  16;
                                                   ç
                                                                                             Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                               deficiency
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                                                 Gaps
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blood
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RESULT 5
AAR74089
ID AAR7
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ID AAR7
XX
AC AAR7
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AC AAR7
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DT 04-N
DT 04-N
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Homma
KW thro
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Homo

                        XEXEEXEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents N-terminal residues 1-720 of a human Factor-
UIII heavy chain. The sequence is shorter than the A1-A2 domain,
and is produced by treating a polypeptide containing the full A1-A2
domain of full-length Factor-VIII with a protease, e.g. thrombin.
The fragment has the same specific activity as full-length
Pactor-VIII in a chromogenic assay and the activity is a factor of two
clower in a clotting assay, and the fragment is activated by thrombin
at a slower rate and to a lower level than fragments 1-740 (AAR74090),
clower in a clotting assay and the fragment is produced
recombinantly to reduce production costs and improve safety, and
production levels and stability are higher than for the full-length
form. The fragment may be used to treat patients who have developed
antibodies against epitopes in the C-terminal part of the heavy chain.
(Updated on 25-MAR-2003 to correct pN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                   25-MAR-2003
04-NOV-1995
                                        Factor-VIII heavy chain N-terminal fragment.
                                                                                                                                                                                              AAR74089;
                                                                                                                                                                                                                                                   AAR74089 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Factor VIII polypeptide(s) comprising a heavy chain shorter than native A1-A2 domain - are easier to produce recombinantly and retain coagulant activity, may be used to treat patients who have developed antibodies to C-terminal epitope(s) of Factor VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 24-26; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ezban Rasmussen M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12~NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9513300-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; Factor VIII; heavy chain; N-terminal fragment; thrombin cleavage; blood-clotting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
04-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Factor-VIII heavy chain N-terminal fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR74088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR74088 standard;
                                                                                                                                                                                                                                                                                                                                                                                                            697
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FRNRGMTALLKVSSCD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     FRNRGMTALLKVSSCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            720 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93DK-0001280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-DK00423.
                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kjalke M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 82; D)
100.0%; Pred. No. 8.
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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PRINCE PR
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AAR76959
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Misc-difference Misc-difference

/label= Asp 482

absent or

Asn,

Ser, Ser,

Ala Ala Ala

'label= Asp absent or Asn,

Location/Qualifiers

label= Asp

absent or Asn,

Thr,

Factor-VIII; Homo sapiens Human Factor-VIII/Factor-VIIIa derivative

therapeutic; blood-clotting

AAR76959; 25-MAR-2003 09-MAR-1996

(updated) (first entry) AAR76959 standard; protein; 740

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0

Misc-difference

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Best Loc
Matches
                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                             and is produced by treating a polypeptide containing the full 11-A2 domain of full-length Factor-VIII with a protease, e.g. thrombin. The fragment has the same coagulant specific activity as full-length Factor-VIII in a chromogenic assay, and is activated by thrombin at a similar rate. The fragment may be produced recombinantly to reduce production costs and improve safety, and production levels and stability are higher than for the full-length form. The fragment may be used to treat patients who have developed antibodies against epitopes in the C-terminal part of the heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Factor VIII polypeptide(s) comprising a heavy chain shorter than native A1-A2 domain - are easier to produce recombinantly and retain coagulant activity, may be used to treat patients who have developed antibodies to C-terminal epitope(s) of Factor VIII
                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents N-terminal residues 1-729 of a human Factor-VIII heavy chain. The sequence is shorter than the A1-A2 domain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ezban Rasmussen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9513300-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; Factor VIII; heavy chain; N-terminal fragment; thrombin cleavage; blood-clotting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NOVO ) NOVO-NORDISK AS
     697
                                 1 FRNRGMTALLKVSSCD 16
                                                                                                16;
                                                                                                                       Similarity
FRNRGMTALLKVSSCD
                                                                                                                                                                                              729 AA;
                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-29; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93DK-0001280
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                                                                                                                  100.0%;
     712
                                                                                           0;
                                                                                                               Score 82; I
Pred. No. 8.
                                                                                                Mismatches
                                                                                                               DB 16;
8.6e-07;
                                                                                                                                      Length 729;
                                                                                         Indels
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                                                                                           Gaps
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RBSULT 7
AAR76961
ID AAR7
XX AAR7
AC AAR7
XX AAR7
XX BP Hume
DB Hume
DB Hume
DB Hume
CX Home
CX Home
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The new Factor-VIII/Factor-VIIIa derivative comprises a functional A2 domain in which amino acid residues, as indicated in the Features, are deleted or substituted by another amino acid so as to increase the overall positive charge. Asp-403, Asp-404, Asp-433, Asp-482 and Asp-500 are preferably substituted by Asn, Glu-434 and Glu-440 are preferably substituted by Gln. The new derivative has the same activity as the wild-type Factor-VIII but with improved stability (the activity is maintained for a longer period compared to the rapid decline of the activity of wt Factor-VIII). The new derivative can be used in a composition for treating diseases caused by an absence or deficiency of Factor-VIII, especially haemophilia. (Updated on 25-MAR-2003 to correct DR field.)
                                                                                                                                                                                                                                                                      Human Factor-VIII derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel factor VIII derivative used to treat haemophilia - and comprises a functional A2 domain containing a mutation at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                       Misc-difference
                                                                Misc-difference
                                                                                                           Misc-difference
                                                                                                                                                                                  Homo
                                                                                                                                                                                                                        Factor-VIII;
                                                                                                                                                                                                                                                                                                                 09-MAR-1996
                                                                                                                                                                                                                                                                                                                                                              AAR76961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ezban Rasmussen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9518829-A1
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                                                                                                                                                                                                                                                                                                                                                                                                      AAR76961 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 11-14; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-255041/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                             sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cys residues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRNRGMTALLKVSSCD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRNRGMTALLKVSSCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       740 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                        therapeutic; blood-clotting.
                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95WO-DK00010
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                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Asp absent
500
/label= absent or Val, Ala or Ile
                                          'label= absent or Gln,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Glu absent or Gln, Ser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label= Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label= Asp
                                                                                   label= absent or Ala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nicolaisen EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      712
                                                                                                                                                                                                                                                                                                                                                                                                         740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 82; DE
Pred. No. 8.7
D; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
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K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gln,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Asn,
                                          Ser,
                                                                                   Thr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16;
8.7e-07;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel factor VIII derivative used to treat haemophilia - and comprises a functional A2 domain containing a mutation at one
                       07-JAN-1994;
                                                                     06-JAN-1995;
                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Factor-VIII; therapeutic; blood-clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Factor-VIII derivative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 14-17; 30pp;
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                                                                                                                   13-JUL-1995.
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16; Conserv
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                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 692
                                                                                                                                                                                                                   /label= absent or Val,
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                                                                                                                                                                                                                                                                 label= absent or Gln,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; 740
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Pred. No.
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8.7e-07;
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RESULT 9
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Best Local S
Matches 16
                                                                               Crosslinked Factor VIII polypeptide which is stable - is prepd. using bis(sulphosuccinimydyl) suberate or disuccinimydyl suberate in the presence of polysorbate 80 to produce a coagulant with long lasting
                                              Disclosure;
                                                                                                                                       WPI; 1995-194038/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The new Factor-VIII derivative comprises a functional A2 domain in which Cys-692 is replaced with Ser. For other (less preferred) substitutions at this site, see AAR76961. Alternatively, Gu-720 and/Tyr-729 are deleted or substituted with various amino acids (as in the Features). The new derivative has the same activity as the wild-type Factor-VIII but with improved stability (the activity is maintained for a longer primotored to the rapid decline of the activity of wt Factor-VIII). The new derivative can be used in a composition for treating diseases caused by an absence or deficiency of Factor-VIII, especially haemophilia.
                                                                                                                                                                                                                    12-NOV-1993;
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                                                                                                                                                                                                                                                                      18-MAY-1995
                                                                                                                                                                                                                                                                                                WO9513301-A1
                                                                                                                                                                                                                                                                                                                                              Factor-VIII; blood-clotting; blood; coagulant; haemophilia-A
                                                                                                                                                                                                                                                                                                                                                                          Human Factor-VIII N-terminal fragment.
                                                                                                                                                                                                                                                                                                                        Homo sapiens
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21-NOV-1995
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                                                                                                                                                                                         (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 18-20; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprises a functional A2 domain containing a mutation at one or more Cys residues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          740 AA;
                                           Page 21; 36pp; English
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[larity 100.0%;
Conservative 0
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(first entry)
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Pred. No. 8.7e-07;
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This is the N-terminal fragment of human Factor-VIII which crosslinked resulting in increased stability and retention activity over extended periods of time after activation by

n may be n of high / thrombin.

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FRNRGMTALLKVSSCD

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RESULT 10
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Best Local S
Matches 16
                                                                                                                                                                  The sequence represents N-terminal residues 1-740 of a human Factor-VIII heavy chain. The sequence contains entire A1 and A2 domains, and truncated forms (1-720 in (AAR74088)) and 1-729 in (AAR74089)) may be produced by treatment with a protease, e.g. thrombin. The C-terminally truncated fragments have the same coagulant specific activity as full-length Factor-VIII, and may be produced recombinantly to reduce production costs and improve safety, giving higher production levels and stability than for the full-length form. The fragments may be used to treat patients who have developed antibodies against epitopes in the C-terminal part of the heavy chain. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Factor VIII polypeptide(s) comprising a heavy chain shorter than native A1-A2 domain - are easier to produce recombinantly and retain coagulant activity, may be used to treat patients who have developed antibodies to C-terminal epitope(s) of Factor VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 30-32; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-194037/25.
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04-NOV-1995
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(Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombin cleavage; blood-clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; Factor VIII; heavy chain; N-terminal fragment;
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                              Similarity
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100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93DK-0001280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ž
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
Score 82; DB 16;
Pred. No. 8.7e-07
; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 82;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90
                                                       16;
                                                    Length 740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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697

FRNRGMTALLKVSSCD

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                                                                                                                        RESULT 11
AAR76982
                                                                                                                                                              This sequence represents the A2 domain of a human factor VIII derivative.

C Factor VIII is a large glycoprotein which is present in plasma at low concentrations. Factor VIII is an essential part of the clotting reaction in response to a wound. Factor VIII is susceptible to cleavage by thrombin, activated protein C, plasmin, and other serine proteases. Full length factor VIII consists of three repeats of the A-domain, a B-domain and 2 repeats of the C-domain. Active factor VIII has the A1 domain cleaved off. Factor VIII is too unstable for use in recombinant techniques. Factor VIII containing this sequence has improved stability and shows resistance against enzymatic activity present in mammalian cells. This means that factor VIII containing this sequence can be used in recombinant techniques. A factor VIII derivative can be used for treating diseases caused by an absence or deficiency of factor VIII (in the same way as normal factor VIII) e.g. haemophilia. The advantage with using a recombinant factor VIII also includes no need for lots of domors in order to get a sufficient amount. Also, there is no long purification process, and there is no risk of transmission of blood-bourne diseases
                                                           Matches
                                                                          Query Match
Best Local
                                                                                                                      Sequence
                                                                                                                                                      such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel factor VIII derivative with resistance to enzymatic cleavage and comprises a functional A2 domain where Glu720 and/or Tyr729 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-255040/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ezban Rasmussen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Factor VIII; human; haemophilia; thrombin; protein C; plasmin; serine protease; recombination; therapy; deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    deleted/substituted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9518828-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human factor VIII A2-domain derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR76982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR76982 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NOVO ) NOVO-NORDISK AS
697
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Page 11-14; 26pp; English.
                                                         16;
                                                                        Similarity
FRNRGMTALLKVSSCD 712
                          FRNRGMTALLKVSSCD 16
                                                                                                                      740 AA;
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94DK-0000031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Val, Ala, Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Gln, Ser, Thr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nicolaisen EM,
                                                                      100.0%;
                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        740 AA
                                                                      Score 82;
Pred. No.
                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Persson
                                                                      ; DB 16;
. 8.7e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ala
                                                        o,
                                                                                    Length 740;
                                                        Indels
                                                      0;
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RESULT 12
AAW33227
PROPERTY OF THE PROPERTY OF TH
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Region
                    WPI; 1997-535830/49.
                                                            Amano
                                                                                                                                            15-MAY-1996;
24-APR-1996;
                                                                                                                                                                                                            24-APR-1997;
                                                                                                                                                                                                                                                      30-0CT-1997.
                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recombinant secretion; pro-coagulant activity; resistance; activated protein C cleavage; APC; B domain; A2 domain; A3 domain; on Willebrand factor binding site; binding affinity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW33227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW33227 standard; protein; 1383
                                                                                                                                                                                                                                                                                          WO9740145-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pro-coagulant active factor VIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Procoagulant-active human factor VIII:C (FVIII) mutant protein.
                                                                                                    (IMMI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replacement
                                                                                                    UNIV MICHIGAN
                                                         Kaufman RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                         96US-0017785
96US-0016117
                                                                                                                                                                                                          97WO-US06563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "C1 |
1226..1378
/note= "C2 |
372..373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "A3 (
1073..1221
                                                                                                                                                                                                                                                                                                                                                                                                                       528..554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "/
711..746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153..179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            notes "plastocyanin-like
746..1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380..554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "a spacer of the sequence
SFSQNSRHPSTRQXQFNATTIPENDIEKTDPWF
AHRTPWFKIQNVSSSDLLMLL is inserted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                  note= "wild type Arg replaced with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "plastocyanin-like domain
187..329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "factor VIIIA heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "by thrombin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "Al domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           741..1383
                                                                                                                                                                                                                                                                                                                                                          .abel= R740A
                                                       Pipe SW;
                                                                                                                                                                                                                                                                                                                                                                                                "probable"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "plastocyanin-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "factor VIIIA light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                      "probable"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "plastocyanin-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between domains A2 and A3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FVIII; haemophilia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC VIII (FVIII) mutant protein, comprising a deletion of the B domain and CC von willabrand factor binding site, a mutation at Arg740 and an addition CC of an amino acid sequence spacer between the A2 and A3 domains. Factor CC VIII, along with calcium and phospholipid, acts as a cofactor for factor CC IXA, when it converts factor X to the activated form (factor XA). FVIII CC is the coagultion factor deficient in the X-chromosome-linked bleeding CC disorder haemophilia A. Several other mutant FVIII proteins have also CC been created (see AAW33222-29). The FVIII mutant F309S (AAW33225) is CC capable of recombinant secretion at higher levels than typically obtained CC with wild type FVIII and retains pro-coagulant activity. The FVIII caprotein C (APC) cleavage. The present FVIII mutant can form a more coagulant configuration, and have an approximate 5-fold increase in Specific activity compared to purified wild type FVIII, while increasing their binding affinity to von Willebrand factor improves their coagulactive compared to purified wild type FVIII, replacement therapy, while the nucleic acid molecule can be used for grant therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                              Misc_feature
                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW33228 standard; protein; 1383
                                                                                                                                                          Domain
                                                                                                                                                                                       Region
                                                                                                                                                                                                                                       Κey
                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                   FVIII replacement
                                                                                                                                                                                                                                                                                                                                    von Willebrand
                                                                                                                                                                                                                                                                                                                                               recombinant secretion; pro-coagulant activity; resistance; activated protein C cleavage; APC; B domain; A2 domain; A3
                                                                                                                                                                                                                                                                                                                                                                                                                 Procoagulant-active human factor VIII:C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified human pro-coagulant active administered to haemophiliacs, i.e.
                                                                                                                          Domain
                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                               Pro-coagulant active factor VIII; FVIII; haemophilia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Page -; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence represents a novel pro-coagulant active factor (FVIII) mutant protein, comprising a deletion of the B domain
                                                                                                                                                                                                                                                                     sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    this sequence does not appear in the specification; it was created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRNRGMTALLKVSSCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRNRGMTALLKVSSCD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1383 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                  factor binding site; binding affinity;
                              /note= "/
711..746
                                                                                                                                                          1..329
                                                                                              187..329
                                                                                                                                                                                                                                    Location/Qualifiers
                                                                           note=
                                                                                                                                        /note= "A1 domain"
                                                                                                                                                                       /note= "factor VIIIA light chain"
                                                                                                                                                                                                      /note= "factor VIIIA heavy chain"
                                                                                                                                                                                                                                                                                                                   therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                         "plastocyanin-like
"a spacer of the sequence SFSQNSRHPSTRQKQFNATTIPENDIEKTDPWF
                                               "A2 domain
                                                                                                        "plastocyanin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     given references.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 82; DB 18;
Pred. No. 1.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor VIII - can be factor VIII replacement therapy
                                                                                                                                                                                                                                                                                                                                                                                                            (FVIII) mutant protein
                                                                                                         domain
                                                                           domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                   domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Modified human pro-coagulant active factor VIII - can be administered to haemophiliacs, i.e. factor VIII replacement therapy
                                                                                                                                                                                                             WPI; 1997-535830/49
                                                                                                                                                                                                                                                      15-MAY-1996;
24-APR-1996;
                                                                                                                                                                                                                                                                                       30-OCT-1997.
                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                           Claim 18; Page -; 57pp; English.
                                                                                                                                                                                                                          Amano K,
                                                                                                                                                                                                                                                                         24-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                  Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                         (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                   WO9740145-AJ
                                                                                                                                                                                                                                                                                                                                                                                                               Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                          Kaufman RJ,
                                                                                                                                                                                                                                                      96US-0017785
96US-0016117
                                                                                                                                                                                                                                                                         97WO-US06563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380..554
/note= "
                                                                                                                                                                                                                                                                                                                                                                                    528..554
                                                                                                                                                                                                                                                                                                                                                                                                  153..179
                                                                                                                                                                                                                                                                                                                                                                                                               372..373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     564..711
                                                                                                                                                                                                                                                                                                                                                                                                                            1226..1378
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "C1 domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                'note= "wild type Arg replaced with Ala
                                                                                                                                                                                                                                                                                                                                     'note=
                                                                                                                                                                                                                                                                                                                                                        label= R336I
note= "wild type
                                                                                                                                                                                                                                                                                                                                                                              note=
                                                                                                                                                                                                                                                                                                                                                                                          'note= "probable"
                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "C2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note=
                                                                                                                                                                                                                                                                                                                                            label= R562K
                                                                                                                                                                                                                                                                                                                        label= R740A
                                                                                                                                                                                                                                                                                                                                    "wild type
                                                                                                                                                                                                                                                                                                                                                                                                        "by thrombin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A3 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "plastocyanin-like
                                                                                                                                                                                                                                                                                                                                                                              "probable"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "plastocyanin-like domain 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AHRTPMPKIQNVSSSDLLMLL is inserted between domains A2 and A3"
                                                                                                                                                                                                                          SW
                                                                                                                                                                                                                                                                                                                                                        Arg replaced with Ile"
                                                                                                                                                                                                                                                                                                                                     Arg replaced with Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain
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The present sequence represents a novel pro-coagulant active factor CC VIII (FVIII) mutant probein, comprising a deletion of the B domain and CC von Willebrand factor binding site, mutations R3361, R562K and R740A and CC an addition of an amino acid sequence spacer between the A2 and A3 CC domains. Factor VIII, along with calcium and phospholipid, acts as a CC cofactor for factor IXA, when it converts factor X to the activated form CC (factor XA). FVIII is the coagultion factor deficient in the CC X-chromosome-linked bleeding disorder haemophilia A. Several other CC mutant FVIII proteins have also been created (see AAW33222-29). The FVIII CC mutant F309S (AAW33225) is capable of recombinant secretion at higher CC levels than typically obtained with wild type FVIII and retains CC pro-coagulant activity. The FVIII mutant R3361 (AAW33223) and R562X CC (AAW332223) are resistant to activated protein C (APC) cleavage. The FVIII comparising a deletion of the B domain and von Willebrand factor binding site, a mutation at Arg740 and an addition of an amino acid CC sequence spacer between the A2 and A3 domains can form a more stable CC configuration, and have an approximate 5-fold increase in specific CC binding affinity to von Willebrand factor improves their stability. CC The FVIII proteins can be administered to haemophiliacs, i.e. FVIII CC replacement therapy, while the nucleic acid molecule can be used for cote: this sequence does not appear in the specification; it was created using sequences from the given references.

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Sequence

1383

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RESULT 14
AAW33229
ID AW33229
XX AAW33
AC AAW33
XX DT 30-AP
XX Proc
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                    WO9740145-A1
                                                                                                          Misc-difference
                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                              Disulfide-bond
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                                                                                                                                                                                                                                                                                                      Cleavage-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FVIII replacement therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pro-coagulant active factor VIII; FVIII; haemophilia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRNRGMTALLKVSSCD 712
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                                                                                                                                                                                                                                                                                                                                                                                            /note= "A3 domain"
1073..1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= ", 711..746
                                                                                                                                                                                                                                                                 153..179
                                                                                                                        /label= F309S
/note= "wild type
                                                                                                                                                                                                                                                                                                                                                    1226..1378
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                                                                                                                                                                                              note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "plastocyanin-like domain 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Al domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "factor VIIIA light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  741..1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "factor VIIIA heavy chain"
                                                                                                                                                                                                                                     "probable"
                                                                                                                                                                                                                                                                                                                             "C2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "plastocyanin-like domain 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "plastocyanin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "a spacer of the sequence SFSQNSRHPSTRQKQFNATTIPENDIEKTDPWF AHRTPMPKYQNVSSSDLAWIL is inserted between domains A2 and A3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "plastocyanin-like
                                                         "wild type Arg replaced with Ala"
                                                                                                                                                                                              "probable"
                                                                                                                                                                                                                                                                                 "by thrombin"
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Pred. No. 1.8e-06;
; Mismatches 0;
                                                                                                                             Phe
                                                                                                                          replaced with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and A3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                      CC The present sequence represents a novel pro-coagulant active factor CC VIII (FVIII) mutant protein, comprising a deletion of the B domain and CC von Willebrand factor binding site, mutations F309S, R740A and addition CC of an amino acid sequence spacer between the A2 and A3 domains. Pactor CC VIII, along with calcium and phospholipid, acts as a cofactor for factor CC IXA, when it converts factor X to the activated form (factor XA). FVIII CC is the coagulation factor deficient in the X-chromosome-linked bleeding CC disorder haemophilia A. Several other mutant FVIII proteins have also CC capable of recombinant secretion at higher levels than typically obtained CC with wild type FVIII and retains pro-coagulant activity. The FVIII CC mutant R3361 (AAW33222-29). The FVIII mutant can form a more stable configuration, and have an approximate 5-fold increase in C App) cleavage. The present FVIII mutant can form a more CC stable configuration, and have an approximate 5-fold increase in C specific activity compared to purified wild type FVIII, while increasing CC stability. The FVIII proteins can be administered to haemophiliacs, i.e. CFVIII replacement therapy, while the nucleic acid molecule can be used CC for gene therapy.
                                                                                 Query Match
Best Local (
                                                                   Matches
                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified human pro-coagulant active factor VIII - can be administered to haemophiliacs, i.e. factor VIII replacement therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 19; Page -; 57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAY-1996;
24-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-OCT-1997
                                                                                                                                                                                                          for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UNMI ) UNIV MICHIGAN
                                                                                                                                                                       sequences from
                                                                                                                                                                                        this sequence
                                1
                                                                                   Similarity
                              FRNRGMTALLKVSSCD 16
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                                                                                                                                     1383 AA;
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0017785
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                                                                                                                                                                                      does not appear in the
                                                                                100.0%;
                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pipe
                                                                                                                                                                   given
                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SW.
                                                                              Score 82; DB 18;
Pred. No. 1.8e-06;
                                                                                                                                                                       references.
                                                                 Mismatches
                                                                                                                                                                                      specification;
                                                                                              Length 1383;
                                                                 Indels
                                                                                                                                                                                      it was created
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                                                             Gaps
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697
FRNRGMTALLKVSSCD 712
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AAPROZER
XX
AC AAPR
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AC AAPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
10-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP80268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP80268 standard; protein; 1424 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (updated)
(first entry)
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Modified factor VIII:C; maturation polypeptide; haemophilia; blood coagulation; RD deletion; procoagulant. Modified factor VIII:C sequence with the R740-D1658 deletion.

Homo sapiens

W08800831-A.

11-FEB-1988.

31-JUL-1987; 87WO~US01814.

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Search completed: November 7, 2003, 07:27:05
Job time: 7.89987 secs
                                                                      밁
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                                                                                                                                     Query Match 100.0%; 9 Best Local Similarity 100.0%; F Matches 16; Conservative 0;
                                                                                                                                                                                                                                         The RD deletion removes the DNA from Ser 741 to Ser 1657. A major part of the sequence encoding the maturation polypeptide of factor VIII:C is deleted, i.e. Gln 744 - Asp 1563. The full lenght Factor VIII:C cDNA has two changes with respect to the published sequence (EPO application 160457):

CTG to CTA at Leu 242 and TTC to CTC change at mino acid residue 1880 (Phe to Leu). The product is produced in approx. 20 times higher yields than previous recombinant produced factor VIII:C and are more easily purified. The peptide is used for treating haemophilia A, both acute and prolonged bleeding.

See also AAN80444 and AAN80446. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 60-61-62-63; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New DNA sequences encoding modified factor VIII:C - with deletion of DNA encoding maturation polypeptide, useful for high yield transformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1988-049866/07.
N-PSDB; AAN80447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pasek MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BIOJ ) BIOGEN NV. (PASE/) PASEK M P.
                                                                      697 FRNRGMTALLKVSSCD 712
                                                                                          1 FRNRGMTALLKVSSCD 16
                                                                                                                                                                                                             1424 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86US-0893375.
                                                                                                                                     Score 82; DB 9; Length 1424;
Pred. No. 1.9e-06;
Mismatches 0; Indels (
                                                                                                                                       ?
                                                                                                                                     Gaps
                                                                                                                                     0;
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# OM protein protein search, using sw model November GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. 7, 2003, 07:21:18; Search time 1.29506 Seconds (without alignments) 742.581 Million cell updates/sec

Perfect score: US-09-661-992B-5 58 1 YGNSPKGFAY 10

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB Maximum DB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database PIR\_76:\* pir1:\*
pir2:\*
pir3:\*
pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

#### SUMMARIES

29	28	27	26	25	24	23	22	22	20	19	18	17	16	15	14	13	12	11	10	φ	80	7	φ,	ហ	44	ω	N	Ļ	NO.	Result
36	ω	36	36	36	36	37	37	37	37	37	37	37	37	37	37	37	38	38	38	38	38	38	39	39	41	41	41	42	score	
62.1	62.1	62.1	62.1		62.1	63.8	٠		63.8	63.8		63.8	63.8	63.8	63.8	63.8	65.5	65.5	65.5	65.5	65.5	65.5	67.2	67.2	70.7	70.7	70.7	72.4	Macch	
381	199	196	181	117	17	712	422	394	394	390	390	346	331	306	223	205	588	583	488	488	488	402	568	401	2515	453	389	626	Length	
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C90395	\$38867	A95890	A96762	C83576	I67526	F97012	A98172	WHPSBA	WHPSBF	AD3115	G96028	C86413	D86413	S59863	B70372	T19356	JC7206	B87204	B96521	AG0621	AD0735	D90034	A55377	H82175	A41519	875579	H90083	B70749	[ ] [ ]	}
DNA repair protein	т.		probable RNA-bindi	erved by	CD33 antigen homol	hypothetical prote	4-hydroxybenzoate	4-hydroxybenzoate	4-hydroxybenzoate	•			cysteine proteinas	polyA binding prot	řein ,	hypothetical prote		നം	protein F21D18.20	probable bacterion		prot	3		o	hypothetical prote		probable Acyl-CoA	ption	

i	4.	44	3	42	41	40	39	38	37	36	35	34	33	32	31	30
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;	, O	60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3	62.1	62.1	62.1	62.1	62.1	62.1
ļ	285	270	258	217	204	166	157	113	112	109	1928	1414	910	670	611	452
2	v	N	N	Ŋ	Ŋ	N	N	N	N	N	N	Н	N	N	N	Ŋ
	R82450	AE1497	\$25624	T50004	T29489	T39586	876232	F84671	JUOISI	F30607	JS0610	S23809	S38167	T02019	S60914	864211
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### ALIGNMENTS

# RESULT 1 B70749

probable Acyl-CoA Synthetase - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000
C;Accession: B70749
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; G
R;Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hol
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70749

A;Residues: 1-626 <COL> A;Cross-references: GB:Z74697; GB:AL123456; NID:g3261602; PIDN:CAA98985.1; PID:g A;Experimental source: strain H37Rv A; Molecule type: A; Status: preliminary; nucleic acid sequence not shown; translation not shown DNA

C; Genetics:

A;Gene: fadD26 C;Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology F;103-610/Domain: acetate-CoA ligase homology <ACL>

Matches Query Match y Match 72.4%; Score 42; DB 2; Length 626; Local Similarity 77.8%; Pred. No. 8.5; hes 7; Conservative 1; Mismatches 1; Indels 0

Gaps

0

밁 S 73 YGSDPKGFA 81 1 YGNSPKGFA 9

#### RESULT 2 H90083

polyadenylate-binding protein [imported] - Guillardia theta nucleomorph (Species: nucleomorph Guillardia theta A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24-May-2001 C;Accession: H90083
R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, Nature 410, 1091-1096, 2001
R;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
A;Accession: H90083

A; Status: preliminary

A; Molecule type: DNA A; Residues: 1-389 < DOU>

A; Cross-references: GB: AF165818; NID: g13794428; PIDN: AAK39803.1; GSPDB: GN00150

A; Map position: 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Drosophila melanogaster)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1999
C;Accession: A41519; S19019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:D90911; GB:AB001339; NID:g1653083; PIDN:BAA18140.1; PID:g165322 A;NOTE: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 C;Superfamily: hypothetical protein s110804; translation elongation factor Tu homology C;Keywords: GTP binding; nucleotide binding; P-loop F;62-176/Domain: translation elongation factor Tu homology <FTU>F:68-75/Region: nucleotide-binding motif A (P-loop) F;173-176/Region: GTP-binding NKXD motif F;367-369/Region: GTP-binding SAK/L motif
                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-2515 <GCL>
A;Cross-references: GB:X62420; NID:g8753; PIDN:CAA44286.1; PID:g8754
                                                                                                                                                                                                                                                                                                                                                                         A;Title: tudor, a posterior-group gene of Drosophila melanogaster, encodes a novel prote
A;Reference number: A41519; MUID:92038995; PMID:1936993
A;Accession: A41519
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(;Species: Symechocystis sp.
A;Variety; PCC 6803
(;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 02-Feb-2001
(;Accession: $75579
                                                                                                                                                                                                    C; Superfamily: posterior-group
                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Golumbeski, G.S.; Bardsley, A.; Tax, Genes Dev. 5, 2060-2070, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 posterior-group protein tudor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasudd DNA Res. 3, 109-136, 1996
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-453 < KAN>
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C;Keywords: nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: $74322; MUID: 97061201; PMID: 8905231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: A41519; S19019
                                                                                                                                                                                                                                Cross-references: FlyBase:FBgn0003891
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Best Local :
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               YGNSPKSF 2178
                                                             YGNSPKGF 8
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                                                                                                             Conservative
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Conservative 0;
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87.5%;
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70.0%;
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0; Mismatches
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Pred. No. 58;
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Pred. No. 7
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7.9;
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                    C;Accession: D90034
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekim C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
                                                                                                                                 hypothetical protein SA2135 [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001-
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A; Title: Whole genome sequencing
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A;Residues: 1-568 <HAK>
A;Residues: 1-568 <HAK>
A;Cxoss-references: GB:U14169; NID:g987224; PIDN:AAA80483.1; PID:g624634
C;Superfamily: African clawed frog CPE-binding protein; ribonucleoprotein
F;314-388/Domain: ribonucleoprotein repeat homology <RRM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Alternate names: cytoplasmic polyadenylation element-binding protein C;Species: Xenopus laevis (African clawed frog) (C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000 C;Accession: A55377
                                                                                                                                                                                                                                                                                                                                                             R;Hake, L.B.; Richter, J.D.

Cell 79, 617-627, 1994

A;Title: CPBB is a specificity factor that mediates cytoplasmic

A;Reference number: A55377; MUID:95042759; PMID:7954828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 1
C;Superfamily: bicyclomycin resistance protein
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Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholera A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
H82175
                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                             A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                         A; Accession: A55377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CPE-binding protein - African clawed frog
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A;Experimental source: serogroup
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A; Residues: 1-401 <HEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    multidrug resistance protein VC1634 [imported] - Vibrio cholerae (strain N16961
C;Species: Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
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                                                                                                                                             Query Match
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                                                2 GNSPKGFAY 10
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                                                                                                                    67.2%;
Similarity 66.7%;
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GNMPKGYVY 365
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                                                                                             1; Mismatches
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                                                                                                                    Score 39; DB
Pred. No. 28;
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Pred. No. 19;
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of meticillin-resistant Stapylococcus aureus

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, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AG0621
                                  A;Cross-references: GB:AL513382; PIDN:CAD05441.1; PID:g16502202; C;Genetics:
                                                                          A; Molecule type: DNA
A; Residues: 1-488 < PAR>
                                                                                                                                                                                                                                                     C;Accession: AG0621
C;Accession: AG0621
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, S.; Moule, S.; O'Gaora, P.
                                                                                                                                                                                                                                                                                                                                  probable bacteriophage protein STY1048 [imported] - Salmonella enterica subsp. C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein STY2039 [imported] - Salmonella enterica subsp. (;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AD0735
                                                                                                                    A;Status: preliminary
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C;Superfamily: Haemophilus influenzae hypothetical protein HI1409
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A;Accession: AD0735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Nolecule type: DNA
A; Molecule type: DNA
A; Residues: 1-402 < KUR>
A; Cross-references: GB:BA000018; PID:g13702296;
A; Cross-references: strain N315
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C;Superfamily: sodium-glutamate
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A; Accession: D90034
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Best Local
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6; Conservat
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75.0%;
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Pred. No.
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Pred. No. 36;
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Salmonella enterica
                                                GSPDB:GN00176
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, L.; White,
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RESULT 11
B87204
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O., Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; De ansen, N.F.; Hughes, B., Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Maiti, R.; M.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; M.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: B96521
A;Accession: B96521
                                                                                                                                                                                                                                                                  eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.;
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: B87204
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A;Map po
                                                                                                    A;Gene: fadD26
C;Superfamily:
                                                                                                                                                   A;Cross-references: GB:AL450380; NID:g13093967; PIDN:CAC31874.1; GSPDB:GN00147
C;Genetics:
                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-583 <STO>
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R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 24-Aug-2001
                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable acyl-CoA synthase [imported] - Mycobacterium leprae C;Species; Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-488 <S'
A; Cross-references: (
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Best Local :
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6; Conserv
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                                                                                               Synechocystis long-chain-fatty-acid-CoA ligase;
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75.0%;
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  Score 38; DB
Pred. No. 44;
1; Mismatches
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Pred. No.
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Pred. No. 36;
2; Mismatches
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    Indels
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A.; Hamlin, N.;
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YGNSPKGF

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RESULT 14
B70372
B70372
C;Species: Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: B70372
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus A;Reference number: A70300; MUID:98196666; PMID:9537320
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A;Map position: 1
A;Introns: 22/3; 120/2
                                                                           R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:Z81037; PIDN:CAB02750.1; GSPDB:GN00019; CESP:C17E4.5
A;Experimental source: clone C17E4
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, A;Reference number: Z19113
A;Accession: T19356
                                             Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-205 <WIL>
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C;Superfamily: phosphoprotein phosphatase 65K regulatory
C;Keywords: phosphoric monoester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Ishizaki, T.; Yokoyama, H.; Kajiwara, S.; Shishido, K. Biosci. Biotechnol. Biochem. 64. 438-442, 2000 A;Title: Basidiomycete fungal gene encoding a regulatory A;Reference number: JC7206; MUID:20199469; PMID:10737208 A;Accession: JC7206
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JC7206
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A; Residues: 1-588 <ISH>
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60.0%;
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Pred. No.
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Pred. No. 44;
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Search completed: November Job time: 3.39506 secs

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S59863
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                                                                                                                                                     A;Cross-references: EMBL:X89969; NID:g1065677; PIDN:CAA62006.1; PID:g1051125
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1995
C;Superfamily: bovine polyA binding protein II; ribonucleoprotein repeat homology
F;173-239/Domain: ribonucleoprotein repeat homology <RRM2>
                                                                                                                                                                                                                                        A;Accession: 859863
A;Status: preliminary; nucleic acid sequence not shown, translation not shown A;Molecule type: mNNA
A;Residues: 1-306 <NEM>
                                                                                                                                                                                                                                                                                                                   R;Nemeth, A.; Krause, S.; Blank, D.; Jenny, A.; Jenoe, P.; Lustig, A.; Wahle, Nucleic Acids Res. 23, 4034-4041, 1995
A;Title: Isolation of genomic and cDNA clones encoding bovine poly(A) binding A;Reference number: 859863; MUID:96071160; PMID:7479061
                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Nov-1999 C;Accession: S59863
                                                                                                                                                                                                                                                                                                                                                                                                                                             polyA binding protein II - bovine
C;Species: Bos primigenius taurus (cattle)
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-223 <AQF>
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18; Search time 0.720961 Seconds (without alignments) 652.278 Million cell updates/sec

Title: Perfect score: US-09-661-992B-5 58

Sequence: 1 YGNSPKGFAY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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# ALIGNMENTS

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between the Swiss Institute of Bioinformatics and the EMBL outeration the Buropean Bioinformatics Institute. There are no restrictions on i use by non-profit institutions as long as its content is in no w modified and this statement is not removed. Usage by and for commerci entities requires a license agreement (See http://www.isb-sib.ch/announc or send an email to license@isb-sib.ch).  EMBL; Z74697; CAA98985.1; ALT_INIT. EMBL; Z74697; CAA98985.1; ALT_INIT. EMBL; R2007122; AAK47327.1; Tigr; MT2999; Tuberculist; Rv2930; InterPro; IPR000873; AMP-bind.	INCE FROM N.A.  (IM=CDC 1551 / Oshkosh;  (IM=CDC 1551 / Oshkosh;  Schmann R.D., Alland D., Eisen J.A., Carpenter L., White schmann R.D., Alland D., Eisen J.A., Carpenter L., Hickey as Chann J. DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey lay J.P., Welson W.C., Umayam L.A., Ermolaeva M.D., Salzi per A., Utterback T., Weidman J., Khouri H., Gill J., Mil per A., Utterback T., Weidman J., Khouri H., Gill J., Mil w., (1998)  18 W., (1998)	SEQUENCE FROM N.A.  STRAINHAISTRY, MEDLINE=98295987; PubMed=9634230; MEDLINE=98295987; PubMed=9634230; MEDLINE=98295987; PubMed=9634230; MEDLINE=98295987; PubMed=9634230; MEDLINE=98295987; PubMed=9634230; MEDLINE=98295987; PubMed=1 J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Comnor R., Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S., Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S., Davies R., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Diver S., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Butter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).	1 6

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P25823;
01-MAY-1992
                                                                                                                                                                                                                                                                                     entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92038995; PubMed=1936993; Golumbeski G.S., Baxdeley A., Tax F., Boswell R.E.; "Tudor, a posterior-group gene of Drosophila melanogaster, encodes novel protein and an mRNA localized during mid-oogenesis."; Genes Dev. 5:2060-2070(1991).
         DOMAIN
                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; pr00501; AMP-binding; 1.

PROSITE; PS00455; AMP_BINDING; FALSE_NEG.

Hypothetical protein; Ligase; Fatty acid metabolism;

Complete proteome.
                                                               DOMAIN
                                                                                                                                                                                                                                 EMBL; X62420; CAA44286.1; -. 
FIR; A41519, A41519, HSSP; Q1637; 1G5V. 
FlyBase; FBgn0003891; tud.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                        GO; GO:0019090; P:mitochondrial rRNA, mitochondrial export; IMP. GO; GO:0007315; P:pole plasm assembly; IMP. InterPro; IPR001097; Maternal_tudor. InterPro; IPR002999; Tudor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
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                                                                                           DOMAIN
                                                                                                         DOMAIN
                                                                                                                                                 SMART:
                                                                                                                                                             Pfam; PF00567; TUDOR; 10
                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SIMILARITY: Contains 9 Tudor domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                     DOMAIN
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wes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           es Dev. 5:2060-2070(1991).

FUNCTION: REQUIRED DURING COGENESIS FOR THE FORMATION OF FUNCTION: REQUIRED DURING COGENESIS FOR THE FORMATION OF PRIMORDIAL GERM CELLS AND FOR NORMAL ABDOMINAL SEGMENTATION.

DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT THE LIFE CYCLE.

MISCELLANEOUS: THE TUD MRNA ACCUMULATES WITHIN THE POSTERIOR REGION OF THE DEVELOPING COCYTE DURING THE EARLY TO MIDDLE STAGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 YGSDPKGFA 38
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TUDÓR; ...
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_PSEAE
PHHY, PSEAE STANDARD; PRT; 394 AA
P20586;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 392:353-358 (1998).

-! FUNCTION: INVOLVED IN THE ASSEMBLY PROCESS OF THE P-RING PORMATION. IT MAY ASSOCIATE WITH FLGF ON THE ROD CONSTITUTING A STRUCTURE ESSENTIAL FOR THE P-RING ASSEMBLY OR MAY ACT AS A MODULATOR PROTEIN FOR THE P-RING ASSEMBLY (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Periplasmic (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Eyer M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V., "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Flagella basal body P-ring formation protein flgA precursor.
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067005;
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PF03240; FlgA; 1.
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                                                                                                                                                                                 Score 37; DB 1; Length 223; Pred. No. 13; 2; Mismatches 2; Indels
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Pred. No. 26;
                                                                                                                                                                                                                                                            PROTEIN FLGA
                                                                                                                                                                                                                                                                         FLAGELLA BASAL BODY P-RING FORMATION
                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                              98C0A5189D8254CD CRC64;
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                                                394 AA
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STRAIN=ATCC 15692 / PAO1;

MEDLIND=20437337; PubMed=10984043;

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"Crystal structures of mutant Besudomonas aeruginosa
p-hydroxybenzoate hydroxylases: the Tyr201Phe, Tyr385Phe, and
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                                                      EMBL; M23173; AAA88455.1; -.
EMBL; AE004463; AAG03636.1; -
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P-hydroxybenzoate bydroxylase (EC 1.14.13.2) (4-hydroxybenzoate 3-
                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MUTANTS.
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Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                              CATALYTIC ACTIVITY: 4-hydroxybenzoate + NADPH + O(2) = protocatechuate + NADP(+) + H(2)O.

COFACTOR: FAD:
COFACTOR: FAD:
PATHWAY: DEGRADATION OF BENZOATE TO SUCCINATE AND ACETYL-COA.
SUBUNIT: Homodimer.

SIMILARITY: TO P. PUTIDA SALICYLATE HYDROXYLASE.
    1DOB; 30-NOV-94.
1DOC; 30-NOV-94.
1DOD; 30-NOV-94.
                                         JT0384; WHPSBA
                                                                                                                                                          a collaboration
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PDB; 1IUS; 03-APR-96.

PDB; 1IUF; 03-APR-96.

PDB; 1IUF; 03-APR-96.

PDB; 1IUW; 20-UN-96.

PDB; 1IUW; 11-JUL-96.

PDB; 1PXA; 27-FEB-95.

PDB; 1PXA; 27-FEB-95.

PDB; 1ROI; 27-FEB-02.

PDB; 1ROI; 27-FEB-02.

R PDB; 1KOI; 27-FEB-02.

R PDB; 1KOI; 27-FEB-02.

R PDB; 1KOI; 27-FEB-02.

R PDB; 1KOI; 27-FEB-03.

R InterPro; IPR002938; MONY_FAD_binding.

PR InterPro; IPR002942; Rng_moxygenase.

PS InterPro; IPR003042; Rng_moxygenase.

PS Fam; PF01364; FAD binding 3; 1.

DR PFAm; PF01369; MONOXYGENASE.

R PFANTS; PR00420; RNGMNOXGNASE.

KW Aromatic hydrocarbons catabolism; Oxidoreductase; Monooxygenase; KW Plavoprotein; FAD; NADF; 3D-structure; Complete proteome.

MN BIND 4 32

FAD (POTENTIAL).
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21-JUL-1986
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SEQUENCE
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Wierenga R.K., Drenth J.;
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                                                                                                                            Hofsteenge J., Weijer W.J., Jekel P.A., Beintema J.J., "p-hydroxybenzoate hydroxylase from Pseudomonas fluorescens. Completion of the elucidation of the primary structure.";
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01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last amotation updat
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SEQUENCE OF CNBR PEPTIDES AND STRUCTURE OF MEDLINE=83209623; PubMed=6406227; Weijer W.J., Hofsteenge J., Beintema J.J.,
                                                                                                                                                                                                                SEQUENCE OF CNBR PEPTIDES AND TERTIARY STRUCTURE MEDLINE=83209654; PubMed=6406229;
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-52; 53-65 AND 66-110. MEDLINE=81114232; PubMed=6780353;
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"Primary structure of p-hydroxybenzoate hydroxylase from Pseudomonas
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15-APR-92. 30-SEP-94. 30-SEP-94. 30-SEP-94. 30-SEP-94. 30-SEP-94. 31-MAR-95. 112-AUG-98.

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use by non-profit institutions as long as its content
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"Structure and function of mutant Arg44Dys of 4-hydroxybenzoate
hydroxylase implications for NADPH binding.";
Eur. J. Biochem. 231:157-165(1995).
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Hol W.G.J., Drenth J.;
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MEDLINE=99148809; PubMed=10025942;
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Proteins 14:178-190(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS)
MEDLINE=88172509; PubMed=3351945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pinding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98237589; PubMed=9578477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT LYS-42 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95354684; PubMed=7628466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Crystal structure of the reduced form of p-hydroxybenzoate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF REDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Crystal structure of p-hydroxybenzoate hydroxylase complexed with its reaction product 3,4-dihydroxybenzoate.";
                                                                                                                                                                                                                                                                                                              PATHWAY: DEGRADATION OF BENZOATE TO SUCCINATE AND ACETYL-COA. SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                  SIMILARITY: TO E.COLI UBIH/VISB AND VISC.
                                                                                             1РНН;
2РНН;
1РВВ;
                                                                                                                                       ; X68438; CAA48
A90643; WHPSBF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biochem. 253:194-201(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. 199:637-648(1988)
                                                                                                                          15-JAN-93.
                                                                                                                                                     CAA48483.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=1409567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hol W.G.J., Drenth J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Swarte M.B.A.,
                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF MUTANT LYS-44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hol W.G.J.,
hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kalk K.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drenth .";
                                                                                                                                                                                                                             restrictions on
tent is in no
                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                        EMBL
                                                                                                                                                                                                                                                       a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SER-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NADPH
                                                                                                                                                                                                               tot
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DR PDB. 1863; 12-AUG-98.
DR PDB. 1863; 12-AUG-98.
DR PDB. 1863; 12-AUG-99.
DR PDB. 1864; 22-UUL-98.
DR PDB. 1865; 13-AUR-99.
DR PDB. 1863; 13-AUR-99.
DR PDB. 1864; 13-AUR-
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RESULT 6
RNT1_DROME
                                                                                                                                                RX MEDLINE-2019606; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Schever S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Schever S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Schever S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Bordon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Boyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bessley E.M.,
RA Ballew R.M., Basu A., Buller H., Cadleu E., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Burbin K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.C.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Woshrefi A.,
RA Mount S.M., Welson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Lasko P., Lei Y., Levitcky A.A., Li J., Li Jang Y., Lin X.,
RA Kalmel B.E., Sylar-Kiamos I., Singson M., Stupski M.P., Smith T.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Sider-Kiamos I., Singson M., Stupski M.P., Smith T.,
RA Sher B.C., Yang S., Nollong R., Zhou X., Zhou S., Zhou X., Zhou S., Zhou X., Zhou S., Zhou X., Zhou S., Zho
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Best Local S
Matches 6
STRAIN=Berkeley;
MEDLINE=22456069; PubMed=12537572;
Mills=22456069; PubMed=12537572;
Millburn S. Campbell K.S.,
Millburn G.H., Prochnik S.E.
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu J., Berman B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNT1_DROME STANDARD; PRT; 1180 AA.

GOVYS3; Q95RG9;
16-OCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Regulator of nonsense transcripts 1 homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. NCBI TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UPF1 OR CG1559.
                                                                                                                       REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 YANHPRGFA 209
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Similarity 66.7%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB : Pred. No. 22; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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             B.P.,
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HOS2/FAR
HOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEAST STANDARD; PRT; 452 AA. P53096; O1-OCT-1996 (Rel. 34, Created) O1-OCT-1996 (Rel. 34, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Probable histone deacetylase HOS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.A.,
Gonzalez M., Guarin H., Li P.W., Liao G., Miranda A., Mungall C.J.,
Munco J., Pacleb J.M., Paragas V., Park S., Phouanenavong S.,
Wann K.H., Yu C., Lewis S.E., Rubin G.M., Celniker S.E.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                     "Sequencing of a 40.5 kb fragment located on the left arm of chromosome VII from Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97197971; PubMed=9046087;
Coglievina M., Klima R., Bertani I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=S288c / FY1679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOS2 OR YGL194C OR G1330.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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EMBL; AY061379; AAL28927.1; -.
      MEDLINE=97121415; PubMed=8962081;
                                                                                                                                                                                                                                                                                                                                               Bruschi C.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
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                                                                   GENE NAME
                                                                                                                                                              Yeast 13:55-64(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ewis S.
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SUBCELLULAR LOCATION: Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE DNA2/NAM7 HELICASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      957 YGNSPLGY 964
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FBgn0630354; Upf1.

FBgn0630354; Upf1.

FBgn0630354; Upf1.

FBgn0630354; Upf1.

FBgn0630354; Upf1.

FBgn0630354; Upf1.

FBgn0630354; Upf1.

FBgn0630354; Upf1.

FBGN630354; ATP-binding; Zing-finger.

FCH2-TYPE (ATYPICAL) (POTENTIAL).

FBGN630354; Upf1.

FFGN630354; Upf1.

FFGN63030354; Upf1.

FFGN6303035
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75.0%;
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Pred. No. 66;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          Delneri D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1180;
                                                                                                                                                                                                                                                                                                                                                                                                Zaccaria P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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RESULT 8
LYP1_YEAST
ID LYP1_YEAST
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                                                                                                                                                                   片
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Requirement of Hos2 histone deacetylase for gene activity in yeast."; Science 298:1412-1414(2002).
-I- FUNCTION: Responsible for the deacetylation of lysine residues on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "HDA1 and RPD3 are members of distinct yeast histone deacetylase complexes that regulate silencing and transcription."; Proc. Natl. Acad. Sci. U.S.A. 93:14503-14508(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0000118; C:histone deacetylase complex; IPI.
GO; GO:0017136; F:NAD-dependent histone deacetylase activity; IDA.
GO; GO:0045129; F:NAD-independent histone deacetylase activity; IDA.
GO; GO:0015575; P:histone deacetylation; IDA.
GO; GO:0016575; P:negative regulation of meiosis; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 272716; CAA96906.1; -. EMBL; X91837; CAA62950.1; -. PIR; S64211; S64211. SGD; S0003162; HOS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :
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                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Nuclear protein; Chromatin regulator; Transcription regulation; Activator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000286; His deacetylse. Pfam; P900850; Hist deacetyl; 1. PRINTS; PR01270; HDASUPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION, AND MUTAGENESIS OF 195-HIS-HIS-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jenes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Responsible for the deacetylation of lysine residues on the N-terminal part of the core histones (H2A, H2B, H3 and H4). In contrast to other histone deacetylase proteins, which give a tag for epigenetic repression, it is apparently involved in transcriptional activation.

SUBUNIT: Identified in a Set3C complex with SET3, HST1, SNT1, SUBCELULAR LOCATION: NUClear.

SUBCELULAR LOCATION: NUClear.

SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA FAMILY. HD SUBFAMILY 1.
                                                                                                                                                                   163 NSPSGFCY 170
                                                                                                                                                                                                                             3 NSPKGFAY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                           452 AA;
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197
196
352
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197
                                                                                                                                                                                                                                                                                                                                                                                                                           51455 MW;
                                                                                                                                                                                                                                                                                                                     62.1%;
75.0%;
                                                                                                                                                                                                                                                                                          Score 36; DB
Pred, No. 39;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; CAA62950)
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HH->AA: LEADS TO HYPERACETYLATION
PERDSEGEDYSLY -> HSGTHSGRITHFI (I)
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                                                                                                                                                                                                                                                                                                                                                                                                                    024E8AEA0A445A08 CRC64;
                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 452;
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STANDARD;

611 AA

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TRANSMEM
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                                                                                                                                                    Transport;
TRANSMEM
TRANSMEM
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GO; GO:0015274; F:basic amino acid transporter activity; IDA.

GO; GO:0015802; P:basic amino acid transport; IDA.

INTERPRO; IPR002293; AA/rel_permease1.

InterPro; IPR004840; AAc_permease.

InterPro; IPR004841; Permease.

InterPro; IPR004782; Yeast_AA_perm.
                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Suropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                 InterPro, IPR004762; Yeast_AA_perm.
Pfam; PP00324; aa_permeases; 1.
TIGREAMS; TIGR00913; 2A0310; 1.
PROSITE; P800218; AMINO_ACID_PERMEASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                         EMBL; X67315; CAA47729.1; -.
EMBL; X94494; CAA63230.1; -.
EMBL; Z71544; CAA96175.1; -.
PIR; S60914; S60914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Regenberg 8., During-Olsen L., Kielland-Brandt M.C., Holmberg S.; "Substrate specificity and gene expression of the amino-acid permeases in Saccharomyces cerevisiae"; Curr Genet 36:317-328(1999).
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STRAIN-ATCC 28583 / FL100;
MEDLINE-93377414; PubMed=8368011;
Sychrova H., Chevallier M.R.;
"Cloning and sequencing of the Saccharomyces cerevisiae gene LYP1 coding for a lysine-specific permease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- FUNCTION: High-affinity permease for lysine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=10654085;
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LYP1 OR YNL268W OR N0790.
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15-SEP-2003
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             TRANSMEM
                              TRANSMEN

    -!- SIMILARITY: Belongs to the amino acid permease family.

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(Rel. 34, Last sequence update)
(Rel. 42, Last annotation update)
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RESULT 10
LPH_RAT
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AC Q0240
DT 01-JU
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CONFLICT
LPH_RAT STANDARD;
Q02401; Q63712; Q63719;
01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=94262327; PubMed=8203164;

Garcia-Cantalejo J., Baladron V., Esteban P.F., Santos M.A., Bou G.,

Garcia-Cantalejo J., Baladron V., Esteban P.F., Santos M.A., del Rey F.;

"The complete sequence of an 18,002 bp segment of Saccharomyces
cerevisiae chromosome XI contains the HBS1, MRP-L20 and PRP16 genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-JUN-1994 (Rel. 29, Last sequence update)
16-JCT-2001 (Rel. 40, Last annotation update)
Hypothetical 102.7 kDa protein in PRP16-SRP40 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; 227116; CAA81640.1; -.
EMBL; 228314; CAA82168.1; -.
EMBL; 38167; S38167; S38167; SGD; S0001797; YKRD89C.
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                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: TO YEAST YMR313C AND S.POMBE SPCC1450.16C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and six new open reading frames."; Yeast 10:231-245(1994).
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P36165;
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                                                                                                                                                                                                                                                                                                                                                                                                                    910 AA;
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310
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93
561
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                                                                                                                                                                                                                                                                                                    62.1%; Score 36; DB 75.0%; Pred. No. 77; cive 0; Mismatches
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> D (IN REF. 1).
> M (IN REF. 1).
                                                        1928 AA
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DOMAIN
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REPEAT
REPEAT
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TRANSMEM
                                                                                                                                                                                                                                  Hydrolase;
SIGNAL
PROPEP
                                                                                                                                                                                                                                        InterPro; IPR001360; Glyco_hydro_1.

Pfam; pF00222; Glyco_hydro_1; 5.

PRINTS; PR00131; GLHYDRIASE1.

PRODOm; PD000650; Glyco_hydro_1; 4.

PROSITE; PS00572; GLYCOSYL_HYDROL_F1_2; 2.

PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 2.

Hydrolase; Glycosidase; Zymogen; Signal; Transmembrane; Repeat.

SIGNAL 1 19

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                  EMBL; X56748; CAA40070.1; -.
EMBL; X56747; CAA40069.1; -.
EMBL; L04635; AAA41539.1; -.
EMBL; L04610; JS0610.
HSSP; P26205; 1CBG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-acylsphingosine. Glycosyl-N-acylsphingosine + H(2)O = a :
SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN. BRUSH BORDER.
-!- TISSUS SPECIFICITY: INTESTINE.
-!- DOMAIN: THE SECUENCY COMMISSIONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene.";
DNA Seq. 3:119-121(1992).
-!- EUNCTION: LPH SPLITS LACTOSE IN THE SMALL INTESTINE.
-!- CATALYTIC ACTIVITY: Lactose + H(2)O = D-glucose + D-galactose.
-!- CATALYTIC ACTIVITY: Glycosyl-N-acylsphingosine + H(2)O = a sug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Sprague-Dawley;
MEDLINE=93091244; PubMed=1339333;
Boukamel R., Freund J.-N.;
                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 103:275-276(1991).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The rat LPH gene 5' region: comparative structure with the gene.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Wistar; TI
MEDLINE=91365258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO FAMILY 1 OF GLYCOSYL HYDROLASES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duluc I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Lactase-phlorizin hydrolase precursor (Lactase-glycosylceramidase)
[Includes: Lactase (EC 3.2.1.108); Phlorizin hydrolase (EC 3.2.1.62)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: INTESTINE.

DOMAIN: THE SEQUENCE EXHIBITS 4 REGIONS (I-IV) OF
HOMOLOGY; THEREFORE LPH MIGHT HAVE EVOLVED BY TWO
PARTIAL GENE DUPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OR LPH
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58; PubMed=1909681;
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175
849
1366
1842
11842
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Rodentia; Sciurognathi; Muridae; Murinae; Rattus
PROTON DONOR (POTENTIAL).

NUCLEOPHILE (BY SIMILARITY).

PROTON DONOR (POTENTIAL).

NUCLEOPHILE (BY SIMILARITY).

A -> R (IN REF. 1; AAA41539).

Q -> E (IN REF. 1; AAA41539).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cei N., Semenza G., Raul F., Freund J.-N., of intestinal lactase-phlorizin hydrolase
                                                                                                                                                                     POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL);
                                                                                                                                                                                                                               BETA-GLUCOSIDASE.
                                                                                                                                                                                                                LACTASE-PHLORIZIN HYDROLASE
                                                                                                                                                       APPROXIMATE REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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Best Local &
Matches
                                                                                                                                                                                                                          EMBL; J04996; AAA26010.1; -.

PIR; F36516; F36516.
HSSP; H7297; IDHY.
InterPro; IPR004360; Gly_bleo_diox.
InterPro; IPR004366; Xdiol_dioxygnse.
Pfam; F760903; Glyoxalase; 1.
ProDom; PD000977; Xdiol_dioxygnse; 1.
PROSITE; PS00082; EXTRADIOL_DIOXYGENAS; 1.
Oxidoreductase; Dioxygenase; Aromatic hydr
INIT_MET
                                                                                                                                                                                                            INIT MET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                 METAL
                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zyletra G.J., Gibson D.T.;
"Toluene degradation by Pseudomonas putida Fl. Nucleotide sequence the todClC2BADE genes and their expression in Escherichia coli.";
J. Biol. Chem. 264:14940-14946(1989).
-i- CATALYTIC ACTIVITY: 3-methylcatechol + O(2) = 2-hydroxy-6-oxo-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sec
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                         ETAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas putida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3-methylcatechol 2,3-dioxygenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATHWAY: Toluene degradation; third step.
SUBUNIT: Homooctamer.
SUBUNIT: Homooctamer.
SUBUNIT: HOMOOCTAMER.
SUBUNIT: HOMOOCTAMER.
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COFACTOR: FERROUS ION.
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  YGNSPKGFA
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Last annotation updat
                                                                                                                                      MW;
                                           Score 35; DB
Pred. No. 38;
l; Mismatches
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1; Mismatches
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hydrocarbons
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                                                                                      Length 290
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185 CRC64;
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RESULT 12
BHC1_RHOCO
RESULT 13
CLC3
CLC3
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ID CLC9
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DT 16-OC
DT 15-SE
DE T-Cell
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Matches 6
                                                             C1C3_CAVPO STANDARD; PRT; 332 AA.

Q9QZY6;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                              CAVPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IFR004360; Gly_bleo_diox.
InterPro; IFR000486; Xdiol_dioxygnse.
Pfam; PF09903; Glyoxvalase; 1.
ProDom; PD000977; Xdiol_dioxygnse; 1.
PROSITE; PS00082; EXTRADIOL_DIOXYMERNAS; 1.
Oxidoreductase; Dioxygenase; Aromatic hydro
METAL 146 146 IRON (BY SIMI)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asturias J.A., Eltis L.D., Prucha M., Timmis K.N.; "Analysis of three 2,3-dihydroxybiphenyl 1,2-dioxygenases Rhodococcus globerulus P6. Identification of a new family
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X75633; CAA53297.1; -. PIR; B53419; B53419.
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                                    CD1C3
                                                    T-cell surface glycoprotein CD1c3 precursor (CD1-c3 antigen).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhodococcus globerulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             radiol dioxygenases.";
Biol. Chem. 269:7807-7815(1994).

Eiol. Chem. 269:7807-7815(1994).

CATALYTIC ACTIVITY: Biphenyl-2,3-diol + O(2) = 2-hydroxy-6-oxo-6-
CATALYTIC ACTIVITY: Biphenyl-2,3-diol + O(2) = 2-hydroxy-6-oxo-6-
phenylhexa-2,4-dienoate + H(2)O.

COPACTOR: FERROUS ION.

PATHMAY: DEGRADATION OF BIPHENYLS AND POLYCHLOROBIPHENYLS (PCB) TO
BENZOIC ACID AND CHLOROBENZOIC ACIDS.

SIMILARITY: BELONGS TO THE EXTRADIOL RING-CLEAVAGE DIOXYGENASE

SIMILARITY: BELONGS TO THE EXTRADIOL RING-CLEAVAGE DIOXYGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAMILY.
                                                                                                                                                                                                                                       250 YGATPSGFA 258
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                                                                                                                                                                                                                                                                                                        l Similarity
6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                291 AA;
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260
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                                                                                                                                                                                                                                                                                                                          60.3%;
                                                                                                                                                                                                                                                                                                        Score 35; DB
Pred. No. 38;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 Aromatic hydrocarbons catabolism; Iron. IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                             DS 1; Length 291;
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DT 28 PE
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Best Local Similarity
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                                                                                                                                                                                                                                          RNFD PASMU
Q9CNF3;
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                             Q9CN03;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
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MEDLINE=20021845; PubMed=10553074;
Dascher C.C., Hiromatsu K., Naylor J.W., Brauer P.P., Brown K.A.,
Storey J.R., Behar S.M., Kawasaki E.S., Porcelli S.A., Brenner M.B.,
LeClair K.P.;
                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF145489; AAF12744.1; -. HSSP; P11609; 1CD1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: ASSOCIATES NON-COVALENTLY WITH BETA-2-MICROGLOBULIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10141;
[1]
  SEQUENCE FROM N.A.
                                          NCBI_TaxID=747;
                                                                                                                     Pasteurella multocida.
                                                                                                                                               RNFD OR PM0384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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J. Immunol. 163:5478-5488(1999).
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BY SIMILARITY.
BY SIMILARITY.
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Pred, No. 44;
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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                                                                                             Pasteurellales;
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Best Local
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NLPD OR STY3050 OR T2826.
                       Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krögh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
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-:- SUBUNIT: Composed of at least six subunits; rnfA, rnfB, rnfC, rnfD, rnfE and rnfG (By similarity).
-:- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR004338; NQR2 RnfD Rn
Pfam; PF03116; NQR2_RnfD_RnfE; 1.
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InterPro; IPR004338; 1
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                                                                                                                                                                                                                                               MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 Enterobacteriaceae; Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                          TaxID=601
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Similarity 60.0%;
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M 42
M 69
M 125
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genome sequence of a multiple drug resistant Salmonella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robbe-Saule V., Norel F.;
"The rpoS mutant allele of Salmonella typhi Ty2 is identical to of the live typhoid vaccine Ty21a.";
FEMS Microbiol. Lett. 170:141-143(1999).
-!- FUNCTION: MAY BE INVOLVED IN STATIONARY-PHASE SURVIVAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95220644; PubMed=7705608;
Robbe-Saule V., Coynault C., Morel F.;
Robe oral typhoid vaccine Ty21a is a xpoS mutant
susceptible to various environmental stresses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIR=TY2 / ATCC 700931;
STRAIR=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Dengland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99118315; PubMed=9919662; Robbe-Saule V., Norel F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                      Pfam; PF01476; LysM; 1.
Pfam; PF01551; Peptidase M37; 1.
SMART; SM00257; LysM; 1.
PROSITE; PS00013; PROKAR LIPOPRO
                                                                                                                                                                                                                                                                                                         MEROPS; M37.UPW; -.
INTERPTO; IPRO02482; LysM,
INTERPTO; IPRO02886; Peptidase_M37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anchor (Potential).
-!- SIMILARITY: BELONGS TO THE E.COLI NLPD / HAEMOPHILUS LPPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 269-373 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEMS Microbiol. Lett. 126:171-176(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Ty21a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 255-373 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLULAR LOCATION: Attached to the inner membrane
                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriol. 185:2330-2337(2003).
 103
                                                                                                                                                                                                                                                                                                                                                     X81641; CAA57297.1; -.
Y17610; CAA76806.1; -.
                                                                                                                                                                                                                                                                                                                                                                                  AL627276; CAD06031.1; -. AE016843; AA070383.1; -.
                           1 YGNSPKG
                                                       ٠<u>.</u>
                                                                     Similarity
YGNIPKG 109
                                                                                                           1
26
26
199
199
199
221
233
240
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCC 700931
                                                                                                              AA;
                                                                                                                                                                                                                     3; PROXAR LIPOPROTEIN; 1.
Lipoprotein; Repeat; Signal; Complete proteome.
25
BY SIMILARITY.
                              Ų
                                                                                                                           26
246
205
227
239
246
                                                                                                            39183 MW;
                                                                    60.3%;
                                                       0
                                                                    Score 35; DE
Pred. No. 49;
                                                                                                                                                                                  LIPOPROTEIN NLPD.
N-ACYL DIGLYCERIDE (BY SIMILARITY)
4 % 7 AA APPROXIMATE REPEATS.
                                                                                                              DD075BB440098FF7 CRC64;
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                   80
                                                                                 Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by a lipid
                                                       0
                                                       Gaps
                                                       0
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Search completed: November Job time : 2,72096 secs

7,

2003, 07:28:04

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
                                                                                                                                  SPTREMBL 23:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_inngi:*
4: sp_invertebrate:*
5: sp_invertebrate:*
5: sp_manmal:*
6: sp_mac:*
6: sp_organelle:*
6: sp_bage:*
8: sp_bage:*
8: sp_nage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  November 7, 2003, 07:21:18; Search time 3.29773 Seconds (without alignments) 782.516 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-661-992B-5
58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YGNSPKGFAY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
sp_plant:*
sp_vrodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         830525
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

16	15	14	13	12	11	10	Q	80	7	6	ហ	4	ω	N	۲	Result No.
39	39	39	39	39	39	39	40	40	41	41	41	42	42	4	44	Score
67.2	67.2	67.2	67.2	67.2	67.2	67.2	69.0	69.0	70.7	70.7	70.7	72.4	72.4	74.1	75.9	Query
568	566	561	559	559	491	401	1312	291	2515	453	389	833	160	294	120	Length DB
13	4	11	73	13	4.	16	16	ψı	ഗ	16	œ	W	w	16	11	B
Q91572	Q9BZB8	P70166	Q9DED5	Q9YGX5	Q9BZB7	Q9KRK6	Q98NH6	Q9VTH9	Q9W2J8	P74064	Q98RZ7	013620	TOLDED	19NX80	Q920E8	Ħ
Q91572 xenopus lae	Q9bzb8 homo sapien	P70166 mus musculu	Q9ded5 carassius a	Q9ygx5 brachydanio	Q9bzb7 homo sapien	Q9krk6 vibrio chol	Q98nh6 rhizobium l	Q9vth9 drosophila	Q9w2j8 drosophila	P74064 synechocyst	Q98rz7 guillardia	O13620 schizosacch	Q9utul schizosacch	Q8xn61 clostridium	Q920e8 mus musculu	Description

0

45	44	43	42	41	40	39	38	37	36	<u>ئ</u>	34	ယ	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	
36	36	36	36	36	9	36	37	37	37	37	37	37	37	37	37	37	37	37	37	37	38	3 8	38	38	38	38	38	39	
62.1	62.1	62.1	62.1	62.1	62.1										63.8												65.5		
183	183	183	181	173	117	69	746	712	422	390	390	346	331	306	306	302	292	258	255	205	588	583	488	488	488	402	402	600	
11	11	4.	10	4	26	1,1	16	16	16	16	N	10	10	Φ	4	11	<u>بر</u> 12	u	w	ψI	ω	16	16	16	10	16	16	13	
070307	Q9R0T9	060572	Q9FX45	Q96G09	Q915X3	Q8CF51	Q8KG23	Q97KK5	Q8U7B0	Q92TL6	Q59744	Q9LP39	Q9LP40	Q28165	043484	035935	Q8CCS6	Q9W086	Q9P4V6	Q93233	Q9P982	Q9Z5K5	Q8Z622	Q8Z7V6	Q9LNG1	Q8NV56	Q99RS8	093386	
070307 mus musculu	Q9r0t9 mus musculu	060572 homo sapien	Q9fx45 arabidopsis	Q96g09 homo sapien	Q9i5x3 pseudomonas	Q8cf51 mus musculu		Q97kk5 clostridium		o.	ĸ	ø	Q9lp40 arabidopsis	god t	OWO	S mus	Q8ccs6 mus musculu	Q9w086 drosophila		Q93233 caenorhabdi	-	Q9z5k5 mycobacteri	Q8z622 salmonella				Q99rs8 staphylococ	O93386 brachydanio	

## ALIGNMENTS

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1 YGNSPKGFAY 10           101 YGNSPAWFAY 110	Query Match 75.9%; Score 44; DB 11; Length 120; Best Local Similarity 80.0%; Pred. No. 1.4; Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps	SEQUENCE 120 AA; 13204 MW; DC4834AB1DE56E3C CRC64;	3 1	SMART; SM00406; IGV; 1. PROSITE; PS50835; IG_LIKE; 1.	0047; ig; 1	InterPro: IPR003006; Ig_MHC.	InterPro; IPR007110; Ig-like.	Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.  RMBL: AP307036: AML09420 1: -	lan Cells.";	of the Idiotope of Pterin-Mimicking A	SECONDER FROM N.M. Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;	CENTENICE EDOM N. A	•	Rodentia; Sciurognathi; Muridae;	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Enteleostomi:		cking anti-idiotope he	01-MAR-2003 (TremBLrel. 23, Last annotation update)	(TrEMBLrel. 19, Last	Q92088; 01-DEC-2001 (TrEMBLrel. 19, Created)	Q920E8 PRELIMINARY; PRT; 120 AA.	ULT 1 0E8

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RESULT
ORNELT
ID X NG1
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ID X NG1
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Q9UTU1
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                                      Query Match
    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 18.1 kDa protein (Fragment).
2257512.
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01-MAR-2002 (TrEMBirel. 20, Created)
01-MAR-2002 (TrEMBirel. 20, Last sequence update)
01-MAR-2003 (TrEMBirel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AP003186; BAB80183.1; ...
InterPro; IPR001173; Glyco trans 2.
Pfam; Pf00535; Glycos trans 2; I.
Transferase; Complete proteome.
SEQUENCE 294 AA; 34356 MW; 390B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium perfringens.
Bacteria; Firmicutes; Clostridia, Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8XN61
                                                                                                                                                   Hypotherical protein.
NON TER 1
NON TER 160 16
                                                                                                                                                                                                                                                    InterPro; IPR000504; RNA_rec_mot.
pfam; pF00076; rrm; 1.
sMART; sM00360; RRM; 1.
pROSITE; pS50102; RRM; 1.
pROSITE; pS50102; RRM; 1.
pROSITE; pS00030; RRM; RNP_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Large-scale screening of intracellular protein localization in living fission yeast cells by the use of a GFP-fusion genomic DNA library."; Genes Cells 5:169-190(2000).
EMBL: AB028003; BAA87307.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=968 h90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     flesh-eater."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1502;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20223868; PubMed=10759889;
Ding D.Q., Tomita Y., Yamamoto A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                      SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222
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                                                                                                                  160 AA;
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                                                                                                                                                        160
                                                                                                                  18116 MW;
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72.48;
87.58;
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Score 42;
Pred. No.
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Pred. No. 5
                                                                                                                  168A1F1D5D5A94F5 CRC64;
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                                      DB 3;
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RESULT
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        REPERT OF CONTRACT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ś
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=972h-;

Murphy L., Harris D., Wood V., Raja Murphy L., Harris D., Wood V., Raja Submitted (APR-2001) to the EMBL/Ge EMBL, AB004535; BAA21408.1; -. EMBL, AL590883; CAC37370.1; -. Genebb Spembe; SPB22H7 02c; -. InterPro; IPR000504; RNA_rec_mot. Pfam; PF00076; rrm; 5.

SMART, SM00360; RNM; 5.
                                                                                                                                                                                                                                                                                                                                                                                       Q98RZ7;
Q98RZ7;
01-OCT-2001
SEQUENCE FROM N.A.

MEDLINE=21223349; PubMed=11323671;

Douglas S., Zauner S., Fraunholz M., Beaton M.,

Wu K., Reith M., Cavalier-Smith T., Maier U.G.;

"The highly reduced genome of an enslaved algal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kushida N., Yamazaki S., Tanaka T., Jinno K., Haikawa Y., Yamazaki J., Yamamoto S., Sekine M., Oguchi A., Nagai Y., Sakai M., Aoki K., Ogura K., Otsuka R., Kudoh Y., Yanagida M., Machida M., Zhang M.Q., Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).

Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 013620 PRELIMINARY; PRT; 833 AA.
013620;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hyporhetical 33, Tag protein (RNA binding protein, recognition MOTIFS).
                                                                                                                                                                                                                                                                                                                               01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                    Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
NCBI_TaxID=55529;
                                                                                                                                                                                                                        Nucleomorph
                                                                                                                                                                                                                                                                                                        Polyadenylate-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50102; RRM; 5.
PROSITE; PS00030; RRM_RNP_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=972 H-;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces.
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                                                                                                                                                                                                                                                   Guillardia theta (Cryptomonas phi).
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tes 7; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 NNPKGFAY 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           833 AA; 93676 MW;
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87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42;
Pred. No.
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  nucleus.";
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                                                       Penny S., Deng L.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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RESULT 7

Q9W2

ID Q9W2

AC Q9W2

AC Q9W2

AC Q9W2

DT 01-M

DT 01-M

DT 01-M

DT 01-M

DT 02-M

DT 01-M

DT 01
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Interpro; IPR000504; RNA_rec_mot.
Pfam; PP00076; rrm; 3.
SMART; SM00360; RRM; 3.
PROSITE; PS00030; RRM; 3.
PROSITE; PS00030; RRM; 1.
SEQUENCE 389 AA; 45171 MW; 721
                                                                                                                                                                                                                                                                                                                                                                                    Q9W2J8
Q9W2J8;
01-MAY-2000
01-MAY-2000
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01-FEB-1997
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D90911; BAA18140.1; .
InterPro; IPR005225; Small GTP.
TIGRPAM9; TIGR00231; small GTP; 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete proteome.
SEQUENCE 453 AA; 49154 MW; 4CFDFAED77536F59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
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P74064;
                                                                                                                                          Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
                                                                                                                                                                                                                                                                       TUD OR CG9450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLL0804
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SEQUENCE FROM N.A.
                                                                                                                Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res
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(TrEMBLrel. 02, Last seq
(TrEMBLrel. 21, Last ann
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                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
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RA Addms M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addms M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addms M.D., Celniker S.E., Holt R.A., Evans C.A., Golle R.P.,
RA Barndon R.C., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barlew R.M., Basu R., Barlet R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Barrandale J., Bayraktaroglu L., Beasley E.M.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Berbios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Solk K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA de Son K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Heim M., Glassex K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Heim M., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Heim M., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Heim M., Houck J.,
RA McLand D.R., Welson K.A., Mixon K., Missern D.R., McPherson D.
RA McLand D.R., Welson K.A., Mixon K., Missern D.R., McPherson D.L.,
RA Halzzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Hang Z.-Y., Masserman D.A., Weinsteck G.M., Weinsen D.R., Weinster B., Shen H.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun B.,
RA Hang R., Per J., Zaveri J.S., Zhan M., Janng G., Zhao Q., Zheng L.,
RA Hang K.R., Per J., Shen H., Shith H.O.,
RA Hang K.R., Per J., Shen H., Shith H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                            Q9VTH9 PRELIMINARY;
Q9VTH9;
01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, I
01-JUN-2002 (TrEMBLrel. 21, I
CG11726 protein.
Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Badopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001097; Maternal_tudor.
InterPro; IPR002999; Tudor.
Pfam; Pf00567; TUDOR; 10
SMART; SM00333; TUDOR; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE003453; AA1
HSSP; Q16637; 1G5V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBgn0003891; tud.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF46693.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.7%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285264 MW; 1218700174D66701 CRC64;
                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 5;
Pred. No. 1.5e+0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .5e+02;
                                                                                                                                                                                                                                                                                                                                  update)
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RESULT 9
Q98NH6
ID Q98N
AC Q98N
AC Q98N
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT Ribo
GN MILO
OS Rhiz
OC Back
OC Back
OX NCB1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RX MEDILINE-20195005; pubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashbunner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell N.D., Zhang Q., Chen L.X.,

RA Barlaw R.M., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Apdayani A., An H.-J., Andrews-Pfamkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Buck J., Brokssein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu B., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Burbin K.J., Bennes P.V., Bennes B.P., Bhandari D., Dew I., Dietz S.M.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Harris N.I., Harvey D., Helman T.J., Wei M.-H., Ibegwam C.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Iai Z.,

RA Harris N.I., Harvey D., Helman T.J., Wei M.-H., Ibegwam C.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Iai Z.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Iai Z.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Iai Z.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Nelson D.R., Nelson K.A., Nusskarn D.R., Pacleb J.M.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Mordage T., Worley A., Weissenbach J.,

RA Sylerkas R., Tector C., Tunner R., Venter E., Mang A.H., Wang X.,

RA Sheng E., Siden F., Sarvat J.S., Zhan M., Zhang G., Zhang V.,

RA Sheng C.Y., Shan M., Zhang G., Zhang Y., Smith T.,

RA Sheng R., Shangoles I.,

RA Mang C., Shan
                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
ML0136.

Rhizobium loti (Mesorhizobium loti).

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

Phyllobacteriaceae; Mesorhizobium.

NCBI_TaxID=381;
                                                                                                              Q98NH6; PRELIMINARY;
Q98NH6; TremBlrel 18,
01-0CT-2001 (TremBlrel 18,
01-0CT-2001 (TremBlrel 18,
                                                                                                 Ribonucleotide reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; 1.
SEQUENCE 291 AA; 32307 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                              119 GKRPKGFAY 127
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                                                                                                                                                                                                                                                                                                                                                                       Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                  GNSPKGFAY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                          69.0%;
                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                          Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    65A1F6D3407AA699 CRC64;
                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                 1312
                                                                                                                                                                                                                                                                                                                                                                                                             DB 5; Length 291;
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                                                                                                                                                                                                                                                                                                                                                                         2; Indels
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RESULT 10
Q9KRK6
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Best Local Similarity
                                                                                                               Matches
                                                                                                                                                                  Query Match
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SEQUENCE FROM N.A.
STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.
Katanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                              InterPro; IPR004812; Efflux_Bcr_CflA.
InterPro; IPR007114; MFS.
InterPro; IPR005828; Sub rransporter.
Pfam; Pr00083; Sugar tr; 1.
TIGRPAMS; TIGR00710; efflux_Bcr_CflA; 1.
PROSITE; PS59850; MFS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=E1 TOR N16961 / Serotype 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., Sellers P.,
McDonald M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Saltberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9KRK6
                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE004241; AAF94785.1; -. TIGR; VC1634; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9KRX6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
SEQUENCE 1312 A#
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Res. 7:331-338(2000).
EMBL; AP002994; BAB47785.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01183; KIBORDTASEM1.
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Pfam; PF02867; ribonuc_red_lgC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drug resistance protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    406:477-483 (2000)
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                                                                                                                                        Similarity
                                                                                                                                                                                                                                                           proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNEPKGFA 1190
                                                  YGNSPKGFAY 10
                                                                                                                                                                                                                                  401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA; 143398 MW; 409464CB9F709F38 CRC64;
                                                                                                                                                                                                                                  42914 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.0%;
                                                                                                                                        67.2%;
70.0%;
                                                                                                                                        Score 39; DB 16; Length 401; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 16; Length 1312; Pred. No. 1.1e+02; O; Mismatches 1; Indels
                                                                                                                                                                                                                                  814CD7A2A86E3BDB CRC64;
                                                                                                               Mismatches
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RESULT 12
Q3YGX
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AC Q3YGX
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DT 01-MA
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CATINA
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Q9BZB
AC Q9BZB
DT 01-JU
DT 01-JU
DT 01-MA
DE CPEBI
OS HOMO
OC BUKAR
OC MAMMA
OX MCBI
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RP SEQUE
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Best Local S
Matches 6
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                                                                                                                                                                         Submitted (MAR-1998) to the EMBL/GenBank/DDBJ EMBL; AB011680; BAA75637.1; -. ZFIN; ZDB-GENB-990927-1; ZOLDA. InterPro; IPR000504; RNA rec_mot. SMART; SM00360; RRM; 1. SMART; SM00360; RRM; 1. PROSITE; PS50102; RRM; 1. PROSITE; PS50102; RRM; 1.
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9BZB7;
Q9BZB7;
01-JUN-2001
01-JUN-2001
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Covary, and Brain;
MEDILINE=2112522; PubMed=11223249;
Welk J.:, Charlesworth A., Smith G.D., MacNicol A.M.;
Helk J.:, Charlesworth A., Smith G.D., MacNicol A.M.;
'Identification and characterization of the gene encoding human cytoplasmic polyadenylation element binding protein.";
Gene 263:113-121(2001).
EMBL; AF329403; AAK01240.1; -.
InterPro; IPR000504; RNA rec_mot.
PROSITE; PS50102; RRM; 2.
PROSITE; PS50102; RRM; 2.
PROSITE; PS50102; RRM; 2.
                                                                                                                                                                                                                                                                                                                                                                        Suzuki H., Maegawa S., Murakawa M., Hoshijima K.,
Yasuda K., Inoue K.;
"Identification of zebrafish maternal RNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata
Actinopterygii; Neopterygii;
Cyprinidae; Danio.
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Eukaryota; Metazoa; Chordata;
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                         GNSPKGFAY 10
GNMPKGYVY 356
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3 (TrEMBLrel. 23,
                                                                                        Conservative
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66.7%;
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Pred. No. 68;
1; Mismatches
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element-binding protein
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; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                maternal RNA-binding proteins,
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Pred. No.
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Catarrhini; Hominidae;
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                                                                                                                                                                                36CF42E1AC70A377 CRC64;
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RESULT 13
GDDD5
ID D205
AC Q9DED
D7 01-M2
D7 01-M2
D7 01-M2
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                                                                                                Query Match
Best Local S
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Best Local S
Matches 6
                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                          Gebauer F., Richter J.D.;

"Mouse cytoplasmic polyadenylation element binding protein: An evolutionarily conserved protein that interacts with the cytople polyadenylation elements of c-mos mRNA.";

proc. Natl. Acad. Sci. U.S.A. 93:14602-14607(1996).

EMBL; Y08260; CAA69588.1; -.
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Q9DED5;
01-MAR-2001
01-MAR-2001
01-MAR-2003
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"Goldfish cytoplasmic polyadenylation element binding pr
(CPEB): its interaction with CPE of cyclin B mRNA and pho
by cdk and Eg2 protein kinases.";
submitted (GUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB04534; BAB19051.1;
Interpro; IPR000504; RNA_rec_mot.
SMART; SM00360; RRM; 1.
PROSITE; PS59102; RRM; 1.
PROSITE; PS59102; RRM; 1.
PROSITE; S5950102; RRM; 1.
SEQUENCE 559 AA; 62122 MW; 05507CE5D1568144 CRC64;
                                                                                                                                                                                                                                    InterPro; IPR000504; RNA rec_mot.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10090;
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01-MAR-2003
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Actinopterygii; Neopterygii;
Cyprinidae; Carassius.
NCBI_TaxID=7957;
                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97121433; PubMed=8962099;
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6; Conserva
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GNSPKGFAY
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                                                                Conservative
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66.7%;
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Last sequence update)
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element-binding protein
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element binding prote
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Pred. No.
                                                                                                    Pred.
                                                                                                                                Score 39;
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                                                                                                                                                                                                CB7958885AB13FF6 CRC64;
                                                                Mismatches
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80
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                                                         Gaps
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354

GNMPKGYVY

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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                               Score
           33444558
33944455
378
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

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6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
         100.0
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72.4
70.7
69.0
67.2
63.8
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Gapop 10.0 , Gapext 0.5
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58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Listing first 45 summaries
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:
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Copyright (c) 1993 - 2003 Compugen Ltd.
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      AAB20388
AAB20444
AAB26463
AAB664427
ABB64427
ABB63366
ABP08836
ABP08836
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Anti-FIX/FIXa anti
Anti-FIX/FIXa anti
Anti-FIX/FIXa anti
Protein encoded by
Drosophila melanog
Drosophila melanog
Drosophila melanog
Human ORFX protein
Heavy chain (VH) g
Human breast speci
                                                                                                                                                                                                                           Description
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Human immunopeptid	ABP62216	23	132	60.3		45
Drosophila melanog	ABB68852	22	128	60.3		44
Human polypeptide	AA010811	22	119	60.3		43
Zea mays protein f	AAG18544	21	116			42
Arabidopsis thalia	AAG32223	2	113	60.3	35	41
mays proteir	AAG18545	21	108	•		40
Arabidopsis thalia	AAG49953	21	99	•		39
mays pro	AAG19069	21	96	•		38
Zea mays protein f	AAG35352	21	90	•		37
mays pro	AAG35353	21	82	•		36
	AAG10160	21	74	٠		35
	AAG32222	21	69			34
	AAG49954	21	63	٠		33
Arabidopsis	AAG10161	21	63	•		32
	ABB63009	22	969	٠		31
mela	ABB67398	22	767	٠		30
sp.	AAW90940	21	710			29
Staphylococcus epi	ABP40557	23	484	•		28
Cysteine protease	AAB65770	22	396	4		27
peptide	AAM39480	22	287	•		26
Human MDDT polypep	ABU11773	24	280	٠		25
_	AAM41266	22	271	•		24
Human protein sequ	AAB93180	22	261	٠		23
Novel human diagno	ABG15228	22	238	•		22
Human RNA-associat	AAY70220	21	216	•		21
Amino acid sequenc	AAY84429	21	216	٠		20
	ABG00682	22	198	62.1		19
Human protein sequ	AAB92806	22	183			18
	AAY70228	21	183			17
l human	ABG15227	22	130			16
Novel human diagno	ABG00681	22	118	٠		15
Human ORFX protein	ABP03818	23	117	•		14
ted pr	AAG02102	21	92	62.1		13
novel	\$5	23	365			12
	AAW59884	19	365	٠		11
Drosophila melanog	ABB68781	22	258	٠		10

## ALIGNMENTS

RESULT 1
AABZ0388
ID AABZ
XX AABZ
XX AABZ
XX Fact
XX Fact
XX Fact
XX Fact
XX Haem
Comp
XX Haem
C Factor IX; FIX; Factor IXa; FIXa; antibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse; complementarity determining region; CDR. 14-SEP-1999; 13-SEP-2000; 2000WO-EP08936. 22-MAR-2001. WO200119992-A2 Mus musculus. Anti-FIX/FIXa antibody 193/AD3 CDR3. 21-JUN-2001 (first entry) AAB20388; AAB20388 standard; Peptide; 10 AA. (BAXT ) BAXTER AG. 99AT-0001576

New factor IX/factor IXa antibodies and their derivatives useful for

WPI; 2001-290358/30.

Scheiflinger F, Kerschbaumer

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Falkner F,

Dorner F;

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RESULT 2
AAB20444
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Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide) have Factor VIIIa (FVIIIa) cofactor activity or FIXa activating activity. Administration of the antibodies or their derivatives leads to an increase in the procoagulant activity of FIXa, even in the presence of FVIIIa inhibitors. This allows for rapid blood coagulation even in the absence of FVIII or FVIIIa, and in the case of FVIII inhibitor patients. The antibodies or their derivatives are used in a claimed pharmaceutical composition for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic diathesis.
            WPI; 2001-290358/30
                                       Scheiflinger F.
                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                    Factor IX; FIX; Factor IXa; FIXa; antibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic disthesis; haemostatic; amidolytic; therapy; mouse; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-activated Factor IX (FIXa) activity. It is an example of anti-FIX/FIXa antibodies of the invention. Such antibodies and their derivatives (including those that comprise the present CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of complementarity determining region 3 (CDR3) of the heavy chain of an antibody expressed by mouse hybridoma 193/AD3. This antibody has anti-Factor IX (FIX) or anti-activated Factor IX (FIXa) activity. It is an example of
                                                                                              14-SEP-1999;
                                                                                                                         13-SEP-2000; 2000WO-EP08936.
                                                                                                                                                       22-MAR-2001
                                                                                                                                                                                   WO200119992-A2
                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                           Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-FIX/FIXa antibody CDR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB20444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB20444 standard; Peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coagulation
                                                                    (BAXT ) BAXTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 74; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YGNSPKGFAY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                               99AT-0001576.
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                       Kerschbaumer R,
                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                             /note= "any amino acid"
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                                                                                                                                                                                                                                         note=
                                                                                                                                                                                                                                                                                                "any
                                                                                                                                                                                                                                        "any amino acid"
                                                                                                                                                                                                                                                                      "any amino acid"
                                                                                                                                                                                                                                                                                                  amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 58; DB 22;
Pred. No. 0.0012;
; Mismatches 0;
                                     Falkner F,
                                       Dorner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 10;
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Query Match
Best Local :
                                                                                                                                region 3 (CDR3) of an antibody having anti-Factor IX (FIX) or anti-activated Factor IX (FIXA) activity. Such antibodies and their derivatives (including those that comprise the present CDR3 peptide) have Factor VIIIa (FVIIIa) cofactor activity or FIXA activating activity. Administration of the antibodies or their derivatives leads to an increase in the procoagulant activity of FIXA, even in the presence of FVIIIa inhibitors. This allows for rapid blood coagulation even in the absence of FVIII or FVIIIa, and in the case of FVIII inhibitor patients. The antibodies or their derivatives are used in a claimed pharmaceutical composition for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic diathesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of complementarity determining region 3 (CDR3) of an antibody having anti-Factor IX (FIX)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 74; 138pp; English.
                          Similarity
100.0%;
ilarity 100.0%;
Conservative (
                                                                                              16 AA;
  Score 58; DB
Pred. No. 0.0
); Mismatches
                        0.002;
                                              DB 22;
                                              Length 16;
  0
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RESULT 3
AAB20433
ID AAB32
XX AAB2
XX AAB2
XX AAB2
XX AAT1
XX Fact
XX Chim
XX Chim
XX Chim
XX Chim
XX Fact
FT Regi
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Protein
                                                                                                                                                                                                                                                                                                                                                                              Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse
                                                                                                                                                                                                                                                                                                                                             Chimeric -
Chimeric -
                                                                                                                                                                                                                        Proteir
                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-FIX/FIXa antibody 193/AD3 scfv
                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB20433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB20433 standard; Protein; 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YGNSPKGFAY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YGNSPKGFAY 13
                                                                                                                                                                                                                                                                                                                                                        Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                           /label= VH
98..108
                                                                                                                                                                                                           135..242
/label= VL
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                label= CDR3
                                                                                                                                                                                                                                      label= Linker
                                                                                                                                                                                                                                                  ..134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                ; naemophilia A;
therapy; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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WPI; 2001-290358/30

Scheiflinger F,

Kerschbaumer R,

Falkner F,

Dorner F;

(BAXT ) BAXTER

ត

14-SEP-1999;

99AT-0001576

13-SEP-2000; 2000WO-EP08936.

22-MAR-2001 WO200119992-A2 Region

'label= CDR:

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RESULT 4
AAB6460
ID AAB6
XX AAB6
XX AAB6
XX Prot
XX Myco
XX Myco
XX Myco
XX Myco
XX WO20
XX WO20
XX WO20
XX I1-J
XX II-J
XX II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of a single chain FV (scFV) derivative CC of antibody 193/AD3, comprising the heavy (VH) and light (VL) chain CC variable regions of 193/AD3 joined by an artificial, flexible linker CC peptide. The scFV was obtained by PCR amplification of cDNAs for CC 193/AD3 VH and VL regions and cloning in vector pDAP2. 193/AD3 is CC an example of anti-human Factor IX (FIX)/activated Factor IX (FIX) and their derivatives, CC antibodies of the invention. Anti-FIX/FIX and their derivatives, CC including scFV and CDR3 fragments, have Factor VIIIa (FVIIIa) cofactor CC activity or FIXA activating activity. Administration leads to an CC increase in the procagulant activity of FIXA, even in the presence CC of FVIIIa inhibitors. This allows for xapid blood coagulation even CC in the absence of FVIII or FVIIIA, and in the case of FVIII or FVIII or FVIIIIA, and in the case of FVIII or FVIIII or FVIIIIA, and in the case of FVIII CC claimed pharmaceutical composition for treating patients with blood CC coagulation disorders, especially haemophilia A and haemorrhagic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                              Screening a mutant library for mutants unable to grow under specific conditions and for identifying loci involved in pathogenicity,
                                                                                                                                                                                                                                            Gicquel B,
                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1999;
08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mycobacterial infection; actinomycetales; antibacterial; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUL-2000, 2000WO-IB00950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200102555-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis; attenuated microorganism; fad26; Rv2930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein encoded by Mycobacterium tuberculosis fad26 (Rv2930)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB66460;
                                                                                                                                                                                                                                                                                                        (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              signature tagged transposon mutant; mutant library;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as hasmophilia A and hasmorrhagic diathesis
                                                                                                                                                                                    2001-091804/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                            Guilhot C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                      99US-0142982
99US-0142833.
                          signature
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                                                                                                                                                                                                                                            Camacho
                   tagged transposon mutagenesis
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Pred. No.
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The present sequence is given in a specification relating to a method for CC screening a library of mutants. The method comprises constructing a CC library with insertions in genes and/or regulatory regions of the CC organisms of interest, where the insertion contains a tag and/or a CC transposon associated with a tag. The mutants are identified by CC hybridisation of the tags to known sequences. The method is useful for CC transposon associated with a Mycobacterial infection, CC suspected of being infected with a Mycobacterium, or having been CC exposed to an infectious Mycobacterium. It is also useful for identifying and isolating mutants of actinomycetales and for identifying CC compounds that have antibiotic activity. The method is used to identify CC M. paratuberculosis, M. bovis, M. leprae, M. avium, M. intracellulaire and CC M. paratuberculosis, N. bovis, M. leprae, M. avium, M. intracellulaire and CC It is especially useful for identifying loci involved in pathogenicity. It is useful in constructing vaccines. The method can be used to screen CC multiple libraries concurrently. It can screen libraries of different cryganisms or different strains of the same organism. The present protein is encoded by a gene which is disrupted by the insertion of the relications.
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Query Match Best Local S Matches 7 ABB64427 standard; Protein; 2515 AA. 73 1 YGNSPKGFA Similarity 7; YGSDPKGFA 81 Conservative 72.48; Score 42; DB Pred. No. 60; 1; Mismatches 22 Length 626; Indels 0 Gaps

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Sequence

626 AA;

RESULT 5
ABB64427
ID ABB6
XX ABB6
XX ABB6
XX Dros
YX D Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical. Drosophila melanogaster polypeptide SEQ ID NO 20073. 26-MAR-2002 ABB64427; (first entry)

Drosophila melanogaster.

WO200171042-A2

27-SEP-2001.

23-MAR-2000; 2000US-191637P 11-JUL-2000; 2000US-0614150 23-MAR-2001; 2001WO-US09231.

(PEKE ) PE CORP NY.

Venter JC, Adams M, Ľ PWD. Myers Ħ

2001-656860/75. ABL08530.

New isolated nucleic acid genes from Drosophila and detection reagent for detecting 1000 for elucidating cell signalling and

Disclosure; SEQ ID NO 20073; 21pp + Sequence Listing; English

The invention relates to an isolated nucleic acid detection reagent

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RESULT 6
ABB63366
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                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 16890; 21pp + Sequence Listing; English
                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes from Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL10140-ABL16175) and the encoded proteins (ABB57737-ABB72072).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ ID NO 16890.
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                                                                                                                                            (ABB57737-ABB72072)
                                                   ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid detection reagent for detecting 1000 or more and for elucidating cell signalling and cell-cell
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Pred. No. 3.9e
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3.9e+02;
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CC The present invention describes substantially purified human proteins CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 CC in the specification). ABN15762 to ABN27252 encode the human ORFX CC proteins given in ABP00010 to ABR11500. ORFX proteins are useful for CC treating or preventing a pathology associated with an ORFX-associated CC disorder in humans, and in the manufacture of a medicament for treating a CC syndrome associated in gene therapy. ORFX sequences can be used in gene therapy. ORFX sequences can be used in the CC treatment of cancer, hyperproliferative disorders, chrhosis of liver, CC psociasis, benign tumours, keloid, degenerative disorders related to organ CC transplantation, cardiovascular diseases, diabetes mellitus, systemic CC transplantation thyroiditis, myosthyroidism, cholesterol ester CC storage disease, various immune deficiencies and disorders, infectious CC diseases, autoimmune thyroiditis, myosthenia gravis, graft-versus-host CC useful for treating burns, incisions, ulcers, for treating osteoporosis, CC useful for treatine thyroiditis, incisions, ulcers, for treating osteoporosis, CC useful for treatine disorders, or periodontal disease, and for gut reperfusion injury in various tissues and conditions resulting from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAY-2001; 2001WO-US10836.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; open reading frame; ORFX; gene therapy; cancer; hyperproliferative disorder; psoriasis; benign tumour;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                degenerative disorder; osteoarthritis; neurodegenerative disorder
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nes 7; Conserv
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77.8%;
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Pred. No.
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                                                                                                                  ANY43862-75 represent the amino acid sequences of the heavy chain (VH) gene sequences from antibodies against Bacillus anthracis spores. The antibodies are produced by different hybridomas, The specification describes monoclonal antibodies (especially IgG antibodies) which are highly specific and can discriminate between the spores of the Bacillus family. The antibodies are produced by exposing mice to Bacillus spores. The humoral immune response to Bacillus spores in the monoclonal antibody, and peptide fragments derived from the antibodies are also capable of binding spores. The monoclonal antibody, and peptide fragments of it, can be used to detect Bacillus spores in a field sample. It is particularly uses for detecting anthrax in a field sample.
                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                Monoclonal antibody specific for Bacillus spores, used
                                                                                                                                                                                                                                                                 Example 13; Page 53-54; 64pp; English.
                                                                                                                                                                                                                                                                                                                          WPI; 2000-013435/01
                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VH gene usage; anthrax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heavy chain; VH; IgG; monoclonal antibody; spore; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                systemic cytokine damage.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY43866;
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                                                                     Similarity
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                                   YGNSPKGFAY 10
                 YGNYPAWFAY 86
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                                                                                                    129 AA;
                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene sequence of Bacillus anthracis antibody 7-1.
                                                                    65.5%;
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77.8%;
                                                       Score 38; DB
Pred. No. 56;
0; Mismatches
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Pred. No. 34;
0; Mismatches
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                                                                                                                                                  The present invention provides human breast specific coding sequences and proteins. These are useful for detecting breast tissue and for detecting and treating breast cancer and other breast diseases. The present
                                                                                                                 Sequence
                                                                                                                                                                                                                Claim 11; Page 219; 243pp; English.
                                                                                                                                                                                                                                                         Novel breast-specific polypeptides and polynucleotides encoding polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating breast cancer and non-cancerous disease states in
                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-2000; 2000US-249998P
22-NOV-2000; 2000US-252563P
                                                                                                                                         sequence is a breast specific polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                   Salceda S,
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                        2 GNSPKGFA 9
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                                                                      Similarity
GNGPRGFA 13
                                                                                                               151 AA;
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                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specific gene; breast cancer; gene therapy; breast disease;
                                                                   63.8%;
75.0%;
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                                                    Score 37; DB
Pred. No. 99;
1; Mismatches
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Drosophila; developmental biology; cell signalling; insecticide;

WO200171042-A2

Drosophila melanogaster

pharmaceutical

Drosophila melanogaster polypeptide SEQ ID NO 33135

26-MAR-2002

(first entry)

ABB68781;

ABB68781 standard; Protein;

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AAW59884
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                                                               Feng P,
Su JY;
WPI; 1998-414099/35.
N-PSDB; AAV41925.
                                                                                                                                                                                     21-JAN-1997;
21-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               capable of detecting 1000 or more genes from Drosophila. The inventuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                   21-JAW-1998;
                                                                                                                                                                                                                                                                                            23-JUL-1998
                                                                                                                                                                                                                                                                                                                                    WO9831800-A2
                                                                                                                                                                                                                                                                                                                                                                                                            Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction; immunological disorder; autoimmune disease; anti-infectious agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid
genes from Drosophila and
interactions -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specification, but was obtained in electroni
at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 33135; 21pp + Sequence Listing;
                                                                                                                                                AUCK-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to an isolated nucleic acid detection reagent
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                                                                                                                        AUCKLAND UNISERVICES HUMAN GENOME SCI INC.
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                                                                                 Gentz
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2000US-0614150.
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97US-0034204.
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                                                                                                                                                                                                        11-APR-1997;
11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cerebrovascular disorder; cerebral ischaemia; angiogenesis; sumburn; nervous system disorders; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; tissue regeneration; epithelial cell proliferation; organ transplantation; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; autoimmune disease; chemotaxis; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the amino acid sequence of the CDNA clone Bcl-like (HAICH29) used in the method of the invention. The products of the clone can lused for treating conditions associated with abnormal expression of the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoinmune diseases, inflammatory diseases, various allergies, and as anti-infectious age: The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynuclectides and encoded polypeptides - used develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, all or tumours
                                                                                                                                                                                                                                                                 11-APR-1997;
11-APR-1997;
                                                                                                                                                                                                                                                                                                                              07-MAR
                                                                                                                                                                                                                                                                                                                                                         07-MAR-1997;
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07-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preservative; nutritional.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 FSGHPKGFAY 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YGNSPKGFAY
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97US-04033P
97US-040334P
97US-040334P
97US-04033EP
97US-043311P
97US-043311P
97US-043313P
97US-043314P
97US-043314P
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97US-043568P
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97US-04368P
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97US-040162P.
97US-040163P.
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Pred. No. 2.5e+02;
l; Mismatches 3
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18-AUG-1997

22-AUG-1997

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23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
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23-MAY-1997;
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23-MAY-1997;
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11-APR-1997;
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9718-056636P

9709-056652P

9709-056664P

9709-056664P

9709-056862P

9709-056874P

9709-056874P

9709-0568778P

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9709-056878P

9709-056878P

9709-056889P

9709-056888P

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97US-048974P.
97US-049610P.
97US-051926P.
97US-052874P.
97US-055724P.
97US-056630P.
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97US-047615P.

97US-047617P.

97US-047618P.

97US-047632P.

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97US-047595P.
97US-047596P.
97US-047597P.
97US-047598P.
97US-047599P.
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97US-047612P.
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97US-047587P.
97US-047588P.
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97US-047584P.
97US-047585P.
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97US-043671P.
97US-043672P.
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CC The invention relates to an isolated protein that is one of 186 human CC secreted proteins, given in the specification, encoded by one of CC 309 cDNA sequences also given in the specification. The protein is used CC in a pharmaceutical composition used to prevent, treat or ameliorate a CC medical condition in e.g. humans, mice, rabbits, goats, horses, cats, CC dogs, chickens or sheep. Disorders which are diagnosed or treated include autoimmume diseases e.g. rheumatoid arthritis, hyperproliferative CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, CC angiogenesis, nervous system disorders e.g. Alzheimer's disease, CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, CC angiogenesis, nervous system disorders e.g. Alzheimer's disease, CC e.g. corneal infection. The polypeptides can also be used to aid wound cere consuburn, to maintain organs before transplantation, for supporting cell collure of primary tissues, to regenerate tissues and in chemotaxis. The CC polypeptides can also be used as a food additive or preservative to components. The present sequence represents one of the novel human CC cemponents. The present sequence represents one of the novel human CC cemponents. The present sequence represents one of the novel human CC cemponents. The present sequence represents one of the novel human CC secreted proteins of the invention
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22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
05-SEP-1997;
05-SEP-1997;
12-SEP-1997;
02-CCT-1997;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human secreted protein for diagnosing, preventing, treating or ameliorating medical conditions and used as a food additive or preservative -
                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Column 103; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-634796/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moore
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Duan R, Hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                    proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA, Fischer CJ
A, Yu G, Ni J, Feng
Hu J, Florence KA, O:
Shi Y, Lafleur DW,
365 AA;
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97US-056911P.
97US-056911P.
97US-05761P.
97US-057650P.
97US-057650P.
97US-057669P.
97US-05060P.
97US-05060P.
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Fischer CL,

T, Feng P, Yo.

NA, Olsen HS, L.

NA, Li Y, Zeng Z
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Young PE, Greene JM, Fe;
n HS, Ebner R, Brewer LA;
Y, Zeng Z, Kyaw H;
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Ferrie AM;
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RESULT 13
AAG02102
XX AAG022
XX AAG02
XX AAG02
XX AAG02
XX D6-OC
XX Humar
XX Humar
XX Gene
XX Gene
XX Gene
XX Gene
XX Homo
XX EP10: S S Query Match
Best Local Similarity
Matches 6; Conserv 267 1 YGNSPKGFAY 10 FSGHPKGFAY 276 Conservative 63.8%; Score 37; DB 23; Length 365; Pred. No. 2.5e+02; Mismatches 3; Indels 0, Gaps

0

AAG02102 standard; Protein; 92 ጅ

06-0CT-2000 (first entry)

AAG02102;

Human secreted protein, SEQ ID NO: 6183.

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.

Homo sapiens

EP1033401-A2

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RESULT 14
ABP03818
ID ABP03
XX ABP03
XX ABP03
XX Human
XX Hypex
KW Aypex
KW Aypex
KW Aypex
KW Aypex
KW Hypex
KW
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                                                                                                                                                                                                                                                                                                                                                                       Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30' different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -
30-MAY-2000; 2000US-206132P
                                                                                                                                                                                                                                                         Homo sapiens:
                                                                                                                                                                                                                                                                                                                                                   autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human ORFX protein sequence SEQ ID NO:7618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUN-2002
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                                                        29~MAY-2001; 2001WO-US10836.
                                                                                                                                                                                          WO200192523-A2
                                                                                                                                                                                                                                                                                                                  myasthenia gravis.
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6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB
Pred. No. 88;
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ABG00681

ABG00681 standard; Protein; 118

RESULT 15

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Homo sapiens

WO200175067-A2

Novel human diagnostic protein #672.

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

13-FEB-2002

(first entry

ABG00681;

30-MAR-2001; 2001WO-US08631

11-OCT-2001.

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                                                                                                                                                                                                                                                      The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where x is 1-11491 (see Table 1 ci the specification). ABN15762 to ABN27822 encode the human ORFX CC proteins given in ABR90010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated cd disorder in humans, and in the manufacture of a medicament for treating a cyndrome associated with ORFX-associated disorder. ORFX polymucleotide sequences can be used in gene therapy. ORFX sequences can be used in the ct treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders; haemorrhage, cransplantation, cardiovascular disease, diabetes mellitus, systemic transplantation, cardiovascular disease, diabetes mellitus, systemic transplantation, cardiovascular disease, diabetes mellitus, systemic disease, autoimmune thyroiditis, myasthenia gravis, graft-versus-host cd diseases, autoimmune thyroiditis, myasthenia gravis, graft-versus-host cd diseases and autoimmune thilammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, concertions or regeneration and treatment of lung or liver fibrosis, concertions or regeneration and treatment of lung or liver fibrosis, constemic cytokine damage.

CC N.B. The semmence damage.
                                                                                Matches
                                                                                                 Query Match
Best Local
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                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID 7618; 1037pp; English.
                                                                                                                                                                                                                      N.B. The sequence data for this patent did not specification, but was obtained in electronic for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN CORP.
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                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
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3
                                    1 YGNSPKGF 8
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YGRSPSGF 50
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                                                                                               62.1%;
75.0%;
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                                                                         Score 36; DB 23;
Pred. No. 1.1e+02;
0; Mismatches 2;
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format
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directly from WIPO
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Query Match
Best Local Similarity
Watches 6; Conserve
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                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant procein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC diagnostic amino acid sequences of the invention.

CC Mote: The sequence data for this patent did not appear in the printed CC artity. but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID No 31040; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS64868.
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23-AUG-2000; 2000US-0649167.
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                                                                                                                     1 YGNSPKGFAY 10
                                                                                                                                                                                                                                              118 AA;
                                                                                                                                                             Conservative
                                                                                                                                                                                 62.1%;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Match
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58
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195.799 Million cell updates/sec
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l: /cgn2_6/ptodata/2/pubpaa
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/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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249
306
365
365
373
373
1038
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1257
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         US-10-001-887-96
US-10-153-668-118
US-10-153-668-120
US-09-809-391-696
US-09-882-171-696
US-10-219-220-153
US-10-156-761-13515
US-10-032-585-7154
US-10-284-668-72
US-09-738-626-4750
US-09-738-626-4750
US-09-764-864-953
US-09-764-864-953
US-09-764-864-953
US-09-769-787-40
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96, Appl
118, App
120, App
696, App
696, App
285, App
153, App
13515, A
7151, Appl
12, Appl
14750, Ap
913, Appl
14750, Ap
913, Appl
14750, Ap
913, Appl
14750, Appl
1593, Appl
1693, Appl
RESULT 2
US-10-153-668-118
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ag dy	Query Mat Best Loca Matches	RESULT 1  US-10-001-887-96  Sequence 96, Application US/10  Publication No. US20020155464#  GENERAL INFORMATION:  APPLICANT: Macina, Roberto APPLICANT: Macina, Roberto APPLICANT: Cafferkey, Roberto APPLICANT: Cafferkey, Roberto APPLICANT: Cafferkey, Robert APPLICANT: Liu, Changhua ITITLE OF INVENTION: Compositi FILE REFERENCE: DEX-0269  CURRENT FILING DATE: 2001-11  FRIOR APPLICATION NUMBER: 60 PRIOR FILING DATE: 2000-11-22  PRIOR FILING DATE: 2000-11-22  NUMBER OF SEQ ID NOS: 137  SOCTWARE: Patentin version 3.  SEQ ID NO 96  LENGTH: 151  TYPE: PRT  ORGANISM: Homo sapien	ı	44444000000000000000000000000000000000
6 GNG 6	ത്ത	1-887-96 Lee 96, Application No. US2 LINFORMATION LANT: Salceda LANT: Macina LANT: Recipo LANT: Liu, Caffer LANT: Liu, CAFFER LANT: LIU, GAFFER LANT: LANT, Y LANT, LANT, Y LANT, LANT, Y LA		0 4 4 4 10 10 10 10 10 10 10 10 10 10 10 10 10
GNSPKGFA	larity	1-887-96 ce 96, Application US ce 96, Application US ce 96, Application US caps: US200201554 LINFORMATION: LINFORMATION: CANT: Salceda, Susana CANT: Recipon, Herve CANT: Recipon, Herve CANT: Cafferkey, Rob CANT: Cafferkey, Rob CANT: Liu, Chenghus OF INVENTION: Compos REFERENCE: DEX-0269 TAPPLICATION NUMBER: FILING DATE: 2001-11 APPLICATION NUMBER: FILING DATE: 2000-11 APPLICATION UMBER: FILING DATE: 2000-11 APPLICATION NUMBER: FILING DATE: 2000-11 APPLICATION SAPION NO 96 H: 151 INCOME.		\$
13	63 75 i ve	stion US/100 002015464A1  Susana Susana Herve Key, Robert Ongming Anghua Compositio Compositio V10MBER: US 2001-11-1 V10MBER: 60/2 2000-11-22 2000-11-22 2000-11-22 2000-11-23 version 3.1		44444444444444444444444444444444444444
	. O. 8.	%/1000 64A1 oert ert 111-2 60/24 60/25		112 9 9 10 115 15 15 15 15 15 15 15 15 15 15 15 15
	Score 37; DB 14; Length 1 Pred. No. 46; 1; Mismatches 1; Indels	US/10001887 15464A1 ma rrtb ve tobert ig la la lositions and Methods Relating to 01-11-20 101-11-20 101-11-20 11-22 77 77 77 77 77 77 77 77 77	ALIGNMENTS	US-09-801-368-174  US-10-231-035-6  US-09-530-139-16  US-09-886-429-4  US-09-886-429-4  US-09-886-429-4  US-09-162-435-30  US-09-728-914-16  US-09-530-139-46  US-09-530-139-46  US-09-530-139-49  US-09-530-139-49  US-09-530-139-49  US-09-815-242-11743  US-09-815-242-117-3  US-10-195-117-3  US-10-195-118-3  US-10-195-118-3  US-10
	151; ls 0;	Breast		Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 2 Sequence 3 Sequence 3 Sequence 4 Sequence 4 Sequence 4 Sequence 7 Sequence 7 Sequence 7 Sequence 7 Sequence 3 Sequence 1 Sequence 11 Sequence 11
	Gaps 0;	Specific Gen		e 174, Applie 1, Applie 2, Applie 30, Applie 32, Applie 32, Applie 32, Applie 32, Applie 33, Applie 34, Applie 35, Applie 37, Applie

Gaps

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; ORGANISM: Homo sapiens
US-10-153-668-120
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US-10-153-668-118
                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/316,031
PRIOR FILING DATE: 2001-08-31
PRIOR PELICATION NUMBER: US 60/328,403
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: UF 2001-157043
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: UP 2001-260681
PRIOR FILING DATE: 2001-08-30
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MATSUDA, Akio
APPLICANT: MURAMATSU, Shuji
APPLICANT: ISHIZAWA, Kenya
TITLE OF INVENTION: STAT6 Activating Gene
FILE REFERENCE: 1254-0207P
CURRENT APPLICATION NUMBER: US/10/153,668
CURRENT TILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 60/293,172
PRIOR FILING DATE: 2001-05-25
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PRIOR FILING DATE: 2001-08-31
PRIOR PPLICATION NUMBER: US 60/328,403
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: UF 2001-157043
PRIOR FILING DATE: 2001-05-25
PRIOR PPLICATION NUMBER: UF 2001-260681
PRIOR PPLICATION NUMBER: UF 2001-260681
PRIOR PPLICATION NUMBER: UF 2001-313175
PRIOR PPLICATION NUMBER: UF 2001-313175
PRIOR FILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 488
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                                                                                                                     SOFTWARE: PatentIn Ver.
                                                                                                                                       NUMBER OF SEQ ID NOS: 488
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PRIOR APPLICATION NUMBER: US 60/293,172
PRIOR FILING DATE: 2001-05-25
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CURRENT FILING DATE: 2002-05-24
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APPLICANT: ISHIZAWA, Kenya
TITLE OF INVENTION: STATE Activating Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver.
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Local Similarity 60.0%;
les 6; Conservative
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Pred. No. 77;
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; ORGANISM: Homo sapiens
US-09-809-391-696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 696, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prior application data removed -
NUMBER OF SEQ ID NOS: 761
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 696
LENGTH: 365
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Publication No. US20030049618A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 63.6
Best Local Similarity 60.6
Matches 6; Conservative
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Best Local :
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PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 09/149,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/882,171
CURRENT FILING DATE: 2001-06-18
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CURRENT FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: 186 Human Secreted proteins
                                                                                                    FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,163
FILING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/040, 162
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040, 333
FILING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US98/04493
FILING DATE: 1998-03-06
                                       APPLICATION NUMBER: 60/047,600 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,615
                                                                                                                                                                                            APPLICATION NUMBER: 60/040,334
FILING DATE: 1997-03-07
                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/038,621
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,626
FILING DATE: 1997-03-07
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                                                                                                                                                                         APPLICATION NUMBER: 60/040,336
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5. US20030175858A1
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                      1997-05-23
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60/047,597
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Pred. No.
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Pred. No. 1.
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1.1e+02;
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SEQ ID NO 118

LENGTH: 24 TYPE: PRT

249

Query Match

Sequence 120, A Publication No.

SE() ID NO 120 LENGTH: 306

OR APPLICATION NUMBER: 60/047,502
OR FILING DATE: 1997-05-23
OR APPLICATION NUMBER: 60/047,633
OR FILING DATE: 1997-05-23
OR APPLICATION NUMBER: 60/047,583
OR FILING DATE: 1997-05-23
OR APPLICATION NUMBER: 60/047,617
OR FILING DATE: 1997-05-23
OR APPLICATION NUMBER: 60/047,503
OR APPLICATION NUMBER: 60/047,503
OR APPLICATION NUMBER: 60/047,503
OR FILING DATE: 1997-05-23
OR APPLICATION NUMBER: 60/047,503
OR FILING DATE: 1997-05-23
OR APPLICATION NUMBER: 60/047,503

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, 57 , 67 , 63	7,599 7,588 7,588 7,586 7,590 7,590 7,593	5,911 5,636 5,874 5,910 5,864 5,863 5,845 7,761	5,878 5,662 5,872 5,882 5,882 5,893 5,898

PRIOR APPLICATION NUMBER: 60/047,592
PRIOR PILLING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,581
PRIOR APPLICATION NUMBER: 60/047,581
PRIOR APPLICATION NUMBER: 60/047,581
PRIOR APPLICATION NUMBER: 60/047,584
PRIOR APPLICATION NUMBER: 60/047,587
PRIOR APPLICATION NUMBER: 60/047,582
PRIOR PILLING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,582
PRIOR PILLING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,632
PRIOR APPLICATION NUMBER: 60/043,580
PRIOR APPLICATION NUMBER: 60/043,511
PRIOR APPLICATION NUMBER: 60/043,511
PRIOR APPLICATION NUMBER: 60/043,311
PRIOR APPLICATION NUMBER: 60/043,671

OR APPLICATION NUMBER: 60/043,669
OR FILING DATE: 1997-04-11
OR APPLICATION NUMBER: 60/043,312
OR FILING DATE: 1997-04-11
OR APPLICATION NUMBER: 60/043,313
OR FILING DATE: 1997-04-11
OR APPLICATION NUMBER: 60/043,672
OR FILING DATE: 1997-04-11
OR APPLICATION NUMBER: 60/043,315
OR APPLICATION NUMBER: 60/048,974
OR APPLICATION NUMBER: 60/048,974
OR APPLICATION NUMBER: 60/056,886
OR FILING DATE: 1997-06-26
OR APPLICATION NUMBER: 60/056,877
OR APPLICATION NUMBER: 60/056,889
OR APPLICATION NUMBER: 60/056,889
OR APPLICATION NUMBER: 60/056,889
OR APPLICATION NUMBER: 60/056,889
OR APPLICATION NUMBER: 60/056,893
OR APPLICATION NUMBER: 60/056,630

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APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of p
FILE REFERENCE: 11000.1022c1
CURRENT APPLICATION NUMBER: US/10/219,220
CURRENT PILING DATE: 2002-08-14
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
PRIOR FILING DATE: 1999-06-04
UNUMBER OF SEQ ID NOS: 290
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 285
LENGTH: 373
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US-10-219-220-153
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          Sequence 153, Application US/10219220
Publication No. US20030082724A1
GEMERAL INFORMATION:
APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Geath and their use in the modification of plant development
FILE REFERENCE: 11000.1022c1
CURRENT APPLICATION NUMBER: US/10/219,220
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CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                             62.18;
Local Similarity 60.08;
nes 6; Conservation
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APPLICATION NUMBER: 60/057,669
FILING DATE: 1997-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/057,650 FILING DATE: 1997-09-05 APPLICATION NUMBER: 60/056,884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/056,908
FILLING DATE: 1997-08-22
APPLICATION NUMBER: 60/048,964
FILLING DATE: 1997-06-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,875
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    2002-08-14
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Pred. No.
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Pred. No. 1.8e+02;
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1.1e+02;
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APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Charles, Bussey
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 7154
LENGTH: 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SALAKI, TAMATORI APPLICANT: SALAKI, TOSHIYUKI APPLICANT: HATTORI, MASAHIRA TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UF 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: UF 2001-272697
PRIOR TILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13515
LENGTH: 1038
TYPE: PRT
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US-10-219-220-153
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US-10-156-761-13515
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; Sequence 7154, Application US/10032585
; Publication No. US20030180953A1
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PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 290
SOFTWARE: FBSESEQ for Windows Version 3.0
SEQ ID NO 153
LENGTH: 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 62.1%;
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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APPLICANT:
APPLICANT:
                                                                                                                                                                         APPLICANT: Terry, Roem
APPLICANT: Bo, Jiang
APPLICANT: Charles, E
APPLICANT: Howard, Bu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISBIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
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TYPE: PRT
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6; Conserve
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Pred. No. 5.2e
1; Mismatches
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Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 15; Length 1038;
5.2e+02;
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Best Local Similarity
Matches 6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-284-668-12
; Sequence 12, Application US/10284668
; Bublication No. US20030106100A1
; GENERAL INFORMATION:
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RESULT 11
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                                                                                                                       Matches
                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                            NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Agrevo-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEPHONE: 212-596-9090
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                     Local Similarity hes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/836,567

FILING DATE: 24-UUL-1997

APPLICATION NUMBER: PCT/EP95/04415

FILING DATE: 09-NOV-1995

APPLICATION NUMBER: DE 744 41 408.0

FILING DATE: 10-NOV-1994

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/284,668
FILING DATE: 29-Oct-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZIMES
INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                  45
                                                                                   2 GNSPKGF 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YGNSPKGF 8
                                                  GSSPKGF 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                            LENGTH: 1197 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kossmann, Jens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Springer, Franziska
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1251 Avenue of the Americas
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75.0%;
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Pred. No. 3.8e+02;
                                                                                                                                    Score 35; DB 15
Pred. No. 9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                        DB 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 521;
                                                                                                                                                      Length 1197;
                                                                                                                       Indels
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Sequence 12, Application US/09852870A
Patent No. US20020165132A1
GENERAL INFORMATION:
APPLICANT: Goodman, Murray
APPLICANT: Goodman, George
FITLE OF INVENTION: Lanthionin Bridged Proteins
FILE REFERENCE: LKR 9122-D
CURRENT APPLICATION NUMBER: US/09/852,870A
CURRENT APPLICATION NUMBER: US/09/852,870A
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/384,601
PRIOR FILING DATE: 1999-08-26
NUMBER OF SEQ ID NOS: 24
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US-09-738-626-4750
                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: Cys-Ser lanthionine bridge
US-09-852-870A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-852-870A-12
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APPLICANT: SENOH, AKHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION UMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UF/09/377484
PRIOR APPLICATION NUMBER: UF/09/377484
PRIOR APPLICATION NUMBER: UF/09/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UF/00/159162
PRIOR FILING DATE: 2000-04-07
                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.0 SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn ver.
SEQ ID NO 4750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4750, Application US/09738626 Publication No. US20020197605A1
                                                                           Matches
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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TYPE: PRT
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nes 5; Conserv
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3 FGNSPRG 9
                                   1 YGNSPKG 7
                                                                         Similarity
5; Conserv
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OCHIAI, KBIKO
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                                                                                        58.6%;
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                                                                                        Score 34; DB 10;
Pred. No. 5.8e+05;
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Pred. No. 9.5e+02;
                                                                           Mismatches
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es 0;
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APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
ITILE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129WO
CURRENT APPLICATION NUMBER: US/09/769,787
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: GB 9816337.1
PRIOR APPLICATION NUMBER: US 60/125164
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: US 60/125164
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 388
SOFTWARE: PATENTIN CHARTER: 284
TYPE: PRT
OFCANION: CHARTER CONTINUED: DETERMINE CHARTER CONTINUED: DRT
                     RESULT 15
US-10-272-419-18
Sequence 18, Application US/10272419
FUBLICATE 18, Application US/10272419
FUBLICATE 18, Application US/0030087403A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: THOMAS, STUART
APPLICANT: NACARAJAN, VASANTHA
TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
TITLE OF INVENTION: GITTERS TO THE PRODUCTION OF ADIPIC ACID AND
TITLE OF INVENTION: GITTERS TO THE PRODUCTION OF ADIPIC ACID AND
TITLE OF INVENTION: GITTERS TO THE PRODUCTION OF ADIPIC ACID AND
TITLE OF INVENTION: GITTERS TO THE PRODUCTION OF ADIPIC ACID AND
THE REFERENCE: CL1341-A
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US-09-769-787-40
US-09-769-787-40
Sequence 40, Application US/09769787
Publication No. US20030091577A1
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-953
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US-09-764-864-953
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Patent NO. US2002012753A1
GENERRAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 58.6%;
Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local &
CURRENT ARPLICATION NUMBER: US/10/272,419
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Search completed: November 7, 2003, 08:16:49 Job time: 10.7717 secs
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                                                                                                                                                                                       ; TYPE: PRT ; ORGANISM: Acinetobacter sp. US-10-272-419-18
                                                                                                                                                                                                                                   CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 09/252,553
PRIOR FILING DATE: 1999-02-19
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Microsoft Office 97
SEQ ID NO 18
LENGTH: 324
                                                                                                                           Matches
                                                                                                                                         Query Match
Best Local Similarity
                                                            : |:||||
31 FSNTPKGF 38
                                                                                           1 YGNSPKGF 8
                                                                                                                           Conservative
                                                                                                                                          58.6%;
62.5%;
                                                                                                                        ; Score 34; DB:
; Pred. No. 3.5e.
2; Mismatches
                                                                                                                                          DB 15;
3.5e+02;
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Result
No.
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
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Query
Match Length !
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Gapop 10.0 , Gapext 0.5
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58
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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YGNSPKGFAY 10
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                       US-09-149-476-696
US-09-152-991A-32215
US-09-252-991A-19973
US-09-252-991A-19973
US-09-325-932A-153
US-09-325-932A-153
US-09-325-991A-29391
US-08-866-542C-35
US-08-866-542C-35
US-08-866-542C-35
US-08-467-72C-12
US-08-467-72C-12
US-08-467-472C-12
US-08-467-472C-12
US-08-467-472C-12
US-08-467-472C-12
US-08-467-472C-12
US-08-467-472C-12
US-08-464-11
US-09-194-0844-11
US-09-194-084-11
US-09-194-084-11
US-09-198-452A-118
US-09-198-452A-118
US-09-198-452A-11
US-07-969-875A-27
US-08-441-507-13
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Sequence 32215, A
Sequence 19973, A
Sequence 153, App
Sequence 5402, Ap
Sequence 29391, A
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                                                12, Appl
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13, Appl
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6336, Ap
4138, Ap
21004, Ap
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21004, Appl
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US-08-639-237-2	US-09-107-532A-5048	US-09-134-078-16	US-09-277-078-2	US-09-252-991A-26771	US-07-969-875A-15	US-08-441-507-15	US-09-134-001C-5008	US-08-435-998-32	US-08-155-171B-32	US-07-969-875A-21	US-08-441-507-21	US-09-252-991A-30103	US-09-107-532A-3702	US-09-339-972-57	US-08-928-692-57	US-09-252-991A-31838	US-09-025-769B-16
Sequence 2, Appli	Sequence 5048, Ap	Sequence 16, Appl	Sequence 2, Appli	Sequence 26771, A		Sequence 15, Appl	Sequence 5008, Ap		Sequence 32, Appl		Sequence 21, Appl	Sequence 30103, A	Sequence 3702, Ap	Sequence 57, Appl	Sequence 57, Appl	Sequence 31838, A	Sequence 16, Appl

## ALIGNMENTS

88	US-09-149-4	76-696
	Patent No.	090, ADDIICACION 03/091494/0 ), 6420526
**	GENERAL	ORMATION:
	APPLICANT:	TIVENTION: 186 Himan Secreted proteins
~ ~	FILE REI	ERENCE: PZ002P1
••	I (73)	TION NUMBER: U
••	CURRENT	ILING DATE: 1998-09-08
٠.,	EARLIER	PPLICATION NUMBER: F
** **	BARLIER	APPLICATION NUMBER: 60/040,162
•	EARLIER	: 1997-03-07
٠.	EARLIER	PPLICATION NUMBER: 6
••	EARLIER	: 1997-03-07
**	KARLIKK	PPLICATION NUMBER: 6
	EARLIER	APPLICATION NUMBER: 60/040.626
•	EARLIER	: 1997-03-07
••	BARLIER	ATION NUMBER: 6
•	EARLIER	APPLICATION NUMBER: 60/040.336
••	EARLIER	: 1997-03-07
•••	EARLIER	NUMBER: 6
•••	EARLIER	APPLICATION NUMBER: 60/047,600
٠.	EARLIER	: 1997-05-23
٠,	BARLIER	ATION NUMBER: 6
•	EARLIER	: 1997-05-23
	BARLIER	FILING DATE: 1997-05-23
٠, .	BARLIER	ATION NUMBER: 6
••	EARLIER	: 1997-05-23
••	EARLIER	ATION NUMBER: 6
•	BARLIER	ADDITION NUMBER: 60/047 583
•	BARLIER	: 1997-05-23
••	EARLIER	ATION NUMBER: 6
	RARLIER	APPLICATION NIMBER: 60/047.618
٠	BARLIER	: 1997-05-23
~	BARLIER	ATION NUMBER: 6
•••	BARLIER	APPLICATION NUMBER: 60/047.592
•	EARLIER	1997-05-23
**	EARLIER	PPLICATION NUMBER: 6
• •	RAPI.TER	WIMBER - U
	EARLIER	FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 91
EARLIER APPLICATION NUMBER: 60/056, 636
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-06-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING

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PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32215
                                                                             ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-19973
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US-09-252-991A-32215
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US-09-252-991A-32215
                                                                                                                                                                                                                                                                                                                                                         Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J.
                                                                                                                                                   SEQ ID NO 19973
                                          Query Match
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                     APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 107
                                                                                                                  LENGTH: 149
TYPE: PRT
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       Local Similarity 66. es 6; Conservative
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WENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
WENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
NNCE: 107196.136
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                     62.1%;
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66.7%;
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   Score 36; DB 4;
Pred. No. 29;
1; Mismatches ;
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Pred. No.
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Pred. No.
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   Indels
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

FITIE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAF

FITIE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/064,799

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR PILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

LENGTH: 484

TYPE: PRT

COLUMN OF SECULO NOS: 5674
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APPLICANT: Lasham, Annette
FITTLE OF INVENTION: Compositions affecting p
FITLE OF INVENTION: Compositions affecting p
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 153
LENGTH: 396
TYPE: PRT
ORGANISM: Pinus radiata
                                                                                                                       RESULT 6
US-09-252-991A-29391
           GENERAL INFORMATION:
APPLICANT: MAIC J.
TITLE OF INVENTION:
TITLE OF INVENTION:
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US-09-325-932A-153
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                                                                                   Sequence 29391, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                            Query Match
Best Local
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Patent No. 6451604
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                                                                                                                                                                                                                                                                                          Local
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Rubenfield et al.
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDO
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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66.7%;
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Pred. No. 1e+02;
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Pred. No.
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the modification of forestry pla
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    Query Match
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                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/836,567
FILING DATE: 24-UUL-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/EP95/04415
FILING DATE: 09-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 41 408.0
FILING DATE: 10-NOV-1994
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                                                                                                                INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1197 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Pseudomonas aeruginosa
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MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC comparible
COMPUTER: LEM PC comparible
COMPUTER: PC-DOS/MS-DOS
COMPUTER: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Ag:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kossmann, Jens
APPLICANT: Springer, Franziska
APPLICANT: Abel, Gernot
                                                             COLECULE TYPE:
                                                                                                                                                                                                   TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 NAPKGFA 251
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                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08836567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                  212-596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FISH & NEAVE
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85.7%;
  60.3%;
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  Score 35;
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Pred. No. 1.5e+02
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US-08-968-542C-35; Sequence 35, Application US/08968542C; Patent No. 5981728
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Best Local Similarity
""" thes 6; Conserv
                                                                                                                 RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/09606304 Patent No. 6483010 GENERAL INFORMATION:
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Matches 6; Conserv
                       GENERAL INFORMATION:
APPLICANT: Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212-596-9090 INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
   APPLICANT: Myers,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION NUMBER: US/09/606,304
FILING DATE: 28-Jun-2000
CLASSIFICATION : CUnkmowns
PRIOR APPLICATION DATE: 08/836,567
FILING DATE: <Unkmowns
APPLICATION NUMBER: 08/836,567
FILING DATE: <Unkmowns
APPLICATION NUMBER: DE P 44 41 408.0
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: Agrevo-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
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TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRAN
PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
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ADDRESSEE: FISH & NEAVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1197 amino acids
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dull1 Codes For A No. 5981728el Starch
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1; Mismatches 0;
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DESCRIPTION: ami
HYPOTHETICAL: no
HYPOTHETICAL: no
HANTI-SENSE: no
FRAGMENT TYPE:
US-08-968-542C-35
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US-08-750-152A-2
                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08750152A Patent No. 5977331
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                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 1230 amino acid res
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                     APPLICANT: ABB. CHIZU
APPLICANT: KAWAHARA, YOSHIO
APPLICANT: NAKAMATSU, TSUYOSHI
TITLE OF INVENTION: ALPHA-KETOGLUTARATE DEHYDROGENASE GENE
                                                                                                                                                                                                                                                                               APPLICANT: ASAKURA, YOKO
APPLICANT: KIMURA, EIICHIRO
APPLICANT: ABE, CHIZU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D.,
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: 06036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft Word 6.0.1 for Macintosh CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/968,542C
FILING DATE: No. 5981728ember 12, 1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UMBER:
FILING DATE:
                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 floppy d.
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macinto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUMBER OF SEQUENCES:
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CTTY: Houston
TX
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                                                                                                                CITY: ARLINGTON
STATE: VA
                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 6; Conserv
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TOPOLOGY: linear
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ZIP: 7707:
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8011 Candle Lane
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ilarity 85.7%;
Conservative
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Pred. No. 4.2e+02;
1; Mismatches 0
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US-08-467-472C-12
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Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/742,
FILING DATE: 9-AUGUST-1991
APPLICATION NUMBER: US 08/021,
APPLICATION NUMBER: US 08/021,
APPLICATION NUMBER: US 08/021,
APPLICATION NUMBER: US 08/021,
APPLICATION NUMBER: 27, 224
REFERENCE/DOCKET NUMBER: 27, 224
REFERENCE/DOCKET NUMBER: LKR-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/08467472C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6028168
                                                                 TELEFAX: (212) 557-563
TELEX: NONE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1257 amino acids
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MEDIUM TYPE: 3.5" FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA: US/08/750,152A
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOPTWARE: ASCII
                                                                                                         TELEPHONE: (212) 557-5635
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/467,472C FILING DATE: 6-JUNE-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: NEW YORK
STATE: NY
                 rype: amino acid
ropology: linear
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                                                   ENGTH:
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VENTION: LANTHIONINE BRIDGED PEPTIDES
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Pred. No. 4.3e+02;
3; Mismatches 2
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Gaps

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DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES:
RELEVANT RESIDUES:
US-08-467-472C-12
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                                                            Matches
                                                                        Query Match
Best Local
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RELEVANT RESIDUES IN SEQ ID NO: 12:
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DESCRIPTION:
HYPOTHETICAL: 1
ANTI-SENSE: N/I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES MITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
FORTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE - ORIGINAL SOURCE: INC., ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE:
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DENTIFICATION METHOD:
                              1 YGNSPKG 7
                                                          Similarity 5; Conserv
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1990
FGNSPRG
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                                                                                                                                                                                                                                                                                                   TANDEM MASS SPECTROMETRY: PROCEEDINGS OF THE 11TH AMERICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : BIOPOLYMERS
JOHN WILEY AND SONS,
SUPPLEMENTARY
                                                                                                                                                                                                                            443 - 445
                                                                                                                                                                                                                                                                                                                                          IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
                                                          Conservative
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PE: INTERNAL
MINO P
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SYMPOSIUM
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                                                     Score 34; DB 3; Lo
Pred. No. 2.5e+05;
2; Mismatches 0;
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STRUCTURE
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RESULT 12

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US-09-384-061-12
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PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
PRELEVANT RESIDUES IN SEQ ID NO: :
PUBLICATION INFORMATION:
                                                                                                                                                                                                                     OTHER INFORMATION: wat OTHER INFORMATION: the OTHER INFORMATION: a - PUBLICATION INFORMATION AUTHORS: JUNG, GUNTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: GOODMA
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SEQUENCE CHARACTERISTICS:
LENGTH: 9
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FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE
ORIGINAL SOURCE: INC.,
ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
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APPLICATION NUMBER: U
FILING DATE:
APPLICATION NUMBER: U
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CURRENT APPLICATION DATA:
US/09/384,061
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MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
COMPUTER: MS-DOS Version 6.2
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 697-3355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 28-JANUARY-
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFFNER
                                                                                                                                                                                                                                                                                                                                                                        POSITION IN GENOME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 99 PARK
CITY: NEW YORK
STATE: NY
                                                                                                                                                   AUTHORS: JUNG, GUNTHEK
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
                                                                                                                                                                                                                                                                                                       IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESCRIPTION: PEPTIDE POTHETICAL: N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: AMINO ACID
TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                       NAME/KEY: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 27, REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NONE
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LANTHIONINE BRIDGED PEPTIDES
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                   CYS-SER
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COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASUSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
CLASSIFICATION HOME: 435
PRIOR APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 464, Application US/08858207A Patent No. 6348328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                 APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Knowles, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
ADDRESSES: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6348328
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
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FILING DATE:
FUBLICATION DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 12:
PUBLICATION INFORMATION:
FUTURE: IDENTIFICATION OF A THIOETHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES 1
RELEVANT RESIDUES 1
                                                                                                                                                                                                                                                     CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISSUE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YGNSPKG 7
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1986
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CHEMISTRY OF LANTHIONINE PEPTIDES
BIOPOLYMERS
JOHN WILEY AND SONS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TANDEM MASS SPECTROMETRY PROCEEDINGS OF THE 11TH
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; Pred. No. 2.5e+05;
commatches 0;
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STRUCTURE
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Best Local Similarity
Watches 6; Conserve
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                                                                                                                                                                                                                                                                                                                                            PCT-US94-00844-11
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                                                                                                       Sequence 18, Applica
Patent No. 6498242
GENERAL INFORMATION:
           APPLICANT: CHEN, QIONG
APPLICANT: THOMAS, STUART
APPLICANT: NAGARAJAN, VASANTHA
TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
TITLE OF INVENTION: INTERMEDIATES
                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Applicat GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 29-JAN-19
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION NUMBER: US/09/648,004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/010403
FILING DATE: 29-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/0084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEPHAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Method of Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 11
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                           TYPE: ami
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
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                                                                                                                                        Application US/09648004
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85.7%;
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Pred. No. 1.2e+02;
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Pred. No.
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49;
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CURRENT FILING DATE: 2000-04-25;
PRIOR APPLICATION NUMBER: 09/252,553
PRIOR FILING DATE: 1999-02-19;
NUMBER OF SEQ ID NOS: 32;
SOFTWARE: Microsoft Office 97
SEQ ID NO 18
LENGTH: 324
TYPE: PRT;
ORGANISM: Acinetobacter sp.
US-09-648-004-18

Query Match
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps O;

Qy 1 YGNSPKGF 8
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Db 31 FSNTPKGF 38

Search completed: November 7, 2003, 07:30:05
Job time: 2.46862 secs
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ALIGNMENTS

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hypothetical prote hypothetical prote zinc transporter: l probable RNA-bindi hypothetical prote conserved hypothetical prote chorion protein si Ig heavy chain v r hypothetical prote hypothetical prote hypothetical prote synaptophysin - hu probable exported single stranded D

B84745 T49963 D89798 S06612 S25047 E71334 AH2432 AH2432 AJ5699 AC0821 S56750

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB seq length: 0
DB seq length: 2000000000
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Query
Match
              US-09-661-992B-6
72
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pir2:*
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H32513
T04310
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PH1733
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                    glycine/tyrosine-r
glycine/tyrosine-r
Ig heavy chain V-r
Ig heavy chain V-r
Ig heavy chain pre
strong gravity str
RNA binding motif
matrix protein M1
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K-kininogen, LMW p
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Ig heavy chain V r
                                                                                                                                                                                                                                                                                                                                          hypothetical prote
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probable iron-sulf
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W.Alternate names: protein K10A8 130
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: T51469
R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata
submitted to the Protein Sequence Database, August 2000
A;Reference number: Z25394
A;Accession: T51469
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <SAT>
A;Cross-references: EMBL:AL391151
A,Experimental source: cultivar Columbia; BAC clone K10A8
C;Genetics:
                                                                                A;Cross-references: GB:AE005673; NID:gl3424664; PIDN:AAK24986.1; GSPDB:GN00148
C;Genetics:
                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-205 <STO>
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A;Introns: 97/1
A;Note: K10A8_130
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Best Local S
Matches 8
                                                           ;Genetics:
;Gene: CC3024
Query Match
Best Local Similarity
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es 8; Conservative
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69.4%;

score 50; DB; Pred. No. 0.84

d 2;

Length 173; Indels

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Gaps

0;

Result

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Score

65.3**%**; 70.0**%**;

Score 47; Pred. No.

DB 2; 3;

Length 205;

44444444444444444444444444444444444444

Minimum

Maximum

Database

Scoring table:

Sequence: Perfect score: Run on: OM protein -

Searched:

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C;Accession: C64757

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; E
R;Bose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: C64757
                                                                                     C;Superfamily: conserved hypothetical iron-sulfur protein HP0138; ferredoxin 2[4Fe-4S] C;Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein F;312,315,318,377/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted F;322,362,365,368/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                 A;Cross-references: GB:AE000137; GB:U00096; NID:g2367108; PIDN:AAC73410.1; PID:g1786498
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-475 < BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable iron-sulfur protein ykgF - Escherichia coli (strain K-12) C;Species: Escherichia coli (c;Species: Escherichia coli (c;Species: Escherichia coli (c;Species: L-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002 C;Accession: C64757
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R;Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

pela, D; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

Science 293, 668-672, 2001

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,

hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039, MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                   A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows, KAlman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: D95384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Genome: plasmid
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A;Residues: 1-456 <KUR>
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Best Local
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.bate: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
.Accession: D95384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: GB:AB006469; PIDN:AAK65638.1; PID:g14524124; GSPDB:GN00165
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       Similarity 77.8
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7; Conserva
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87.5%;
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77.8%;
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A;Accession: E85522
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A; Residues: 1-475 < HAY>
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CCHCYCSIY
              GGHGYGSSF
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hypothetical protein ECs0345 [imported] - Escherichia coli (strain 0157:H7, sub 

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Rasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Tille: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7

A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: A90672

A; Status: preliminary

A;Cross-references: GB:BA000007; PIDN:BAB33768.1; PID:gl3359802; (A;Experimental source: strain O157:H7, substrain RIMD 0509952 C;Genetics: A;Gene: ECs0345 C;Superfamily: conserved bypothetical iron-sulfur protein HP0138; GSPDB:GN00154

ferredoxin N

7; Conserv Conservative 61.1%; 77.8%; 1; Mismatches Score 44; Pred. No. Indels 0, Gaps

0

DВ

2

Length 475

hypothetical protein ykgF [imported] - C;Species: Escherichia coli Escherichia coli (strain O157:H7, substra

C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001 C;Accession: E85522

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001 × 0

A;Title: Genome sequence of enterohemorrhagic Escherichia A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Residues: 1-475 <STO> A;Cross-references: GB:AE005174; NID:g12513108; PIDN:AAG54641.1; A;Experimental source: strain O157:H7, substrain EDL933 GSPDB:GN00145;

conserved hypothetical iron-sulfur protein HP0138;

61.1%; 77.8%;

Score 44;

8

2;

Length 475

2

0

Gaps

0

Pred. No. 21; l; Mismatches

GGHGYGSSF 10

RESULT 7

B83824

Language Protein BH1397 [imported] - Bacillus halodurans (strain C-125)

Language Protein BH1397 [imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans

C;Acte: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001

C;Accession: B83824

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fi

N., Fuji,

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-235 <BEC>
                                                                                                                                                                                                                                                                                                                C;Accession. T33380
C;Rccession. T33380
C;Rccession. Expeler, N.
R;Beck, C.; Wamsley, P.; Keppler, N.
submitted to the EMBL Data Library, July 1998
A;Description: The sequence of C. elegans cost
A;Reference number: Z21333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein DKFZp586F0222.1 - human
C;Species: Homo sapiens (man)
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
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A;Molecule type: DNA
A;Residues: 1-35 <STO>
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Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MVID:20512582; PMID:11058132
A;Accession: E83824
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A;Residues: 1-215 <KOE>
A;Cross-references: EMBL:AL117395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: Z18722
A;Accession: T17207
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A;Experimental source: strain C-125
                                                                                          A; Introns: 35/1; 79/1; 128/1
                                                                                                                A;Map position: X
                                                                                                                                   A; Gene: CESP: H22Kll.3
                                                                                                                                                                               A; Experimental source: strain Bristol N2;
                                                                                                                                                                                                       A;Cross-references: EMBL:AF077544; PIDN:AAC64619.1; GSPDB:GN00028; CESP:H22K11.3
                                                                                                                                                                                                                                                                                               A; Accession: T33380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein H22K11.3 - Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Species: Caenorhabditis elegans
;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
                                           Query Match
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Local Similarity 77.8%;
les 7; Conservation
Local Similarity
res 7; Conserv
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mes 7; Conserv
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    Conservative
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Pred. No. 14;
1; Mismatches
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                     Score 43; DB 2; Length 235;
Pred. No. 15;
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Pred. No. 2.2;
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    Mismatches
                                                                                                                                                                                 clone H22K11
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C;Accession: T02661
R;Kim, C.Y.; Cheon, S.Y.; Jeong, S.Y.; Cheong, Y.H.; Han, C.D.; Cho, M.J.
Submitted to the EMBL. Jata Library, December 1997
                submitted to the EMBL Data Library, January 1996
A;Description: The sequence of C. elegans cosmid C54D1.
A;Reference number: Z20527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-390 <BEV>
A;Cross-references: EMBL:AL163814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lysophospholipase-like protein - Arabidopsis thaliana
N;Alternate names: protein T22P220
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
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C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
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A; Accession: T28808
                                                                                                     hypothetical protein C54D1.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000 C;Accession: T28808
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A; Introns: 127/2; 140/2; 164/1; 185/3; 215/3; 246/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
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A;Accession: T48524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession:
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A; Residues: 1-304 < KIM>
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A; Accession: T02661
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Pred. No.
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A;Molecule type: DNA
A;Residues: 1-702 <CLA>
A;Residues: 1-702 <CLA>
A;Residues: 1-702 <CLA>
A;CCAS: references: EMBL:L22015; NID:g1339990; PIDN:AAC04962.1; PID:g349754; MIPS:YAR01.
R;Davies, C.J.; Hutchison III, C.A.
Wucleic Acids Res. 19, 5731-5738, 1991
Willeic Acids Res. 19, 5731-5738, 1991
A;Title: A directed DNA sequencing strategy based upon Tn3 transposon mutagenesis: appl.
A;Reference number: S20121; MUID:92051323; PMID:1658741
A;Accession: S20121
A;Molecule type: DNA
A;Residues: 1-142 <DAV>
A;Cross-references: EMBI
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                C;Accession: $40904; $20121
R;Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Fortin, N.; Zeng, B.; Delaney, submitted to the SMBL Data Library, November 1993
                                                                                                                                                                                                                                                                                                                                     A;Description: Sequencing of chromosome I of Saccharomyces cerevisiae: Analysis of the A;Reference number: $40891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUN2 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YAR014c
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A/Molecule type: DNA
A/Residues: 1-492 <STO>
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A;Accession: A84863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable carboxyphosphonoenolpyruvate mutase [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A84863
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A;Cross-references: EMBL:U46673; PIDN:AAC48153.1; GSPDB:GN00028; CESP:C54D1.3
A;Experimental source: strain Bristol N2; clone C54D1
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A;Introns: 44/1; 121/3; 145/3; 191/3; 250/1; 291/2; 330/3; 393/2; 483/2; 557/2; 603/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: CESP:C54D1.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Saccharomyces cerevisiae
;Date: 13-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics:
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Best Local
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54.5%;
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Pred. No. 1.1e+02;
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Search completed: November Job time: 4.65407 secs

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R;MCHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V. J. Exp. Med. 178, 295-307, 1993
A;Title: Antigen-driven B cell differentiation in vivo.
A;Reference number: PH1875; MUID:93301607; PMID:8315385
A;Recession: PH133
A;Recession: PH133
A;Mclecule type: mRNA
A;Residues: 1-25 <MCH>
A;Residues: 1-25 <MCH>
A;Experimental source: B cell
A;Note: the authors translated the codon ACA for residue 13 as Ala C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: beterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                         Ig heavy chain V region (clone GCC-13) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1733
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PH1733
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A;Cross-references: SGD:S0000069
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YGSSFDY 25
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                                                            100.0%; F1
                                                              55.6%; Score 40; DB
100.0%; Pred. No. 4.
tive 0; Mismatches
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Pred. No. 95;
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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
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P27637
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P36702
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P092334
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P07522
P34407
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       2 methanococc
7 stachybotry
1 escherichia
2 dioscorea j
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5 escherichia
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9 bacillus su
1 drosophila
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7 oryctolagus
8 ovis aries
2 homo sapien
7 oryza sativ
6 mus musculu
9 homo sapien
9 sonchus yel
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       RESULT 1
YKGF_ECOLI
ID YKGF_ECOLI
AC P77536;
                                                                      EMBL; AE000137; AAC73410.1; -.
EMBL; U73857; AAB18034.1; -.
PII; C64757; C64757.
Ecodene; EG13583; ykgF.
InterPro; IPR001450; 4fe4S ferredoxin.
InterPro; IPR001452; Fe S_binding.
InterPro; IPR001452; Fe S_binding.
Pfam; PF00037; fer4; 2.
TICRFAMB; TICR00273; TIGR00273; 1.
PROSITE; PS00198; 4FE4S FERREDOXIN; 2.
Hypothetical protein; Electron transpo
     Complete
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                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

DUNCAN M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis Pederspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.

-i- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF 'BACTERIAL-TYPE' 4FB-4S FERREDOXINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ul-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Putative electron transport protein ykgf,
YKGF OR B0307.
Escherich
                                                                                                                                                                                                                                                                                                                                                                                                           Science
                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
Enterobacteriaceae; Eschei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
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  IRON-SULFUR
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YAKG SCHPO
CH38_DROME
RO31_XENLA
RO32_XENLA
K1CQ_HUMAN
KNOB_PLAFA
K1CJ_BOVIN
HLY HAL17
PICF_PSESR
K1CJ_HUMAN
VP1_BPCHP
                                                                          transport;
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Q04695
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5 homo sapien
7 plasmodium
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Result No.

Query Match

Length

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YKGF BCOLI
ROH3-HUMAN
YA14 YEAST
KRHA, RABIT
KRHA, SHEBF
HYJK HUMAN
GRA1 OKYSA
RBM3-HUMAN
RRPP SYNV
Y355-TREPP
ROVIN
NAHH MICVI
YUML BACSU
RX DROMB
DMPI BOVIN
RAFI
CAMBL
CHIG DROMB
SYPH BOVIN
RYPH SOVIN
RYPH SOVIN
RYPH SOVIN
SYPH MOUSE
Y209-METUA
SYPH MOUSE
Y217-METUA
RYPH MOUSE
Y218-STACH
PHSG BCOLI
CHIT DIOJA
PHK STRCO
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Post-processing: Minimum Match 0% Maximum Match 100 Listing first 45

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SwissProt 41:\*

Minimum DB Maximum DB

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length:

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Total number of hits satisfying chosen parameters:

127863 seqs, 47026705 residues

Scoring table:

BLOSUM62 Gapop 10.0 ,

Gapext 0.5

Title: Perfect score:

US-09-661-992B-6 72

DGGHGYGSSFDY 12

Sequence:

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GenCore version Copyright (c) 1993 - 2003

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RESULT ROHS HIT ID DE LE RESULT ROHS HIT ID DE LE RESULT 
                                                                     RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschall S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hesleh F.,

RA Histchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RI Histoneko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Histoneko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Histoneko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Histoneko L., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Hownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Wullahy S.J.,

RA Brownstein M.J., Wackernan K.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Wassa K.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Bulkes J., Wassa M.A.,

Ra Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Wassa R.A.,

Ra Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Bulkes J., Kalan R., Kalan R., Schen J., Lu X., Gibbs R.A.,

Ra Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Bulkes J., Wassa R.A.,

Ra Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Bulkes J., Wassa R.A.,

Ra Richards S., Wassa R.A., Kalan R., Schen R., J., Wassa R.A.,

Ra Richards S., Wassa R.A., Malek J., Wassa R.A.,

Ra Richards S., Wassa R.A., Malek J., Wassa R.A.,

Ra Richards S., Wassa R.A., Malek
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Best Local :
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P31942; Q98EX1; Q9NP53; Q9NP96; Q9NPA7; Q9NPI4; Q9UFU4
01-JUL-1993 (Rel. 26, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3)
              SEQUENCE OF 94-104 AND 288-298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              multiply spliced gene.";
Biochim. Biophys. Acta 1492:108-119(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1; 2; MEDLINE=20461765; PubMed=10858537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Relation with splicing and early heat J. Biol. Chem. 272:1827-1836(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fuchs J.-P.; "Cloning of human 2H9 heterogeneous nuclear ribonucleoproteins." "Cloning of human 2H9 heterogeneous nuclear ribonucleoproteins are contained and early heat shock-induced splicing are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97153147;
Mahe D., Mahl P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Uterus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 137-346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The hnRNP 2H9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ionore
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGHGYGSIY 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SEP-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGHGYGSSF
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368
372
475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene, which is involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD; PRT; 346 AA.
Q9NE53; Q9NE96; Q9NEA7; Q9NEI4; Q9UFU4; Q9Y4J5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A. (ISOFORM 1), AN
; PubMed=8999868;
, Gattoni R., Fisc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368
368
372
53052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
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77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mewes H.-W., Gassenhuber J., Wiemann
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W.
                                                    99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IRON-SULFUR 2 (4FE-4S) (B)
IRON-SULFUR 2 (4FE-4S) (B)
IRON-SULFUR 1 (4FE-4S) (B)
682429D387336F72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fischer N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; 4; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the splicing reaction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mattei M.-G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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(BY SIMILARITY).
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ARTHMAN,
InterProj IPRUVVVI
InterProj IPRUVVVI
Pfam; P900076; xrm; 2.
PROSITE; P950102; RRM; 2.
PROSITE; P9501030; RRM RNP_1; FALSE NEG.
PROSITE; P900030; RRM, PALSE NEG.
PROSITE; P900030; RRM; PALSE NEG.
PROSITE; P900030; PROSITE; PROSI
            VARSPLIC
                                                                    VARSPLIC
                                                                                                                             VARSPLIC
                                                                                                                                                                                  VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:5043; HNRPH3.
GK; P31942; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC004511;
PIR; T17207; T1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Microsequences of 145 proteins recorded in the two-dimensional protein database of normal human epidermal keratinocytes.";

Electrophoresis 13:960-969 (1992)
-1- FUNCTION: Involved in the splicing process and participates early heat shock-induced splicing arrest. Due to their great structural variations the different isoforms may possess diffunctions in the splicing reaction.
-1- SUBCELLULAR LOCATION: Nuclear.
-1- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tana,
                                                                                                                                                                                                                                                 /ARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Keratinocytes;
MEDLINE=93162043; PubMed=1286667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=5; Synonyms=2H9D;
IsoId=31942-5; Sequence=VSP_005839, VSP_005843, VSP_005844;
Name=6; Synonyms=2H9E;
IsoId=311942-6; Sequence=VSP_005841, VSP_005842, VSP_005843,
VSP_005844;
SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P31942-3; Sequence=VSP_005838;
Name=4; Synonyms=2H9C;
IsoId=P31942-4; Sequence=VSP_005839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=2; Synonyms=2H9A;
IsoId=P31942-2; Sequ
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      138
                                                                                                                                                                                                                                                                    195
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                                                                                                                                                                                                                                           344
270
49
                                                           137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               splicing; Named isoforms=6;
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/FTId=VSP 005840.
Missing (in isofo
                                                                                                                                                   Missing (in isoform 4 and /FTId=VSP_005839.
                                  /FTId=VSP
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                                                                                                                                                                                                                                                                    GLY-RICH.
RNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M., Gesser B.,
      P_005841
      MCFSLNYT
                                                        isoform 6).
                                                                                                                    isoform 2)
                                                                                                                                                                                                                                 isoform 3).
                                                                                                                                                                                                                                                                    (RRM)
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   ar)
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   isoform
                                                                                                                                                                            isoform
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RESULT 3

YAI4 YEAST STANDARD; PRT; 702 AA.

ID YAI4 YEAST STANDARD; PRT; 702 AA.

AC P27637;

DT 01-EMB-1992 (Rel. 23, Created)

DT 01-EMB-1995 (Rel. 31, Last sequence update)

DT 28-EBB-2003 (Rel. 41, Last annotation update)

DE Hypothetical 78.3 kDa protein in SEN34-ADE1 intergenic region.

GN YARO14C OR FUN2.
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                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92051323; PubMed=1658741;
Davies C.J., Hutchison C.A. III;
"A directed DNA sequencing strategy based upon Tn3 transposon mutagenesis: application to the ADEI locus on Saccharomyces cerevisiae chromosome I.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-S288c / AB972;
MEDLINE-95028152; PubMed=7941740;
Clark M.W., Keng T., Storms R.K., Zhong W., Fortin N., Zeng B.,
Delaney S., Ouellette B.F.F., Barton A.B., Kabaok D.B., Bussey H.;
"Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of
the 42 kbp_SP07-CENI_CDC15 region.";
Hypothetical protein; SH3 domain.
DOMAIN 259 320
                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EWEL outstatis the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                  GO; GO:0005935; C:bud neck; IDA.
GO; GO:0005934; C:bud tip; IDA.
GO; GO:0000131; C:incipient bud site; IDA.
GO; GO:0000282; P:bud site selection; IMP.
GO; GO:0030447; P:filamentous growth; IMP.
                                                                                                                                                                                PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
                                                      InterPro; IPR001452; SH3. 
Pfam; PF00018; SH3; 1. 
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                              EMBL; L22015; AAC04962.1; -.
EMBL; M67445; AAA34397.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-142 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yeast 10:535-541(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                $40904; $40904.
$0000069; BUD14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 GGHGÝGGAGD 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N
                                                                                                                                                                                                                                                                                                                                                                                                  Acids Res. 19:5731-5738(1991).
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KRHA SHEEP STANDARD;
Q02958;
Q1-JUN-1994 (Rel. 29, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93179467; PubMed=7680040; Repline A., Powell B.C., Rogers G.E.; Fratini A., Powell B.C., Rogers G.E.; "Sequence, expression, and evolutionary conservation of a gene encoding a glycine/tyrosine-rich keratin-associated protein of encoding a glycine-rich keratin-associated protein a glycine-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
MCBI_TaxID=9986;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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SUCH AS WOOL AND HAIR CONSIST OF MICROFIERIES EMBEDDED IN A RIGID
MATRIX OF OTHER PROTEINS. THE MATRIX EMPOTEINS INCLUDE THE HIGH-
SULFUR AND GLYCINE/TYROSINE-RICH PROTEINS, HAVING MOLECULAR
WEIGHTS OF 6-20 KDa WHEREAS THE MICROFIERIES CONTAIN THE LARGER,
LOW-SULFUR PROTEINS (40-56 KDa).
DEVELOPMENTAL STAGE: KAP6 PROTEINS ARE FIRST EXPRESSED IN
DIFFERENTIATING HAIR SHAFT KERATINOCYTES A CONSIDERABLE DISTANCE
ABOVE THE PROLIFERATIVE ZONE OF THE FOLLICLE BULB.
SIMILARITY: BELONGS TO THE KAP6 GLYCINE/TYROSINE-RICH TYPE II
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Pred. No. 57;
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Pred. No. 8.7;
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Fratini A., Powell B.C., Rogers G.E.;
"Sequence, expression, and evolutionary conservation of a gene encoding a glycine/tyrosine-rich keratin-associated protein of hair.";
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Mammalia; Eutheria; Ceta
Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
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28-FEB-2003 (Rel. 41, Last annotation update)
28-FE 11, glycine/tyrosine-rich of hair.
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Ann. N.Y. Acad. Sci. 642:64-81(1991)
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DEVELOPMENTAL STAGE: THE KAP6 FOOTEINS ARE FIRST EXPRESSED IN DIFFERENTIATING HAIR SHAFT KERATINOCYTES, A CONSIDERABLE DISTANCE ABOVE THE PROLIFERATIVE ZONE OF THE FOLLICLE BULB.

SIMILARITY: BELONGS TO THE KAP6 GLYCINE/TYROSINE-RICH TYPE II
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TURN
STRAND
HELLX
STRAND
TURN
STRAND
                                                                                                                                                                                                                                                                                                                                      Immunoglobulin '
DOMAIN 1
DOMAIN 1
MOD_RES 1
DISULFID 22
DISULFID 105
                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.8 g
                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00396; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Mol. Biol. 141:369-391(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marquart M., Deisenhofer J., Huber R., Palm W.; "Crystallographic refinement and atomic models of the intact immunoglobulin molecule Kol and its antigen-binding fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.; "Three-dimensional structure determination of antibodies. structure of crystallized monoclonal immunoglobulin IgG1 F. Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A02055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=81072295; PubMed=7441755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=83289131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2FB4; 12-JUL-89.
2IG2; 12-JUL-89.
99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .0-A resolution."
                                                                                                                                                                                                                                                                                                                                                               M00400;
; PS50835; lo
lin V region;
112
                                     Similarity
7; Conser
DGGHGFCSS
                 DECHCYCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND DISULFIDE BONDS
                                                                             126
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIHUKT.
                                                                                                                                                                       66
68
74
78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=6884994;
                                                                                                                                                                                                                                                                                                                                                                                       IG_LIKE;
                  φ
                                                                                                                    13718 MW;
                                             55.6%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                           3D-structure; Pyrrolidone carboxylic
                                                                                                                                                                                                                                                                                                                                                                                       ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunoglobulin-like domain
                                    Score 40; DB
Pred. No. 14;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                        PYRROLIDONE CARBOXYLIC ACID
                                                                           E4D71B52B16F8776 CRC64;
                                                       ļ.
                                                       Length 126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primary KOL, I.";
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                                   Gaps
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RESULT 7

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RESULT 8
REM3 MOUSE
ID REM3
AC 0896
DT 15-J
DT 15-J
DT 28-F
DE Puta
GN REM3
OC Buta
GN REM3
CO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           용
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
MEDLINE=21463050; PubMed=11470798; Chappell S.A., Owens G.C., Mauro V.P.; Pader of Rbm3, a cold stress-induced mRNA, mediates internal initiation of translation with increased efficiency under condition of mild hypothermia.", J. Biol. Chem. 276:36917-36922(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RBM3_MOUSE STANDARD; PRT; 153 AA.

089086;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative RNA-binding protein 3 (RNA binding motif protein 3).
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Danno S., Matsuda T., Fujita J.;

"Isolation and characterization of mouse rbm3
"Submitted (JUL-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Gravity specific protein GSC 233.
01-yza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Emrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kwon S., Kikuchi S., Oono K.;

"Molecular cloning and characterization of gravity specific rice (Oryza sativa L.) suspension callus.";

Upn. J. Genet. 67:335-348(1922).

-i- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN CALLUS.

-i- INDUCTION: BY GRAVITY STRESS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRA1
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MEDLINE=93199820; PubMe
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                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rođentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15563 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A1C302F1988AC864 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ed. No. 16;
Mismatches
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                                    efficiency under conditions
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Best Local
Strausberg R.L., Feligold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.K.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.
Stapleton M., J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RBM3 HUMAN
P98179;
01-OCT-1996
01-OCT-1996
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                           RBM3 OK KNEL.
Homo sapiens (Human).
Metazoa; Chordata;
                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Placenta;
                                                                                                                                                                                                                                                                                           "RBM3, a novel human gene in Xp11.23 with a domain.";
                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-S-SEP-2003 (Rel. 42, Last annotation update)
Putative_NNA-binding protein 3 (RNA binding m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
                                                                                                                                                  MRDLINE=22388257; PubMed=12477932;
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                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=96177665;
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                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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InterPro; IPR000504; RNJ
Pfam; PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BMBL; AB016424; BAA32060.1; -.
EMBL; AY052560; AAL10707.1; -.
HSSP; P09651; IHA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the Buropean Bioinformatics Institute. There are no rest
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1;
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                                                                                                                                                                                                            lechschmidt K., Nya
bindl A., Rosenthal
ibmitted (OCT-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 RNA recognition motif (RRM)
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7; Conserv
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GYGYGRSRDY
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88
153 AA;
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                                                                                                                                                                                                                                  Nyakatura G.,
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145 G
; 16605 MW;
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70.0%;
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GLY-RICH.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                 Strom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C54A66A1A9E4FF3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                T.M., Drescher B., Menzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157
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17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                   putative RNA-binding
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                                                                                                                                                                                                         databases
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                                                                   Scheetz T.E.,
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 3) (RNPL)

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                S.W.
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RESULT 10

REP SYNV

RRPP SYNV

STANDARD; PRT; 286 AA.

AC 22129;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE RNA polymerase alpha subunit (EC 2.7.7.48) (Nonstructural protein) (M1
DE phosphoprotein).

GN M1.

OC Viruses; SSRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Nucleorhabdovirus.

OC Viruses; SSRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Nucleorhabdovirus.

NCBI_TaxID=11307;
RN [1]
RP SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
STRAIN=91021022; PubMed=2219720;
RX MEDLINE=91021022; PubMed=2219720;
RA Hilman B.I., Heaton L.A., Hunter B.G., Modrell B., Jackson A.O.;
RX MEDLINE=91021022; PubMed=2219720;
RA Hilman B.I., Heaton L.A., Hunter B.G., Modrell B., Jackson A.O.;
RY Virus.";
PUTTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE CC -:- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE CC -:- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
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Best Local
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SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U28686; AAB17212.1; -.
EMBL; AF196969; AAF06803.1; -.
EMBL; BC006825; AAF06825.1; -.
EMBL; BC006825; G01859.
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'''Μις'
''Γ.
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88
157 AA;
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149 G
17170 MW;
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70.0%;
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GLY-RICH.
; 91C12E2A3E32CFA4 CRC64;
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Pred. No.
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RESULT 11

Y359 TREEP

ID Y359 AC 08337

PT 16-00

PT 16
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Best Local S
Matches 6
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Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDINE-9832770; PubMed=9665876;
MEDINE-98332770; PubMed=9665876;
Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.
McDonald L., Artiach P., Bowman C., Cotton M.D., Pujii C., Garland
McDonald L., Artiach P., Bowman C., Sandusky M., Weidman J., Smith H.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y359 TREPA
083378;
16-0CT-2001
16-0CT-2001
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                                                                                                                                                                                                          Hypothetical SEQUENCE 2
                                                                                                                                                                                                                                                            EMBL; AE001215; AAC65354.1; -. PIR; E71334; E71334. TIGR; TP0359; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 281:375-388(1998).
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Bacteria; Spirochaetes;
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286 AA; 31775 MW;
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EMBL; M35689; AAA47897.1; -.
PIR; A45350; A45350.
Transferase; RNA-directed RNA polymerase; Phosphorylation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of Treponema pallidum, the syphilis
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114 GGHGWHTSLDH
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211 AA; 23888 MW; 91FFE8824C630327 CRC64;
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(Rel. 40, Last sequence up
(Rel. 40, Last annotation
                                                                                                   Conservative
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124
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85.7%;
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Pred. No. 34;
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                                                                                                                                                DB 1; Length 211;
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RESULT 12
SYPH_HUMAN
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D'Urso M., Craig I.W.;
"Sequence-based exon prediction around the synaptophysin locus
"Sequence-based exon prediction around the synaptophysin locus
"Sequence-based exon prediction around the synaptophysin locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oezcellk T., Lafreniere R.G., Archer B.T. III, Johnston P.A., Willard H.F., Francke U., Suedhof T.C.; "Synaptophysin: structure of the human gene and assignment to the X chromosome in man and mouse."; Am. J. Hum. Genet. 47:551-561(1990).
                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
MIM; 313475; -.
GO; GO:0030285; C:integral to synaptic vesicle membrane; NAS
InterPro; IPR001285; Synaptophysin.
                                                                                  EMBL; X06389; CAA29686.1; -.
EMBL; U93305; AAB92358.1; -.
PIR; A35699; A35699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-88067787; FubMed-3120152;
Suedhof T.C., Lottspeich F., Greengard P.,
"The cDNA and derived amino acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1988 (Rel. 08, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Synaptophysin (Major synaptic vesicle protein P38).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYPH HUMAN
P08247;
                                                                Genew; HGNC:11506; SYP.

    -!- SUBUNIT: HOMOHEXAMER OR HOMOTETRAMER.
    -!- SUBCELLULAR LOCATION: Integral membrane protein. Synaptic

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomics 45:340-347(1997).
-!- FUNCTION: POSSIBLY INVOLVED IN STRUCTURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synaptophysin."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98008923; PubMed=9344658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 15:9607-9607(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                 DOMAIN: THE CALCIUM-BINDING ACTIVITY IS THOUGHT TO BE LOCALIZED IN THE CYTOPLASMIC TAIL OF THE PROTEIN.

SIMILARITY: HIGHLY CONSERVED FROM CARTILAGENOUS FISH TO HUMANS; NO HOMOLOGY IS FOUND TO OFHER KNOWN CALCIUM-BINDING PROTEINS. THE GLYCINB-RICH DOMAIN SHOWS SIMILARITY TO TYPE I AND II CYTOSKELETAL KERATIN AND BOVINE CARTILAGE ALPHA 1 (11) CHAIN.

SIMILARITY: MEMBER OF THE SYNAPTOPHYSIN/SYNAPTOEREVIN CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: CHARACTERISTIC OF A TYPE OF SMALL (30-80 NM) NEUROSECRETORY VESICLES, INCLUDING PRESYNAPTIC VESICLES, BUT ALS VESICLES OF VARIOUS NEUROENDOCRINE CELLS OF BOTH NEURONAL AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER MEMBRANE COMPONENTS OR IN TARGETING PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                                                                 PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPITHELIAL PHENOTYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mehl E., Jahn R.;
for rat and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE VESICLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTIONS AS ORGANIZING
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                                       Matches
                                                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VPAP PRVKA
P36702;
                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                 "Cloning, sequencing, and functional characterization of the two submits of the pseudorables virus DNA polymerase holoenzyme: evidence for specificity of interaction.";

J. Virol. 69:2811-2818(1995).

-I- PUNCTION: ACCESSORY SUBUNIT OF THE DNA POLYMERASE THAT ACTS TO INCREASE THE PROCESSIVITY OF POLYMERIZATION (BY SIMILARITY).
                                                                                         Pfam; PF0228Z; UL42; 2.
DNA-binding; DNA replication.
SEQUENCE 384 AA; 40305 MW;
                                                                                                                                                                                                                                                                                                                                                                                             Berthomme H., Monahan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudorabies virus (strain Kaplan) (PRV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994 (Rel. 29, Last sequence update) 01-OCT-1996 (Rel. 34, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nerve; Synaptosome; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Calcium-binding; Synapse; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00220; SYNAPTOPHYSN. PROSITE; PS00604; SYNAPTOP; 1.
                                                                                                                                                  EMBL; M94355; AAA74384.1; -.
                                                                                                                                                                                                                                                                                                                                                                                      Epstein A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=33703;
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                                                                                                                                                                                                                                                                                      -!- SIMILARITY: TO OTHER HERPESVIRUSES POLYMERASE ACCESSORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95222727; PubMed=7707503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIAMOO
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                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymerase processivity factor (UL42 homolog).
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              1 DGGHGYGSSF 10
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                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGSGYGPQGDY 295
IPR003202; UL42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 AA;
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 29, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26
50
107
131
138
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130
137
141
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223
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305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.2%;
                                                   54.2%; Score 39; DB 60.0%; Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                S.J., Parris D.S., Jacquemont B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEATS, GLY-RICH.
N-LINKED (GLCNAC. . .) (POTENTIAL).
; 592289C43B12EFA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39; DB
Pred. No. 51;
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VESICULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
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                                                                                            FFAC3EF0C1984936 CRC64;
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                                                                DB 1; Length 384;
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                                      Indels
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DMPI BOVIN STANDARD; PRT; 510 MA.

Q95120;
Q95120;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Dentin matrix acidic phosphoprotein 1 precursor (Dentin matrix
                                                                                                              BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            melanogaster.";
J. Cell Biol. 116:257-269(1992).
J. Cell Biol. 116:257-269(1992).
J. Cell Biol. 116:257-269(1992).
J. Cell Biol. 116:257-269(1992).
J. Cell Biol. 1018 SCONCENTRATION OF RIBONUCLEOSOMES. COULD NEEDED TO ORGANIZE A CONCENTRATION GRADIENT OF A DORSALIZING MORPHOGEN (DM) ORIGINATING IN THE GERMINAL VESICLE.
J. SUBCELLULAR LOCATION: NUCLEAR AND/OR CYTOPLASMIC.
J. SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DROME
RB27 DROME
P48809;
01-FEB-1996
                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                     GO; GO:0005654; C:nucleoplasm; IDA.
GO; GO:0030529; C:ribonucleoprotein complex; IDA.
InterPro; IPR000504; RNA_rec_mot.
pfam; pF00076; rrm; 2.
SNART; SN00360; RRM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X62639; CAA44505.1; -. PIR; D41732; D41732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (Some send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Canton-8; TISSUB=Embryo,
MEDLINE=92112968; PubMed=1730754;
Matunis E.L., Matunis M.J., Dreyfuss
"Characterization of the major hnRNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0004838; Hrb27C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P09651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heterogeneous nuclear ribonucleoprotein
HRB27C OR HRP48.
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                                                                                                                                                                                                                                  6; Conserv
                                                                                                                                                                          GYGSGYDY 347
                                                                                                                                                                                           GYGSSFDY 12
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385 AA;
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                                                                                                                                                                                                                                                                                              41030 MW;
                                                                                                                                                                                                                                               54.2%;
75.0%;
                                                                                                                                                                                                                                 Score 39; DB
Pred. No. 63;
1; Mismatches
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                                                                                                                                                                                                                                                                                           RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
7543E50FA96C9D4E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                              DB 1; Length 385;
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Search completed: November Job time: 2,86515 secs

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Matches 7
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CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                    phosphoprotein gene.";

J. Dent. Res. 76:754-760(1997).

-i- FUNCTION: COULD BE INVOLVED IN THE INDUCTION OF MINERALIZATION EXTRACELLULAR MATRIX AND IN DENTINOCENESIS.

-i- TISSUB SPECIFICITY: EXPRESSED IN FETAL BRAIN, BONE AND TOOTH PARTICULARLY IN ODONTOBLAST, BUT NOT IN AMELOBLAST. NOT EXPRESS
                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Cei
Bovidae; Bovinae; Bos.
NCBI TaxID=9913;
                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                    Extracellular
                                                                                                                                                                                                                                                  EMBL; U47636; AAB09412.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hirst K.L., Ibaraki-O'Connor K., Young M.F., Dixon M.J.; "Cloning and expression analysis of the bovine dentin matrix acidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hirst K.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97263952; PubMed=9109824;
                                                                                                                                                                                                                                                                                                                                                                                               IN LIVER AND SKIN.
201
                                                      7; Conserv
DSSHGDGSEFD
                           DGGHGYGSSFD
                                                                                                                510 AA;
                                                                                                                                                          17
351
370
427
                                                       Conservative
                                                                                                                                                                                                                                   matrix;
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$10
351
370
427
464
366
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                                                                                                                55491 MW;
                          11
                                                                     54.2%;
211
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                                                                                                                                                         DENTIN MATRIX ACIDIC PHOSPHOPROTEIN
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                       Score 39;
Pred. No.
                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                9BFA9A74F6450865 CRC64;
                                                       Mismatches
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                                                      .<u>4</u>.
                                                                                   Length 510;
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                                                                                                                                         (POTENTIAL).
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein -
                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                          Score
                                      protein search, using
                                                                                                                                                                                                                                                                                                                SPTREMBL 23:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungd:*
4: sp_numan:*
5: sp_invexteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel:
9: sp_organel:
9: sp_plant:*
11: sp_rodent:
11: sp_vexteb:
12: sp_vixus:*
13: sp_vexteb:
14: sp_unclass
15: sp_vacheap
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2003 Compugen Ltd.
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sp_virus:*
sp_urclassified:*
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       Q91f59 arabidopsis
Q9a419 caulobacter
Q40925 kaposi's sa
P88917 kaposi's sa
P88917 kaposi's sa
Q98139 kaposi's sa
Q98199 ixodes rici
Q8xih9 clostridum
Q8x651 oryza sativ
Q925h2 mus musculu
Q93wz6 prunus pers
Q50000 prunus arme
Q8iqe1 drosophila
Q92ya4 rhizobium m
Q9cjy4 pasteurella
Q92ya7 escherichia
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	Q9BDT9	σ	902	•	41	<b>4</b> 5
bradyrhizob	Q9AN56	Ŋ	781	•	41	44
1 rhizobium	Q98AV1	16	623	•	41	43
	Q8KJ49	N	617	56.9	41	2
Q9zw77 arabidopsis	Q9ZW77	10	492	٠	41	41
	Q8S933	٦ ا	486	•	41	40
	QBGYI4	10	479	•	41	ξ 9
Q98pa9 rhizobium l	Q98PA9	16	314	56.9	41	30
	Q8H6Q2	5	260	56.9	41	37
Q9vyp3 drosophila	Q9VYP3	v	119		41	36
drosophila	Q9V5US	ហ	113	•	41	5
0	Q925H9	H	77	•	41	34
	Q18820	Ų	1080		42	33
a	8-TOM8O	IJ	1003		42	2
shewar	Q8EBA6	16	494		42	1
Q8s2q4 oryza sativ	Q8S2Q4	10	395	58.3	42	30
	Q9LYG5	10	390	٠	42	29
	Q8LEE3	10	383	58.3	42	28
solan	Q941H8	10	339		42	27
	Q8LSP5	10	381	59.7	43	26
~1	049147	10	304	•	43	25
	Q8NK76	w	240	•	43	24
caeno	076631	տ	235	59.7	43	23
o mus	Q925I0	1	141	•	4	22
homo	QBIUB9	<b>.</b>	88	59.7	43	21
ans	Q925H6	ቷ	87	59.7	43	20
mus muscu	Q925H5	11	59		43	19
baci	Q9KD22	16	35	٠	43	18
Q8ce96 mus musculu	OSCE96	11	497	61.1	44	7

## ALIGNMENTS

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RESULT 2
Q9A419
ID Q9A4
AC Q9A4
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Matches 8
Q9A419
Q9A419;
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Q9LF59;
Q1-CCT-2000 (TrEMBLrel. 15, Created)
Q1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-CCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                   SEQUENCE FROM N.A.

EU Arabidopsis sequencing project;
EU Arabidopsis sequencing project;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL391151; CAC01909.1; -.

SEQUENCE 173 AA; 18536 MW; E3510947AA98BC0A CRC64;
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,
Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
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          PRELIMINARY;
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Pred. No. 3
          PRT;
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          205 AA.
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RESULT 3
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InterPro; IPR000912; Herpes MCP.
InterPro; IPR003006; IG MHC.
Pfam; PF03122; Herpes MCP; 1.
PRINTS; PR00235; HSVCAPSIDMCP.
PROSITE; PS00290; IG MHC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE=97296220; PubMed=9151804;
Neipel F., Albrecht J.C., Fleckenstein B.;
"Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus human herpesvirus 8: determinants of its pathogenicity?";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.
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Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Eisen J., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

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"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
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           Local Similarity
nes 7; Conserv
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(TrEMBirel. 17, Last sequence update)
(TrEMBirel. 20, Last annotation update)
protein CC3024.
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05 AA; 22665 MW; C03B0E4FC08908E8 CRC64;
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153463 MW;
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Last sequence tast annotated
           2;
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Pred. No.
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1; Mismatches
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              Mismatches
                                                                                                                                             F10B59E380745A49 CRC64;
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Q98139 PRELIMINARY; PRT; 1376 A. Q98139; (TrembLrel. 02, Created) 01-FEB-1997 (TrembLrel. 02, Last sequence 01-MAR-2003 (TrembLrel. 23, Last annotation Major capsid protein.

Kaposi's sarcoma-associated herpesvirus (K. Viruses; dsDNA viruses, no RNA stage; Herp Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RUSSO J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S. Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases. EMBL; U75698; AAC57106.1; ...

InterPro; IPR000912; Herpes MCP.
InterPro; IPR003016; Ig MHC.
Pfam; PF03122; Herpes MCP.
Pfam; PF03122; Herpes MCP.
PRINTS; PR00235; HSVCAPSIDMCP.
PROSITE; PS00239; IG MHC; 1.
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Russo J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalen. Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.; "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus (HHV8).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97094384; PubMed=8939871;
Moore P.S., Boshoff C., Weiss R.A., (
"Molecular mimicry of human cytokine
genes by KSHV.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P88917;
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Knowles D.M., Garber R., Pellett P.E.,
"Primary characterization of a herpesv:
Kaposi's sarcoma.";
J. Virol. 70:549-558(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=37296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gammaherpesvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           science 274:1739-1744(1996).
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                                                                                                                                                                                                                                                                                                       476
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                                                                                                                                                                                                                                                                                                                                                  ,_
                                                                                                                                                                                                                                                                                                                                                                                          Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H
                                                                                                                                                                                                                                                                                                       DEGHGYGLRYE
                                                                                                                                                                                                                                                                                                                                               DGGHGYGSSFD 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  63.64;
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153419 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23,
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Last sequence update)
Last annotation updat
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                herpesvirus agent associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stage;
                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                          annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    413E0CD4A7BB98D2 CRC64;
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E., McGeoch D.J., Chang Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chang Y.,
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                            Herpesviridae,
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                                                    (KSHV)
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                                                 (Human
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1376;
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                                                 herpesvirus
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RESULT 6
Q9GPD
ID 99GP
AC Q9GP
AC Q9GP
DT 01-v
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DT 01-v
CO Eukee
OC Eukee
OC Eukee
OC Fare
OX NCBJ
RN 11J
RP SEQU
RC TISC
RA Godd
RT Godd
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Best Local S
Matches 7
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InterPro; IPR003006; Ig MHC.
Pfam; Pr03122; Herpes MCP; 1.
PRINTS; PR00235; HSVGRSIDMCP.
PROSITE; PS00299; IG MHC; 1.
SEQUENCE 1376 AA; 153401 MW; 1
                                                                                             Q9GP09 PRELIMINARY; PRT; 381 AA.
Q9GP09;
01-MAR-2001 (TYENBLrel. 16, Created)
01-MAR-2001 (TYENBLrel. 16, Last sequence update)
01-OCT-2002 (TYENBLREL. 22, Last annotation update)
11-OCT-2002 (TYENBLREL. 22, Last annotation update)
Hypothetical 37.6 kDa protein.
Ixodes ricinus (castor bean tick).
Enkaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
Parasitiformes; Ixodida; Ixodidae; Ixodes.
 TISSUE-Salivary gland;
Leboulle G., Rochez C., Louahed J., Rutti B.
Godfroid E., Bollen A.;
"Isolation of Ixodes ricinus salivary gland
                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moore P.S, Chang Y., Dominguez G., Pellett P.E..; Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases. EMBL; U40377; AAB08392.1; -.
                                                                                          NCBI_TaxID=34613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaposi's sarcoma.";
J. Virol. 70:549-558(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96099469, PubMed=8523568;
Moore P.S., Gao S.J., Dominguez G., Ce
Knowles D.M., Garber R., Pellett P.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "In vitro establishment and characterization of two acquimmunodeficiency syndrome-related lymphoma cell lines (Econtaining Kaposi's sarcoma-associated herpesvirus-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Detection of herpesvirus-like DNA sequences in Kaposi's sarcoma patients with and without HIV infection.";
Lengl. J. Med. 332:1181-1185(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequences.";
Blood 86:2708-2714(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moore P.S., Chang Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1175-1376 FROM N.A. MEDLINE=95214703; PubMed=7700310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaposi's sarcoma.";
Science 266:1865-1869(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1175-1376 FROM N.A. MEDLINE=95090463; PubMed=7997879;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification of herpesvirus-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=37296;
[1]
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                                                                                                                                                                                                                                                                                                                                                        Similarity 63.
                                                                                                                                                                                                                                                                                                 DGGHGYGLRYE
                                                                                                                                                                                                                                                                                                                         DCGHGYGSSFD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        characterization
                                                                                                                                                                                                                                                                                                                                                                    63.6%;
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                                                                                                                                                                                                                                                                                                                                                      Score 47; DB
Pred. No. 63;
2; Mismatches
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                                Rutti B.,
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E., McGeoch D.J., Chang Y.;
esvirus agent associated with
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                                                                                                                                                                                                                                                                                                                                                              63,
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mRNA encoding factors
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                                Brossard
                                                                                                                                                                                                                                                                                                                                                                                Length 1376;
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ke (KSHV)
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RESULT ID 8651
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ID 98867
ID 701
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DT 01
CO 08 07
CO 08 
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QEXILT 9
QEXILT 9
QEXILT OR 101-M
DT 01-M
DT 
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OSJNBA004A10.17 OR OSJNBA0053D03.17.
Oryza sativa (Rice), and
Oryza sativa (Japonica cultivar-group).
Rukaryota, Viridiplantae, Streptophyta, Embr.
Spermatophyta, Magnoliophyta, Liliopsida, Pc.
Ehrhartoideae, Oryzeae, Oryza.
NCBI_TaxID=4530, 39947;
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Best Local :
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                      Q88651 PRELIMINARY; PRT; 346 Am.
Q88651;
Q1-UUN-2002 (TrEMBLrel. 21, Created)
O1-UUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete
SEQUENCE
                                                   SEQUENCE FROM N.A. SPECIES=0.sativa;
          SPECIES=O.sativa; STRAIN=Nipponbare;
McCombie W.R., de la Bastide M., Spi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF03717; PBP dimer; 1.
Pfam; PF00905; Transpeptidase; 1.
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EMBL; AP003193; BAB81846.1; -.
InterPro; IPR005311; PBP_dimer.
InterPro; IPR001460; Transpeptdse.
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01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2002 (TrEMBLrel. 21,
Probable penicillin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimizu T., Ohtani K., I
Shiba T., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=13 / Type
PubMed=11792842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      induced duringthe blood feeding process."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AJ300192; CAC20599.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence flesh-eater.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8XIH9;
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SEQUENCE 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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8; Conserv
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gasawara N., Hattori M., Kuhara S., Hayashi H.;
enome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al protein.
381 AA; 37570 MW;
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0; Mismatches
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Pred. No.
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Pred. No.
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2; Mismatches
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      Spiegel
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Q93WZ6;
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Gramene; Q8500...
Hypothetical protein.
AMATTENCE 348 AA; 35920 MW;
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Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo
Currie J., Collura K.;
"Rice Genomic Sequence.";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ dat
EMBL; AC096682; AAM01113.1; -.
EMBL; AC131968; AAN04952.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21185977; PubMed=11290294;
Tratchenko A.V., Visconti R.P., Shang L., Papenbrock T., Pruett N.D.,
Ito T., Ogdwa M., Awgulewitsch A.;
I'overexpression of Hoxc13 in differentiating keratinocytes results in
"Overexpression of a novel hair keratin gene cluster and alopecia.";
bevelopment 128:1547-1558 (2001).
Development 128:1547-1558 (2001).
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01-DEC-2001 (TrEMELrel. 19, Last sequence update)
01-OCT-2002 (TrEMELrel. 22, Last annotation update)
Keratin-associated protein 16.9.
KRTAP16-9 OR KRTAP16.9.
Mus musculus (Mouse)
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Dedhia N.;
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Mammalia; Eutheria;
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Santos L., Miller
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7; Conserv
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B., Cunnius D.M., Katzenberger F., Muller S.,
Yang C., Dike S., O'Shaughnessy A., Palmer L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              65
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Rodentia;
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Pred. No. 7.9;
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Pred. No. 27;
1; Mismatches
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Best Local :
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O1-JUN-1998 (TrEMBLrel. 06, Created)
O1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Abscisic stress ripening protein homolog.
Prunus armeniaca (Apricot)
Prunus armeniaca (Apricot)
Enkaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid,
seurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
                                                                                                                                                                                                                                                                                                                                                         STRAIN=Bergeron; TISSUE=Mesocarp, and Exocarp; Mbeguie-A-Mbeguie D., Gomez R.-M., Fils-Lycaon B.; Mbeguie-A-Mbeguie D., Gomez R.-M., Fils-Lycaon B.; Mbedieular Cloning and Nucleotide Sequence of an Abscisic Stress-, Ripening-Induced (ASR)-Like Protein from Apricot (Accession No. U93164). Gene Expression During Fruit Ripen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-cv. Suncrest; TISSUE-Fruit;
Callahan A.M., Morgens P.H., Cohen R.A., Scorza R.;
Callahan A.M., Morgens P.H., Cohen R.A., Scorza R.;
"Regulation of peach gene expression in a peach/almond hybrid.";
submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF317062; AAL26889.1; -
InterPro; IPR003496; ABL26889.1; -
InterPro; IPR003496; ABL26889.1 -
Ffam; PF02496; ABA WDS; I.
SEQUENCE 193 AA; 20760 MW; D08C20DE062D719F CRC64;
                                                                                                                                                                                                                                                          Plant Physiol. 115:1288-1288 (1997).
EMBL; U93164; AAB97140.1; -.
InterPro; IPR003496; ABA WDS;
Pfam; PF02496; ABA WDS; I.
SEQUENCE 200 AA; 21240 MW; C145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I; Rosales, Rosaceae, Amygdaloideae, Prunus.
NCBI TaxID=3760,
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Pred. No. 20;
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Pred. No. 21;
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Q8IQE1; Q8IQE1; 01-MAR-2003 01-MAR-2003

(TrEMBLrel. (TrEMBLrel.

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Q92YA4;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 20, Last annotation update)
11-DEC-2003 (TrEMBLrel. 20, Last annotation update)
12-DEC-2003 (TremBLrel. 20, Last annotation update)
13-DEC-2003 (TremBLrel. 19, Created)
13-DEC-2003 (TrEMBLrel. 19, Last sequence update)
13-DEC-2003 (TrEMBLrel. 19, Last annotation update)
14-DEC-2003 (TrEMBLrel. 20, Last annotation update)
15-DEC-2003 (TrEMBLrel. 20, Last annotation update)
16-DEC-2003 (TrEMBLrel. 20, Last annotation update)
16-DEC-2003 (TrEMBLrel. 20, Last annotation update)
17-DEC-2003 (TrEMBLrel. 20, Last annotation update)
18-DEC-2003 (TrEMBLrel. 20, Last annotation up
                                                                                                                                                      Q9CJY4;
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Plasmid; H
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                                     01-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE007284; AAK65638.1; -.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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Hypothetical protein
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Pred. No.
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B8A67515B59DA02A CRC64;
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                                 update)
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RESULT 15
CRX6EP 10
CRXCEP 10
CRX6EP                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  문
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11205551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533 (2001).
                                         EMBL; AE005208; AAG54641.1; --
EMBL; AP002551; BAB33768.1; --
InterPro; IPR001450; 4Fe45 ferredoxin.
InterPro; IPR001450; 4Fe45 Ferredoxin.
InterPro; IPR001452; Fe 5 binding.
Pfan; PF00037; fer4; 2.
TIGRDAMS; TIGR00273; TIGR00273; 1.
                                                                                                                                                                                                                               Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Muzata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., "Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8X6E7;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
0rf, hypothetical protein.
97KGF OR Z0385 OR ECS0345.
Escherichia coli 0157:H7.
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May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

ENBL; AE006223; AAK03938.1;
InterPro; IPR001452; Pe S binding.
InterPro; IPR004452; Pe S binding.
Plam; PT00037; fer4; 1.—
TIGRPAMS; TIGR00273; 1.
PROSITE; PS00198; 4FE4S FERREDOXIN; 2.
PROSITE; PS00198; 4FE4S FERREDOXIN; 2.
Hypothetical protein; Complete proteome.
SECUENCE 467 AA; 51821 MW; D3DB3395BB560A8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
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STRAIN=0157:H7 / R
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Enterobacteriaceae; Escherichia.
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7; Conserv
                      PS00198; 4FE4S_FERREDOXIN;
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SQ SEQUENCE 475 AA; 53000 MW; F81B64DD6A1C1B0E CRC64;

Query Match
G1.1%; Score 44; DB 16; Length 475;
Best Local Similarity 77.8%; Pred. No. 57;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps
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Search completed: November 7, 2003, 07:34:29
Job time : 6.05728 secs

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GGHGYGSSF 10

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Result
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72
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Kaposi's sarcoma a
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Movel human diagno
Human polypeptide
Novel human diagno
Human ovarian tumo
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AAG42281	ABG67265	AAW28314	ABG02460	ABJ25324	ABJ25306	ABB63930	S.	ABB68139	AAW26799	AAR56233	AAR56234	ABG19363	AAB58292	AAG09148	AAR52062	AAW58489	AAW73527	AAR38613	AAR28746	AAR52047	AAW26796	AAR05980	ABB92093	ABB71029	ABB67899	AAG10768	ABB93436	AAG10769	AAG10770	ABG02073	AAY70222	AAG78409	ABU65034	AAB27161	AAE27023
Arabidopsis thalia	Discosoma 2	Staphylococcus	Novel human diagno	j.	isolate			Drosophila melanog	Anti-qp54 MAb 48-	h67-125/h13-66/l1-	9/112	Novel human diagno		Arabidopsis thalia	Heavy chain variab		Humanised OKT3 va		Heavy chain variab	Heavy chain variab	Anti-cos4 Mab 48-1	Somatic immunoclob	Herbicidally activ	Drosophila melanog	Drosophila me	Arabidopsis thalia	Herbicidally	Arabidopsis thalia	idopsis	humar	RNA-a	acid	secre	gene	Human gene 18

## ALIGNMENTS

RESULT 1 AAB20389

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New factor IX/factor IXa antibodies and their derivatives useful for
                     WPI; 2001-290358/30
                                       Scheiflinger F, Kerschbaumer
                                                                                                                                                                                   Factor IX; FIX; Factor IXa; FIXa; antibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse; complementarity determining region; CDR.
                                                                                  14-SEP-1999;
                                                                                                        13-SEP-2000; 2000WO-EP08936.
                                                                                                                            22-MAR-2001.
                                                                                                                                                 WO200119992-A2
                                                                                                                                                                     Mus musculus.
                                                                                                                                                                                                                                          Anti-FIX/FIXa antibody 193/K2 CDR3.
                                                                                                                                                                                                                                                              21-JUN-2001 (first entry)
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                                                               (BAXT ) BAXTER AG.
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RESULT 2
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                       Scheiflinger F,
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                                                                              (BAXT ) BAXTER
                                                                                                                                                                                    13-SEP-2000; 2000WO-EP08936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
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12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= CDR3
122..135
/label= Linker
                       Kerschbaumer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Pred. No.
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                       Falkner F,
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0.00013;
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The present sequence is that of a single chain Fv (scFv) derivative CC of antibody 193/K2, comprising the heavy (VH) and light (VL) chain CC variable regions of 193/K2 joined by an artificial, flexible linker CC peptide. The scFv was obtained by FCR amplification of cDNAs for CC an example of anti-human Factor IX (FIX)/activated Factor IX (FIXa) and example of anti-human Factor IX (FIX)/activated Factor IX (FIXa) CC antibodies of the invention. Anti-FIX/FIXa and their derivatives, CC including scFv and CDR3 fragments, have Factor VIIIa (FVIIIa) cofactor CC activity. or FIXa activating activity. Administration leads to an CC increase in the procagulant activity of FIXa, even in the presence CC in the absence of FVIII or FVIIIa, and in the case of FVIII (C) inhibitor partients. The antibodies and derivatives are used in a CC claimed pharmaceutical composition for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic
  Sequence
                                                   diathesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Fig 15; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
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249 AA;
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Query Match Best Local Similarity Watches 12; Conserv Conservative 100.0%;

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Score 72; DB 22; Pred. No. 0.0027; ); Mismatches (

DB 22;

Length 249; Indels

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DGGHGYGSSFDY 110 DGGHGYGSSFDY 12

RESULT 3 AAR97835 ID AAR9 AAR97835; AAR97835 standard; Protein; 1376 AA

11-SEP-1996

(first entry)

Kaposi's vaccine; Kaposi's sarcoma; gamma-2 herpesvirus; KSHV; therapy; diagnosis; diagnosis; AIDS. sarcoma associated herpesvirus ORF25 product

Kaposi's sarcoma associated herpesvirus.

Key Region 30-MAY-1996. W09615779-A1 Location/Qualifiers /note= "Ig and MHC protein signature"

21-NOV-1995; 95WO-US15138

11-APR-1995; 21-NOV-1994; 95US-0420235. 94US-0343101.

(UYCO ) UNIV COLUMBIA NEW YORK

Chang Y, Moore PS;

WPI; 1996-268320/27

N-PSDB; AAT30687

Herpes virus associated with Kaposi's sarcoma - also definitive DNA

E E X S X S S S S S S S S X X X

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Query Match
Best Local S
Matches 7
Kaposi's sarcoma associated herpes virus (KSHV) clone KS5 (AAT16806), obtd. from a KS lesion genomic library, includes 15 complete ORFs and 2 incomplete ORFs (AAT16807-23) named according to their herpesvirus saimiri positional homologues. The major capsid protein (AAR93601) is the product of ORF25 (AAT16807). KSHV proteins and peptides may be obtd. by incorporating encoding sequences into a vector and expression in host cells. They are useful in vaccines or for raising antibodies of diagnostic or therapeutic value. (Updated on 25-WAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                           18-AUG-1994;
21-NOV-1994;
11-APR-1995;
                                                                                                                                        Claim 17; Page 188-193; 305pp; English.
                                                                                                                                                                     Herpes:virus DNA associated with Kaposi's sarcoma - also vectors and proteins, used in detection and vaccination.
                                                                                                                                                                                                                                                        Chang Y,
                                                                                                                                                                                                                                                                                (UYCO ) UNIV COLUMBIA NEW YORK. (GRAN/) GRANT D E. (VIEL/) VIELE L.
                                                                                                                                                                                                                                                                                                                                                                                                                              29-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaposi's sarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaposi's sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaposi's sarcoma associated herpesvirus major capsid protein.
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13-AUG-1996
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treatment o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              capsid protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR93601;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 open reading frames (AAT30682-98), 15 of which are complete, including ORF25 (AAT30687). The protein products (AAR87830-46, respectively) of the 17 ORFs can be expressed in eukaryotic or bacterial host cells for use as vaccines, for KS diagnosis, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lambda clone KS5 (AAT30681) is a fragment of a newly identified gamma-2 herpesvirus associated with Kaposi's sarcoma (KS). KS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     raising antibodies.
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7; Conser
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                                                                                                                                                                                                                                                        Moore PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 175-180; 277pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , useful for diagnosis of and to develop prods. of Kaposi's sarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1376 AA;
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94US-0343101.
95US-0420235.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  associated herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSHV; lymphoma; AIDS; vaccine; diagnosis; therapy;
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Pred. No.
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AAH84373 to AAH84499 represent Escherichia coli growth and proliferation CC related DNA sequences (I). AAH84500 to AAH84670 encode the E. coli CC growth and proliferation related proteins given in AAG99993 and AAG98830 CC to AAG98999. (I) can be used as potential targets for the generation of interact with the gene products of (I). In addition the expression of CC interact with the gene products of (I). In addition the expression of CC used to generate reagents and screen small molecule libraries or other CC used to generate reagents and screen small molecule libraries or other CC candidate compound libraries for compounds that can be further developed to yield novel antimicrobial compounds. In addition, nucleic acid probes CC microorganisms can be used to identify particular microorganisms species of CC microorganisms can be used to identify particular microorganism species in clinical specimens, therefore, providing a rapid and dependable CC infection. Also, antibodies generated agents of a bacterial CC infection. Also, antibodies generated agents of a bacterial CC infection also antibodies generated agents of a bacterial compounds. In a second probes considers used in the isolation of E. coll growth and proliferation constituted sequencing which are used in an avamenta from the process.
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Best Local &
Matches
                                          related sequence,
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                                                                                                                                                                                                                                                                                                                                                      Claim 19; Page 467-468; 522pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG98933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coli growth and proliferation related protein sequence SEQ ID NO:403
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                                                                                                                                                                                                                                                                                                                                                                                           acids that inhibit Escherichia coli proliferation, useful for homologous genes and for designing expression vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0164415
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                                          are used
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Pred. No. 99;
2; Mismatches
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                                      in an example
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Query Match Sequence

61.1%;

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RESULT 6
ABG27993
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                                                                                                                                                                    CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polymucleotides are also used in diagnostics as expressed sequence tage for identifying expressed genes. (I) is useful in gene therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical commanding of sites expressing (II). (II) are useful for treating classing of sites expressing (II). (II) are useful for treating classing of sites expressing (II). (II) are useful for treating classing of sites expressing (II). (II) and (II) are useful for treating classories involving aberrant protein expression or biological activity. (II) and (III) are useful for treating classories involving aberrant protein expression or biological activity. (II) and (III) are useful for treating classories in polymucleotide sequences have applications in classories in the prince classories biodiversity and to produce other types of data and products dependent on DNA and conditions of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              닭
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      Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences, (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID No 58352; 103pp; English
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                                                                                                                                                81
                    Conservative
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                                                59.78;
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Mismatches
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                                                                           Length 81;
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                                                                                            RESULT 7
ABP69638
ID ABP69638
AC ABP6
XX ABP6

                                                                                                                                                                    CC The invention relates to an isolated polynucleotide (I) comprising a CC nucleotide sequence selected from any of 948 sequences CC (ABZ11119-ABZ12066) or their mature protein coding portion, active domain CC coding protein or complementary sequences. The polynucleotides are useful CC for identifying expressed genes or for physical mapping of human genome. CC The encoded polypeptides (ABBC68902-ABBC6849) are useful as molecular CC weight markers, as a food supplement, for generating antibodies, in CC medical imaging, screening and diagnostic assays and for treating CC cell-proliferative disorders (cancer), neurodegenerative diseases (Multiple CC sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid CC disorders, platelet or coagulation disorders, wound, burns, incision, CC ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, CC parasitic), arthritis, etc.

Note: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO CC at fro wire. Int/mih/inihi and not segmences.
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Query Match
Best Local Similarity
                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune genetic, myeloid or lymphoid, or platelet or coagulation disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-759812/82.
N-PSDB; ABZ11855.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-SEP-2002
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                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
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AJ, Yang Y, Ma
rman T, Wang J,
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Ma Y, Yamazak
I, Wang D, Dr
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Yamazaki V, Chen
g D, Drmanac RT;
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R, Wang Z,
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, Ghosh M;
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The invention relates to isolated polynucleotide (I) and (I) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The polynucleotides are also used in disposetics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating clisorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID No 58353; 103pp; English
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23-AUG-2000; 2000US-0649167.
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                                                                                                                  139
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
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77.8%;
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                                 ed. No. 42;
Mismatches
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                                                                     DB 22;
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AAY76638
ID AAY7
XX AAY7
XX AAY7
XX Huma
XX Expr
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XX Homo
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XX Homo
XX O9-A
XX O9-A
XX O9-A
XX O9-A
XX O9-A
XX INST
XX I
    RESULT 10
AAE27023
ID AAE27
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                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                      Matches
AAE27023 standard; Protein; 223 AA.
                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 25; Page 299; 310pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosenthal A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY76638 standard; Protein; 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy; treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY76638
                                                                                                     51
                                                                                                                                         2 GGHGYGSSFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGYGYGSGF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGHGYGSSF 10
                                                                                                                                                                                                                                                                  220
                                                                                                                                                                                 Conservative
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                                                                                                   60
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                                                                                                                                                                                                  59.7%;
70.0%;
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                                                                                                                                                                                                Score 43;
Pred. No.
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This invention describes novel nucleic acid (cDNA) sequences (A) which C have anticancer activity and are highly expressed in ovarian tumor Ct tissue (and some also in testis and breast cancer tissue). The products CC of the invention can be used for gene therapy. (A) are used (i) for CC recombinant expression of polypeptides (B) and (ii) to isolate complete CC genes. (B) are used (i) to identify agents suitable for treatment of CC covarian cancer; (ii) directly for treating this form of cancer (CC including expression from gene therapy vectors) and (iii) for generation CC sequence tags) from a particular tissue type before comparison of CC expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated CC with the fact that BSTs from different libraries may represent different CC parts of the same unknown gene, distorting the estimated frequency of CC cragments encoded by the human ovarian tumor cDNA library derived EST CC fragments represented in AAZ77450-Z77572.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid sequences expressed in ovarian, and some other, cancer tissues, and derived polypeptides, for treatment of ovarian cancer and identification of therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ovarian tumor EST fragment encoded protein 134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expressed sequence tag; EST; human; ovarian tumor; anticancer;
                1; Mismatches
                                                    66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schmitt A,
                                                                                20;
        2
                                                                                Length 220;
        Indels
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Gaps
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AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted CC protein genes, and AAE26959-AAE26999 represent the proteins they encode. AAE2700-AAE27025 represent human secreted protein fragments or their variants. The secreted proteins and genes are useful for preventing, CC treating or ameliorating medical conditions, e.g., by protein or gene CC therapy. Specific uses are described for each of the 28 genes, based on the tissues in which they are most highly expressed and include conditions, e.g., by protein or gene CC developing products for the diagnosis or treatment of immunodeficiencies, c.g., x-linked agammaglobulinaemia, B cell immunodeficiencies, severe combined immunodeficiencies, autoimmune disorders e.g., systemic lupus thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome, carythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune the chyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome, including septic shock, sepsis, reperfusion injury, inflammatory conditions including septic shock, sepsis, reperfusion injury, inflammatory bowel disease, haematopoietic disorders, respiratory inflammatory bowel disease, crohn's disease, hematopoietic disorders, respiratory inflammatory bowel disease), cancers e.g., gastric, ovarian, lung, inflammatory bowel disease), central nervous system (CNS) disorders e.g., central nervous system (CNS) disorders e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM,
Soppet DR,
Ferrie AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human secreted polypeptides and polynucleotides for diagnosing, preventing, treating immune, hyperproliferative, cardiovascular, peurological, reproductive disorders and identifying modulators of
                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 205-206; 209pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cance; Grave's disease; diabetes mellitus; haematopoietic disorder; stroke; respiratory disorder; asthma, allergy; gestrointestinal disorder; inflammatory bowel disease; neurodegenerative disorder; hepatitis; Parkinson's disease; Alzheimer's disease; cardiovascular disorder; atherosclerosis; myocarditis; renal disorder; fungicide; virucide; hepatrosclerosis; myocarditis; renal disorder; fungicide; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                           therapeutic use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-598780/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ROSE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hyperproliferative disorder; acute glomerulonephritis; tonsillitis; respiratory disorder; rhinitis; sinusitis; neurological disease; respondentine disorder; addison's disease; reproductive system disorder; endocrine disorder; vulnerary; cytostatic; nootropic; cardian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SOPP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-HIV; tranquilliser; gout; antiparasitic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human gene 18 encoded secreted protein variant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (VEIY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HHIT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immunodeficiency; X-linked agammaglobulinaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE27023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FISC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RUBE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZENG/)
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ROSEN C A.
LI Y.
LI Y.
ZENG Z.
KYAW H.
FISCHER C L.
LI H.
SOPPET D R.
GENTZ R L.
WEI Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen CA,
Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Wei Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zeng Z,
, Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kyaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fischer CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO:116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Greene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            septic shock
disorders e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SK E
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RESULT 1
ADB27161
ADB27161
ADC 7AB
AC AAB
AC AAB
AC AAB
AC Hum
AC Hum
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Matches
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                        Ruben SM,
Soppet DR,
Ferrie AM,
                                                                                                                                                                                                                (GENT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2002076756-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue regeneration; immunosuppressive; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; autoimmune disease; hyperproliferative disorder; rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis; cerebral ischaemia; cardiovascular disorder; nervous system disorder; cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prion disease, cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis, inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis, sarcoidosis and allogenic transplant rejection, blood-related disorder (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative disorders, respiratory disorders e.g. rhinitis, sinustitis, tonsillitis, lung cancer, allergic disorders peumonitis, renal disorders, endocrine disorders e.g., hyperthyroidism, Addison's liver disorders, endocrine disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism, infectious diseases and reproductive system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-MAY-2001; 2001US-0853161.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human gene 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secreted protein variant of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders e.g. endometriosis.
                                                                                                                                                                                                                                                                                      (/HHI1]
                                                                                                                                                                                                                                                                                                                                (KYAW/)
                                                                                                                                                                                                                                                                                                                                                         (ZENG/)
                                                                                                                                                                                                                                                                                                                                                                                                                              (RUBB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection; corneal infection; skin aging; food additive; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkinson's disease and Alzheimer's disease, AIDS-related dementia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11
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                        AM,
                                                                                                                  YOUNG P E.
GREENE J M.
FERRIE A M.
                                                                                                                                                                                                           SOPPET D R. GENTZ R L. WEI Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N
                                                                                                                                                                                                                                                                                                                                ZENG Z.
KYAW H.
                                                                                                                                                                                                                                                                                 FISCHER C L.
LI H.
                                                                                                                                                                                                                                                                                                                                                                                                                              RUBEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
7; Conserv
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                                            Rosen CA,
Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001US-265583P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoded secreted protein fragment, SEQ ID NO:116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 virucide; fungicide; ophthalmological; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                   ≯ 3
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                                            Li Y, ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.7%;
70.0%;
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                                            Zeng Z,
Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a human
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                                            PA,
                                                                   Kyaw н,
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                                          Young PE,
                                                                   Fischer CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 223;
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                                            Greene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wound healing;
                                            닭분
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted protein genes, and AAB27097-AAB27137 represent the proteins they encode. CC AAB27138-AAB27164 represent human secreted protein fragments. The genes CC and their corresponding secreted proteins are useful for preventing, CC treating or ameliorating medical conditions, e.g., by protein or gene CC treating or treatment of disorders fuch as autoimmune diseases (e.g. Cremmatoid arthritis), hyperproliferative disorders (e.g. neoplasms of CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia, CC system disorders (e.g. Alzheimer's disease), infections caused by fungi, CC system disorders (e.g. Alzheimer's disease), infections caused by fungi, CC system disorders (e.g. Alzheimer's disease), infections caused by fungi, CC system disorders (e.g. Alzheimer's disease), infections caused by fungi, CC polypeptides can also be used to aid wound healing and epithelial cell polypeptides can also be used to aid wound healing and epithelial cell polypeptides can also be used to aid wound healing and epithelial cell colliferation, to prevent skin aging due to sunburn, to maintain organs CC before transplantation, for supporting cell culture of primary tissues, CC additives or preservative to increase or decrease storage capabilities, CC additives or preservative to increase or decrease storage capabilities, and other nutritional components. The present sequence represents a human CC secreted protein fragment referred to in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                           Secreted protein; immunodeficiency; multiple sclerosis; severe combined immunodeficiency; autoimmune disorder; cancer; rheumatoid arthritis; diabetes mellitus; haematopoietic disorder; inflammatory condition; septic shock; inflammatory bowel disease; Crohn's disease; respiratory disorder; asthma; allergy; stroke; gastrointestinal disorder; central nervous system disorder; gastrointestinal disorder; central nervous system disorder; ischaemic brain injury; neurodegenerative disorder; parkinson's disease; hazheimer's disease; cardiovascular disorder; atherosclerosis; hlood-related disorder; thrombosis; atherosclerosis; renal disorder; hyperproliferative disorder; auter glomerulomephritis; hydison's disease; endocrine disorder; liver disease; reproductive system disorder; endometriosis; infectious disease; panoreatic disorder; vaccine; cound repair. anniverse disease; panoreatic disorder; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                      11-MAY-2001; 2001US-0852797.
                                                                                                                                                                                                        body height; hair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein gene 18, protein #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU65034 standard; Protein; 223 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 205-206; 209pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-574454/61
                                                                      21-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 GGHGYGGAGD 171
                                                                                                                                                                                                                                 repair; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGHGYGSSFD 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 AA;
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                                                                                                                                                                                                             colour; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.7%;
70.0%;
                                                                                                                                                                                                                                 Lymphatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                 disorder; hair loss; body weight
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14-MAR-1997;
14-MAR-1997;
30-MAY-1997;
30-MAY-1997;
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Ferrie AM;
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05-SEP-1997;
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                                                                                                                                                                                      Ruben SM,
                                                                                                                                                                                                                               (KYAW/)
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                                                                                                                                                                                                                                                   (RUBE/)
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YOUNG P E.
GREENB J M.
FERRIE A M.
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                                                                                                                                                                                                                                                    RUBEN
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97US-040762P.
97US-048100P.
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97US-048357P.
97US-050934P.
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98US-0152060.
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9705-068368P.
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                                                                                                                                                                                 Li Y, Z
Wei Y,
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Moore
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                                                                                                                                                                                 Young PE,
                                                                                                                                                                                      Fischer CL,
                                                                                                                                                                                  Greene
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New human secreted polypeptides and polynucleotides for diagnosing, prognosing, preventing and treating immune, hyperproliferative, liv kidney, reproductive disorders and for identifying modulators of therapeutic use liver,

Disclosure; Page 13; 209pp; English.

cc sequence at least 95 identical to sequence of 28 human secreted corrected.

cc variant, allelic variant, or species homologue, or the encoded sequence concluded in ATCC 97921 and 97922. Also included are the encoding concluded in ATCC 97921 and 97922. Also included are the encoding concluded in ATCC 97921 and 97922. Also included are the encoding concluded in mucleic acids are useful for diagnosing, preventing, prognosing or ameliorating a medical condition e.g. immunodeficiencies (e.g. X-linked agammaglobulinaemia, B cell immunodeficiencies), autoimmune thyroiditis, autoimmune haemolytic anaemia, B cell coodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis), sepsis, reperfusion injury, inflammatory conditions (e.g. septic shock, concers (e.g. sattric, overian, lung, bladder, liver and concers (e.g. sattric, overian, lung, bladder), liver and concers (e.g. sattric, overian, lung, bladder), liver and concers (e.g. sattric, overian, lung, bladder, liver and concers (e.g. sattricons), inflammation (e.g. hepaticis, gout, trauma, bladder (e.g. hapaticis, gout, trauma, bladder (e.g. sattric), endocrers (e.g. sattric), gout, trauma, bladder (e.g. disorders (e.g. satterial thrombosis), and sattricis, allogenic transplant rejection), blood-related disorders (e.g. endometriosis), infectious disease, concers (e.g. and pancreatic disorders, renal disorders (e.g. addison's disease, and pancreatic disorders, liver diseases and disorders are listed in the specification. They also over the redisted cell livers for useful to enhance or inhibit complement mediated cell lysis, invention relates to an isolated polypeptide comprising an amino acid for

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RESULT 13
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                                             fragment specific for at least one epitope comprising a specified sequence. The applications of the anti HSP90 antibodies include fungal strain growth inhibitor, in the preparation of a diagnostic kit for diagnosing at least one fungal infection and also, in a composition for preparing and for treating fungal infections of human or animal body, caused due to a Candida Cryptococcus, Histoplasma, Aspergillus, Torulopais, Mucormycosis, Blastomycosis, Coccidiodomycosis or Paracoccodiodomycosis organism, resistant to the antifungal agent. The antibody may binds at least one epitope of a fungal stress protein and significantly enhances the efficacy of the antifungal agent against fungal infections, allowing for either lower treatment dosages or more effective treatment at the same dose, which allows for reduction of unwanted side-effects. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New composition useful in a composition for the treatment of infections comprises antibody comprising specified sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti HSP90 antibody; intensive care; non-albicans; Candida albican
amphotericin B; heat shock protein; echinocandin antifungal agent;
polyene antifungal agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stimulating wound and tissue repair, angiogenesis, and the repair of vascular or lymphatic diseases or disorders. They are also useful to prevent hair loss, to modulate mammalian characteristics such as body height, weight, hair colour, and to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. The proteins are also useful for identifying binding partners. The present sequence represents a secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to an antibody or an antigen binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-663017/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NEUT-) NEUTEC PHARMA PLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of anti HSP90 antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Page 46-47; 50pp; English.
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                             the anti HSP90 antibody.
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Pred. No. 66;
1; Mismatches
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RESULT 14
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                Hillman JL,
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12-JAN-1999;
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                                                                                                                                                   2000-237651/20.
DB; AAZ51252.
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                                                                                                                                                                                                                                                                                                          INCYTE PHARM INC.
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                                                                                                                                                                                                                                       Baughn
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99US-0115639
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136..2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Potential glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mote=
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63.6%;
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Pred. No.
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                                                                                                                                                                                                                                         Corley NC,
P, Bandman
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74;
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O, Reddy R,
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Azimzai Y;
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Claim 1; Page 81; 123pp; English

Human RNA-associated proteins useful in diagnosing, treating and preventing cell proliferative, autoimmune, inflammatory and infectious

N-PSDB;

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RESULT 15
ABG02073
ID ABG02
XX ABG02
XX ABG02
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XX Homo
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Best Local S
Matches 7
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiarthritic, opthalmological and antimicropial activity.

RNAAP antibodies are useful for diagnosis of diseases associated with altered expression or activity of RNAAP. It is used to treat cell proliferative, autoimmune, inflammatory and infectious disorders, like actinic keratosis, bursitis, arteriosclerosis, artherosclerosis, cirrhosis, hepatitis, myelofibrosis, mixed connective tissue disease (MCTD), psoriasis, primary thrombocythemia and cancer, HIV, allergies, rheumatoid arthritis, uveitis, Crohn's disease, and bacterial, viral and
                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID No 32432; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAS66260.
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                                                                                                                                                                                                                                                                                                                                                                           biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #2064.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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70.0%;
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Best Local :
                                                                                                                                                                                            quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abstrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fip. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                  Sequence
185 GGHGYGGAGD
                                       2 GGHGYGSSFD 11
                                                                                                       Similarity
                                                                                                                                                                    354 AA;
                                                                                 Conservative
194
                                                                                                    59.7%;
                                                                              Score 43; DB 22;
Pred. No. 1.1e+02;
1; Mismatches 2
                                                                                                                      Length 354;
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Search completed: November 7, 2003, 07:26:58 Job time: 7.1749 secs

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Result
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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195.799 Million cell updates/sec
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72
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep;*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep;*

3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep;*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep;*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-25-200A-18
US-09-795-515-10
5 US-10-422-049-10
5 US-10-422-049-10
5 US-10-67-286A-11
US-09-955-302-630
US-09-738-626-6160
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2 US-10-287-274-403

12 US-09-853-161-116

12 US-09-852-659A-116

13 US-09-852-797-116

14 US-09-852-797-116
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                             Sequence 28297, A
Sequence 103, App
Sequence 116, App
Sequence 116, App
Sequence 116, App
Sequence 2, Appli
Sequence 7, Appli
Sequence 8, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 630, Appli
Sequence 640, Appli
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     Description
          Sequence 1, Appli
US-10-287-274-403
; Sequence 403, Applica
; Publication No. US200
; GENERAL INFORMATION:
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<b>в</b> «	Query Matc Best Local Matches	SEGULT 1 Sequence 28297, Appl Publication No. US20 GENERAL INFORMATION: APPLICANT: Penn, Sh APPLICANT: Penn, Sh APPLICANT: Hanzel, TITLE OF INVENTION: FILE REFERENCE: AEC CURRENT APPLICATION CURRENT FILING DATE NUMBER OF SEQ ID NO SOFTWARE: ANDOMAX S SEQ ID NO 28297 LENGTH: 102 TYPE: PAT OCHER INFORMATION:		11114444444 8001446666666666666666666666666666666666
3 Gg 	5	-386-28297, information no. in information no. in information no. in information in information no. in information of invention no inve		38.59 38.59 39 39 39 39 39 39 39 39 39 39 39 39 39
GHGYGSSFDY          GSGYGSSFGY	Similarity 8; Conservat	944 0 3 H 25 H 2 B 2 B 3 B 3 B 3 B 3 B 3 B 3 B 3 B 3 B		55555555555555555555555555555555555555
Y 12	61.1 80.0 ive	7 7 7 7 7 8 7 8 7 7 1 7 1 7 1 7 1 7 1 7		657 657 657 657 657 348 307 382 382 558 588 588 588 588 10 10 10 10 10 19 286 20 20 20 20 30 30 30 30 30 30 30 30 30 30 30 30 30
	****	US/10 MAA1 ENOME SION US/1 12-20 Listi Listi ED IN		95000000000000000000000000000000000000
	Score 44; DB 12; Length Pred. No. 18; 0; Mismatches 2; Inde:	0029386 E-DERIVED SINGLE ANALYSIS TWO 10/029,386 0 ing Engine vers.	ALIGNMENTS	US-10-401-437-2 US-10-402-312-2 US-10-402-067-2 US-10-402-067-2 US-10-156-761-8089 US-09-036-613-7 US-10-062-254-372 US-10-156-761-11262 US-10-156-761-11262 US-10-156-761-7979 US-10-156-761-7979 US-09-771-388-2 US-10-156-761-7979 US-09-572-404B-2864 US-09-572-404B-2874 US-09-572-404B-2874 US-10-425-586-8 US-10-425-586-8 US-10-425-586-9 US-10-425-586-9 US-10-425-586-3 US-10-10-204-887-1389 US-10-102-806-469 US-10-156-761-13993 US-10-102-806-469 US-10-127-629-5
	ngth 102; Indels 0;	EXON NUCLEIC ACID		Sequence
	Gaps			e Control 113, 113, 113, 113, 113, 113, 113, 113
	ω	PROBES		2, Appli 2, Appli 2, Appli 2, Appli 2, Appli 3, Appli 5, Appli 372, Appli 14939, Appli 11939, Appli 12, Appli 2, Appli 2, Appli 2, Appli 1872, Appli 1872, Appli 1872, Appli 1873, Appli 5, Appli 6, Appli 7, Appli 9, Appli 138, Appli 138, Appli 139, Appli 139, Appli 139, Appli
	0;	USEFU		oe 2, Applice 20, Applice 20, Applice 8089, Applice 8089, Applice 11262, Applice 11262, Applice 11262, Applice 1872, Applice 187

Application US/10287274 o. US20030181408A1

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; ORGANISM: Homo sapiens
US-09-853-161-116
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US-10-287-274-403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-853-161-116
                 Query Match 59.7%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                     SOFTWARE: PatentIn Ver. SEQ ID NO 116
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Best Local Similarity 7/...
"Arches 7; Conservative
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NUMBER OF SEQ ID NOS: 469
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 403
LENGTH: 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: PCT/US98/04858
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/853,161
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
                                                                                                                                                                                                                            PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/068,368
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PRIOR APPLICATION NUMBER: 09/152,060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: 28 Human Secreted Proteins FILE REFERENCE: PZ003P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zyskind, Judith
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THEREFOR
FILE REFERENCE: ELITRA.008DV1
CURRENT APPLICATION NUMBER: US/10/287,274
CURRENT FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: US 60/164415
PRIOR APPLICATION NUMBER: US 09/711164
                                                                                                                                                  LENGTH: 2
TYPE; PRT
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APPLICANT: Ohlsen, Kari
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                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1997-05-30
APPLICATION NUMBER: 60/048,357
FILING DATE: 1997-05-30
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FILING DATE: 1997-05-30
APPLICATION NUMBER: 60/048,100
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APPLICATION NUMBER: 60/0
FILING DATE: 1997-09-05
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/048,970 FILING DATE: 1997-06-06
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77.8%;
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                     Score 43; DB 9;
Pred. No. 54;
1; Mismatches
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Pred. No.
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79;
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                   Indels
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GENERAL INFORMATION:

APPLICANT: ROSEN et al.

FILE OF INVENTION: 28 Human Secreted Proteins

FILE REFERENCE: PZ003P2

CURRENT APPLICATION NUMBER: US/09/852,797

CURRENT FILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: 60/265,583

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 69/152,060

PRIOR FILING DATE: 1998-09-11

PRIOR APPLICATION NUMBER: PCT/US98/04858

PRIOR APPLICATION NUMBER: PCT/US98/04858
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RESULT 5
US-09-852-797-116
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Best Local Similarity
7; Conserve
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                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver.
SEQ ID NO 116
LENGTH: 223
TYPE: PRT
Sequence 116, Application US/09852797 Patent No. US20020172994A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION
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CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-09-11
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TITLE OF INVENTION: 28 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                      OR APPLICATION NUMBER: 60/048,189
OR FILING DATE: 1997-05-30
OR APPLICATION NUMBER: 60/057,765
OR FILING DATE: 1997-09-05
OR APPLICATION NUMBER: 60/048,970
OR APPLICATION NUMBER: 60/068,368
OR APPLICATION NUMBER: 60/068,368
OR APPLICATION NUMBER: 60/068,368
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FILING DATE: 1998-03-12
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FILING DATE: 1997-03-14
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70.0%;
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Pred. No.
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US-10-240-819-2
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RESULT 7
US-09-253-794-7
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SEQ ID NO 116
LENGTH: 223
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SEQ ID NO 2
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Best Local :
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CURRENT FILING DATE: 2002-10-07
CURRENT FILING UNIVER: PCT/GB01/01195
PRIOR APPLICATION NUMBER: PCT/GB01/01195
PRIOR FILING DATE: 2001-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BURNIE, JAMES PETER
TITLE OF INVENTION: TREATMENT OF FUNGAL INFECTIONS WITH POLYENE OR BETA GLUCAN
TITLE OF INVENTION: SYNTHASE INHIBITOR ANTI-FUNGALS COMBINED WITH ANTI HSP90
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 050885/0292613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: GB 0008305.5
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 2
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PRIOR APPLICATION NUMBER: 60/057,765
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/048,970
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
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PRIOR APPLICATION NUMBER: 60/048,357
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,189
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PRIOR FILING DATE: 1997-05-30
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PRIOR APPLICATION NUMBER: 60/040,710
PRIOR FILING DATE: 1997-03-14
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                                                                                                                                                                                                                                                                                  PEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic modified OTHER INFORMATION: hsp90 antibody
                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
                                                                                                                                                                                            Local
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                                                                                     102 GGRDFGDSFDY 112
                                                                                                                                                                                                                                                                                                                                                                                                    248
                                                                                                                           2 GGHGYGSSEDY 12
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Similarity 63.6%;
7; Conservative
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70.0%;

    Mismatches

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Pred. No. 60;
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Pred. No. 54;
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                                                                                                                                                                                                                    DB 12; Length 248;
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RESULT 8
US-09-229-200A-8
JS-09-229-200A-8
Sequence 8, Application US/09229200A
Patent No. US20020099179A1
GENERAL INFORMATION: CD4 Specific Recombinant Antibody
ITILE OF INVENTION: CD4 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSE: JOHNSON & JOHNSON
STREET: One JOHNSON & JOHNSON Plaza
CITY: New Brunswick
STATE: NJ
CONNERCY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-253-794-7
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Patent No. US20020018750A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/253,794
FILING DATE: 22-Feb-1999
CLASSIFICATION - CURROWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,157
FILING DATE: 05-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REGISTRATION NUMBER: 28,665
REGISTRATION NUMBER: 18733/464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                      ZIP: 08933-7003
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARMOUR, KATHYN L.
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
MOUSE MONOCLONAL ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HANSEN, Hans J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                               99 DGGHGFCSS 107
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STATE: D.C.
OPERATING SYSTEM: PC-DOS
                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (202)672-5399
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77.8%;
                      183
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Query Match
Best Lccal Similarity
Watches 7; Conserve
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                                                                                               ; SEQUENCE DESCRIPTION: SEQ ID NO: 18: US-09-229-200A-18
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Patent No. US/002099179A1
GENERAL INFORMATION:
APPLICANT: Jolliffe et al.
TITLE OF INVENTION: CD4 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                           TELEFAX: (908) 524-2.
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/229,200A

FILING DATE: 13-Jan-1999

CLASSIFICATION: CURKnown>
ATTORNEY/AGENT INFORMATION:
NAME: John W. Wallen, III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 0RT-948
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 08933-7003
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 13-Jan-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,200A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: John W. Wallen, III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-948
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO:
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DGGHGYGSS 9
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                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New Brunswick
STATE: NJ
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
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TELEFAX: (908) 5
                               Conservative
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77.8%;
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77.8%;
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                           Score 40; DB 9;
Pred. No. 86;
1; Mismatches
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Pred. No. 86;
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                                                           Length 126
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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-795-515-10
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US-09-795-515-10
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                          Sequence 10, Application US/10422049 Publication No. US20030199679A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09795515
Publication No. US20030039645A1
GENERAL INFORMATION:
                                                                                                                             APPLICANT: Adair, John Robert
APPLICANT: Athwal, Dilject Singh
APPLICANT: Emtage, John Spencer
APPLICANT: Boddmer, Mark William
TITLE OF INVENTION: Recombinant Antibodies Specific For TNF-Alpha
CURRENT APPLICATION NUMBER: US/10/422,049
CURRENT FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: US/09/267,281
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 08/456,418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/846,658
APPLICATION NUMBER: 08/846,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10508-3100
                                                                                                                 FILE REFERENCE: CARPOOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (215) 568-34.
INFORMATION FOR SEQ ID NO:
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LENGTH: 126 amino acid
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APPLICANT: Athwal, Dilject S.
APPLICANT: Emtage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645Alris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                99 DGGHGFCSS 107
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77.8%;
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Pred. No. 86;
1; Mismatches
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                                                                                                                                                                                                            US-09-925-302-630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/267,286A
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: 08/557,050
PRIOR FILING DATE: 1998-10-09
PRIOR APPLICATION NUMBER: PCT/US94/06198
PRIOR PILING DATE: 1994-06-01
PRIOR PILING DATE: 1993-06-01
PRIOR PILING DATE: 1993-06-01
NUMBER: 08 SEQ ID NOS: 23
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Sequence 630, Application US/09925302
Patent No. US2002004941A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/10267286A Publication No. US20030108548A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
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                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BLUESTONE, JEFFREY A.
APPLICANT: ZIVIN, ROBERT A.
APPLICANT: JOLLIFFE, LINDA K.
RIPLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
TITLE OF INVENTION: IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
TITLE OF INVENTION: ANTIBODIES
EILE REFERENCE: TOLT:004USC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1995-06-01
PRIOR APPLICATION NUMBER: 08/373,882
PRIOR FILING DATE: 1995-01-17
PRIOR APPLICATION NUMBER: 07/920,378
PRIOR FILING DATE: 1992-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 126
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Local Similarity 77.8%;
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77.8%;
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Pred. No. 86;
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Best Local Similarity
Wetches 7; Conserve
                                                 ; Sequence 1, Application US/09950368
; Patent NO. US20020061580A1
; GENERAL INFORMATION:
APPLICANT: Genemoor International, Inc.
TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes
; FILE REFERENCE: GC511-FCT
                                                                                                                                                                                                                                                                            S
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US-09-738-626-6160
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US-09-925-302-630
                                                                                                                                                                  RESULT 15
US-09-950-368-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
FULE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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SEQ ID NO 630
LENGTH: 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn ver. 3.0 SEQ ID NO 6160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6160, Application US/09738626
Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                     Query Match
CURRENT APPLICATION NUMBER: US/09/950,368
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 09/355,166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-03-08
PRIOR PELICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
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                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 295
                                                                                                                                                                                                                                                                                                                                     Local Similarity
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SENOH, AKIHIRO
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70.0%;
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                                                                                                                                                                                                                                                                                                                 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 9;
Pred. No. 1.1e+02;
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PRIOR FILING DATE: 1999-07-20

NUMBER OF SEQ ID NOS: 21

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 1

LENGTH: 657

TYPE: PRT

NORANISM: Bacillus

US-09-950-368-1

Query Match
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGHGYGSSF 10

Db 469 GSHGYGQEF 477

Search completed: November 7, 2003, 08:16:50

Job time: 11.526 secs
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Sequence 29, Appl
Sequence 29, Appl
Sequence 20, Appli
Sequence 20, Appli
Sequence 2, Appli
Sequence 1, Appli
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Sequence 11, Appli
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US-09-5183-688-18
US-09-519-489-18
US-08-793-624-3
PCT-US95-10194-3
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US-09-152-060-116
US-09-252-991A-19311
US-07-942-245-3
US-08-107-669D-8
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US-08-318-247-11
US-08-557-050-11
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Compugen Ltd.
                                        Sequence 18, Appl Sequence 18, Appl Sequence 18, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 116, App Sequence 118, Appli Sequence 18, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 10, Appli Sequence 11, Appli Sequence 1952, Appli Sequence 1952, Appli Sequence 31892, Appli 
                                              Patent No.
Sequence
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                                                                                                US-08-343-101A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
US-08-343-101A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5830759

GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Moore, Patrick S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma
TITLE OF INVENTION: Virus Sequences And Uses Thereof
NUMBER OF SEQUENCES: 22
        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS:
LENGTH: 861 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RILING DATE:
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4518
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
PELERAN: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,101A
                                                                                                                                                                                                        HYPOTHETICAL:
ANTI-SENSE: N
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1185 AVER
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                 NAME/KEY: Peptide
LOCATION: 1..861
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036
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5830759
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1185 Avenue of the Americas
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linear
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US-08-793-624-29
PCT-US95-10194-29
US-09-255-991A-20968
US-09-215-694-2
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US-08-9173-508-2
US-08-951-742-2
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US-09-183-688-18

Sequence 18, App Patent No. 60935

CORRESPONDENCE ADDRESS:

ADDRESSEE:

COUNTRY: CITY: New York

New York

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Sequence 18, Application US/09519489 Patent No. 6500663 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6093550
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma
TITLE OF INVENTION: Virus Sequences And Uses Thereof
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45185-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09183688
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1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08/343,101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/09/183,688
                                                                                                                                                                                                                       Score 47; DB Pred. No. 32; 2; Mismatches
                                                                                                                                                                                                                                          DB 3; Length 861; 32;
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                                                                                                                                                                                                                                                                                                       US-08-420-235B-3
                                                                                                                                                                         Sequence 3, Application US/08420235B
Patent No. 5801042
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: MOOZE, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 861 amino acids
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                         ADDRESSEE: Cooper &
                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/519,489
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma
TITLE OF INVENTION: Virus Sequences And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
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                                                   CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1.861
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Peptide LOCATION: 1..861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45
                                                                                                           STREET:
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                                                                                                                       DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                       468 DGGHGYGLRYE 478
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                                        10036
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conserv
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Y: U.S.A.
                                                                                                       E: Cooper & Dunham LLP
1185 Avenue of the Americas
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1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                            SEQUENCES
47
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Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 861;
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US-09-519-489-18 RESULT 3

APPLICANT:

Chang, Yuan

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468

DGGHGYGLRYE 478

1 DGGHGYGSSFD 11

US-09-183-688-18

NAME/KEY: Peptide LOCATION: 1..861 OTHER INFORMATION:

ANTI-SENSE: MOLECULE TYPE: YPOTHETICAL:

TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:

TELEPHONE: 214-2-0526

212-278-0400

LENGTH: 861 amino acids
TYPE: amino acid
STRANDEDNESS: single

COPOLOGY:

linear

0

peptide single TELECOMMUNICATION INFORMATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/3
FILING DATE:
ATTORNEY/AGENT INFORMATION:

FILING DATE: CLASSIFICATION: APPLICATION NUMBER:

Best Loc Matches

Local Similarity tes 7; Conserv

Conservative

2

63.6%;

Query Match

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RESULT 6
PCT-US95-10194-3
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CURRENT APPLICATION NUMBER: US/08/793,624C
; CURRENT FILING DATE: 1997-02-18
; NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1376
TYPE: PRT
ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-08-793-624-3
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                                           Sequence 3, Application PC/TUS9510194
GENERAL INFORMATION:
APPLICANT: The Trustees of Columbia University in the City on APPLICANT: City
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS TITLE OF INVENTION: SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chang, Yuan
APPLICANT: MOOTE, Patrick S.
TITLE OF INVENTION: Unique Assoc
TITLE OF INVENTION: Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1376 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      Local Similarity hes 7; Conserv
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New York
                                                                                                                                                                                                                                                                  DGGHGYGLRYE 486
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amino acid
           E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                               The Trustees of Columbia University in the City of New York
                                                                                                                                                                                                                                                                                                                                        Conservative
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Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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US-09-152-060-116
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US-09-152-060-116
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                                                                                                                                                            EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,189
EARLIER APPLICATION NUMBER: 60/057,765
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-06-06
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                                                     SOPTWARE: PatentIn Ver.
SEQ ID NO 116
LENGTH: 223
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Matches 7; Conserv
                                                                                                                      EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/152,060 CURRENT FILING DATE: 1998-09-11
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1376 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4518
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                          EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,100
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               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                             SARLIER APPLICATION NUMBER: 60/040,710 EARLIER FILING DATE: 1997-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SARLIER FILING DATE: 1997-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: PCT/US98/04858
EARLIER FILING DATE: 1998-03-12
                                                                                                                                                                                                                                                                                                                                 ARLIER APPLICATION NUMBER: 60/048,357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARLIER APPLICATION NUMBER: 60/040,762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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CURRENT APPLICATION DATA;
APPLICATION NUMBER: PCT/US95/10194
FILING DATE;
CLASSIFICATION;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ILING DATE: 1997-05-30
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Pred. No.
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Gaps

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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19311
LENGTH: 328
TYPE: nrm
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US-09-252-991A-19311
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AUCUSIOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18, App
Patent No. 56396
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION UNUMBER: US/07/942,245
APPLICATION UNUMBER: US/07/942,245
PILING DATE: 09-SEE-1992
CLASSIFICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000
TELECOMMUNICATIO
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APPLICANT: 1
APPLICANT: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States ZIP: 20037-3202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pensylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 DGGQGHGVGFD 275
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7; Conserva
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GUILD,
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70.0%;
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Michael A.
Braydon C.
SURFACE RESIDUE VENEERING OF RODENT
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Pred. No. 32;
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US-07-942-245-33
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US-07-942-245-33
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                                                                                                                                            TELEPAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 33
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: 105 amino acids
TYPE: 105 amino acids
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Matches
                                                                    Query Match 55.6%;
Best Local Similarity 77.8%;
                                                          Matches
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                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/942,245
FILLING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEPAX: (202) 293-7860
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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99
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                            1 DGGHGYGSS 9
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Y: United States
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                                                        Conservative
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ROGUSKA,
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Michael A.
Braydon C.
Braydon C.
SURPACE RESIDUE VENEERING OF RODENT
ANTIBODIES
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77.8%;
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Stephen M.J.
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                                                                       Score 40; DB
Pred. No. 49;
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Pred. No. 46;
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Avenue, N.W.
                                                     Mismatches
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                                                                                   DB 1; Length 125;
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RESULT 11 US-08-107-669D-8

Sequence 8, Application US/08107669D Patent No. 5766886 GENERAL INFORMATION:

APPLICANT:

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RESULT 12
US-08-472-788A-8
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Patent No. 5770196
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,788A
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/107,669D FILING DATE: 13-AUG-1993 CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/US92/10906 FILING DATB: 14-DEC-1992
                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                            STREET: 1100 New CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: ami
TOPOLOGY:
CLASSIFICATION:
                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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REFERENCE/DOCKET NUMBER: 06
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: protein
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                                                                                                                                                                                                                                                                              Studnicka, Gary M.
VENTION: Modified Antibody Variable Domains
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1100 New York Ave., N.W., Suite 600
                                                                                                                                                                  USA
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VENTION: Modified Antibody Variable Domains (as amended)
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1; Mismatches
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RESULT 13
US-08-477-531B-8
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PILING DATE: 14-DEC-1992
PRIOR APPLICATION NUMBER: US 07/808
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Michele A. Cimbala
REGISTRATION NUMBER: 3,851
REFERENCE/DOCKET NUMBER: 0610
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,531B
                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                      CLASSIFICATION: 436
PRIOR APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
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APPLICATION NUMBER:
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                                                                                                                                                                                      APPLICATION NUMBER: 08/10 FILING DATE: 13-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1100 New CITY: Washington
                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                             FILING DATE:
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ses 7; Conserv
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TELEFAX: 202/371-2540
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1100 New York Ave., N.W., Suite 600
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77.8%;
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Pred. No.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER I IMP PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,569B
FILING DATE: 07-SEP-1994
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
PREFERENCE/DOCKET NUMBER: CARP-0032
TELECOMMUNICATION INFORMATION:
TELEPAN: (215) 568-3190
TELEFAX: (215) 568-3190
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                RESULT 15
US-08-082-842A-8
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Best Local Similarity
Matches 7; Conserve
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US-08-303-569B-10
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; MOLECULE TYPE: protein
US-08-477-5318-8
Sequence 8, Application US/08082842A Patent No. 5869619
GENERAL INFORMATION:
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APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Entage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 31
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acid
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
STREET: One Liberty Place - 46th Floor
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5859205

    126 amino acids
amino acid
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Pred. No.
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Search completed: November 7, 2003, 07:30:06
Job time: 2.76235 secs
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COUNTRY: U.S.

ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/082,842A
FILING DATE: 23-UN-1993
CLASSIFICATION NUMBER: PCT/US92/10906
FILING APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 13-DEC-1992
PRIOR APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000002
TELECOMMINICATION INFORMATION:
RESERBNCE/DOCKET NUMBER: 0610.1000002
TELECOMMINICATION INFORMATION:
TELEPHONE: 202/371-2600
                                                                                                                                                                      Matches
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Best Local
                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 126 amino acids
                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
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                                                                                                                                                                                        Local
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77.8%;
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Pred. No. 49;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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2: pir2:*
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4: pir4:*
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Copyright (c) 1993 - 2003
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        2003, 07:21:18; Search time 15.4112 Seconds (without alignments)
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Compugen Ltd.
Description
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120	119	136	469	122	96	118	135	160	98	98	117	102	134	142	131
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ig neavy chain V r	Ig heavy chain V r	Ig heavy chain V r	Ig gamma-2a chain	Ig heavy chain V r	Ig heavy chain V-I	Ig heavy chain v r	anti-Sm antibody V	v.	Ig heavy chain V r	Ig heavy chain V7	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain pre	Ig heavy chain V $r$

## ALIGNMENTS

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RESULT 2
S33905
Ig heavy chain precursor V region - synthetic
C;Species: synthetic
C;Species: synthetic
C;Date: 13-Jan-1995 #sequence_revision 30-Apr-1998 #text_change 20-Oct-2000
C;Accession: S33905
R;Llu, A:V; Robinson, R.R.; Hellstroem, K.S.; Murray Jr., E.D.; Chang, C.P.; Hell
Proc. Natl. Acad. Sci. U.S.A. 84, 3439-3443, 1987
A;Title: Chimeric mouse-human IgG1 antibody that can mediate lysis of cancer celle
A;Reference number: S33905; MUID:87204152; PMID:3106970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L6 mAb heavy chain V region - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Species: Mus musculus (house mouse)
C/Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C/Accession: B42848; 833903
R/Fell, H.P.; Gayle, M.A.; Yelton, D.; Lipsich, L.; Schieven, G.L.; Marken, J.S.
J. Biol. Chem. 267, 15552-15558, 1992
A;Title: Chimeric L6 anti-tumor antibody. Genomic construction, expression, and A;Reference number: A42848; MUID:92348410; pMID:1639794
A;Recession: B42848
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-120, FRE.
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-120 <FE2>
A;Cross-references: EMBL:M90691
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-120 <FEL>
A;Cross-references: GB:M90690; NID:g195065; PIDN:AAA38146.1;
A;Cross-references extracted from NCBI backbone (NCBIN:109960,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: sequence extracted A;Accession: $33903
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Best Local :
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1 CIQLVQSGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKMMGWINTYTGQPTY
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Pred. No. 1.9
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NCBIP:109961)
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A;Accession: S33905

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A;Residues: 1-118 <WEI>
A;Cross-*eferences: EMBL:X65090
C;Superfamily: immunoglobulin V region; immunoglobulin C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; homology <IMM>
                                                                                                                                                                                            R;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, B.P. submitted to the EMBL Data Library, March 1992
A;Description: Structural characterization of CD4 mAb.
                                                                                                                                                                                                                                                                                    Ig heavy chain V region (M-T406) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:D12736; NID:g220595; PIDN:BAA02228.1; PID:g220596 A;Note: sequence extracted from NCBI backbone (NCBIN:63271, NCBIP:63299) C:Superfamily: immunoglobulin v region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin f;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                        A; Molecule type: mRNA
                                                                                                                             A; Status: preliminary
                                                                                                                                                      A;Reference number: S19963
A;Accession: S19967
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A;Reference number: A53285; MUID:92017897; PMID:1922102
A;Accession: A53285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain V and J regions, monoclonal antibody SCBT.M8.1 - mouse (fragrof/Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C;Accession: A53285
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A;Residues: 1-146 <LTU>
A;Cross-references: EMBL:M16072; NID:g195270; PIDN:AAA38229.1; PID:g195271
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A; Residues: 1-119 < SAW >
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Best Local S
Matches 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKNMGWINTYTGQPTY
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Pred. No. 1e-39;
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Pred. No. 2.3e-40;
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R;Fischer, R.; Voss,
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C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C;Accession: S37204
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mRNA
A;Residues: 1-117 <12U>
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c;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S32190
R;Izui, S.
                                                                                                                                                                                                                A;Residues: 1-118 <FIS>
A;Cross-references: EMBL:X74589; NID:g402599; PIDN:CAA52666.1; PID:g1333981
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                         R;Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, submitted to the EMBL Data Library, August 1993 strain and cloning of TMV-specific monoclonal
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A; Accession: S32190
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A;Accession: $37204
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                                                                                                                                                          Similarity
ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSFKGFAYWGQGTLYTVSA
                                                       QIQLVQSGPELKKPGETVKISCKASGYTFIDYSMHWVKQVPGKGLKWMGWINTETGEAKY
                                                                                          EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY
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81.5%;
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Pred. No. 3.3e-39;
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                                                                                                                                      Score 525.5; DB 2
Pred. No. 6.7e-39;
7; Mismatches 12
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Pred. No. 1.5e-39;
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Ig heavy chain V region C; Species: Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data A; Reference number: $35759 A; Accession: $35759
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S35759
R;Froyen, G.F.V.
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J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26325
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;5-88/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: $26325
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A;Molecule type: mRNA
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Matches 98
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Pred. No. 1.6e-38;
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Pred. No. 9.3e-39;
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A;Accession: S19968
A;Status: preliminary
A;Molecule type: mRNA
                                                                                                                    Ig heavy chain V region (M-T408) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change C;Accession: S19968 R;Weissenhorn, W.; Riethmueller, G.; Weiss, B.W.; Rieber, E.P. submitted to the EMBL Data Library, March 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-117 <IZU>
A;Residues: 1-117 <IZU>
A;Cross-references: EMBL:X70091; NID:g288251; PIDN:CAA49696.1; PID:g288252
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Reference number: S32185
A;Accession: S32187
A;Status: preliminary
                                                                       A; Reference number: S19963
                                                                                             A;Description: Structural characterization of CD4 mAb
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C;Species: Mus muscultus (house mouse)
C;Date: 06-Feb-1955 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S32187
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A;Residues: 1-113 <ZII.>
A;Residues: 1-113 <ZII.>
A;Cross-references: GB:M30458; GB:M30459; GB:M30480; GB:M30481;
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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R;Zilber, B.; Scherf, T.; Levitt, M.; Anglister, J.
Biochemistry 29, 10032-10041, 1990
A;Title: NMR-derived model for a peptide-antibody complex.
A;Reference number: A36259; MUID:91104915; PMID:2271636
                                                                                                                                                                                                                                                                                               RESULT 11
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A;Status: preliminary
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78.2%; Pred. No. 6.4e-
cive 11; Mismatches
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; Pred. No. 1.2e-37;
10; Mismatches 12
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1-115 <WEI:

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S19965
Ig heavy chain V region (M-T321) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: O6.Feb-1995 #sequence_revision O6-Feb-1995 #text_change 21-Jan-2000
C;Accession: S19965
C;Accession: S19965
R;Weissenhorn, W; Riethmueller, G; Weiss, B.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
  A; Status: preliminary
A; Molecule type: mRNA
A; Residuse: 1-115 < WEI>
A; Cross-references: EMBL:X65088
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 8-91/Domain: immunoglobulin
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;10-93/Domain: immunoglobulin homology <IMM>
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A; Accession: $19965
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A; Residues: 1-124 < SHI>
A; Accession: PH1406
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J. Exp. Med. 176, 1209-1214, 1992
A;Title: Heavy chain variable (VH) region diversity generated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region (clone micro m+ 46-12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000
C;Accession: PH1404; PH1404
D;Chicagosion: TH1404; PH1404
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A; Residues: 115-121 <SH2>
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R;Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Fliege Gene 121, 271-278, 1992
A;Title: Combinatoxial functions of two chimeric antibodies directed to human A;Reference number: PH1224; MUID:93077041; PMID:1446824
A;Recession: PH1225
A;Molecule type: mRUA
A;Residues: 1-139 <WEI>
A;Cross-references: GB:550263; NID:9260763; PIDN:AAB24319.1; PID:9260764
A;Note: this mouse sequence was hybridized and fused with a human constant r. C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>F;20-139/Product: Ig heavy chain V region #status predicted <MAT>
F;34-117/Domain: 1mmunoglobulin homology <IPMN>
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H45722
                                                                                                                                                                                                                                    G;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000 G;Accession: H45722  
R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, J. Virol. 67, 489-496, 1993  
J. Virol. 67, 489-496, 1993  
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                                                              A; Note: sequence extracted from NCBI backbone C; Superfamily: immunoglobulin V region; immuno
                                                                                                                                    A;Status: preliminary; not compared with A;Molecule type: nucleic acid A;Residues: 1-119 <SIM>
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C;Species: Mus musculus (house monee)
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C;Date: 17-Apr-1993 #sequence_revision
C;Accession: PH1225
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                                    Keywords: glycoprotein
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immunoglobulin homology < IMM>
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Query Match

Local

l Similarity 96; Conserv

Conservative

9;

Score 504; DB 2; Length 119; Pred. No. 5e-37; 9; Mismatches 10; Indels

8

Gaps

78.0%; 78.0%;

Search completed: November 7, 2003, 07:36:18 Job time: 15.5112 secs

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652.278 Million cell updates/sec
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             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                         homo sapien
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Mammalia; Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-82152818; PubMed-6801765;
Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
Capra J.D.;
                                           P01769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . Match 53.9%; Score 348; DB 1; Length 140; Local Similarity 54.1%; Pred. No. 1.3e-28; es 66; Conservative 24; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain."; finenuoglobulin-111(198-311(198-311); schedus 216:399-311(1982): :- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IG HEAVY CHAIN V REGION 9367.
IG-LIKE.
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140 AA; 15514 MW; 25A4CBBE31DASCB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HV02_MOUSE STANDARD; PRT; 140 AA. P01746.
201746.
21-UUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HESP, PO1810, 2003.

InterPro: IPR007110; Ig-like.

InterPro: IPR003006; Ig_MHC.

InterPro: IPR003596; Ig_v.

Pfam; PF00047; ig; 1.

SMART; SMO046; Ig_v.

Immunoglobulin V region; Hybridoma; Signal.
                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                        HV1A HUMAN
HV41 MOUSE
HV50 MOUSE
HV14 MOUSE
                                                                HV3K HUMAN
HV3D HUMAN
HV34 MOUSE
                                                                                                                                                                                                                                       HV3B_HUMAN
                                         HV3H HUMAN
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122 AA;
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SEQUENCE
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TO THE SAME J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";
Eur. J. Immunol. 12:1023-1032(1982)
-!- MISCELLANBOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VKLVESGPELKKPGETVKISCKASGYIFTNYGMMWVKQAPGKGLKMMGWINTYTGEPTYA
                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
15 heavy chain V region 36-65.
Buka musculus (Mouse)

Bukaryotai Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Muxinae; Mus.
1018_TaxID=10090;
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 weavy chain VII region CAM.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 AA; 13307 MW; FF04E4A167B654AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-83131846; PubMed=6186498;
Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
Marabak-Rothstein A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.3%; Score 344; DB 1;
53.7%; Pred. No. 2.9e-28;
iive 24; Mismatches 28;
                                                                                                                                                                                                                                                                       120 AA
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Bybridoma.
                                                                                                                                                                                                                                                                       PRT;
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InterPro, IPR007110, Ig-like.
InterPro, IPR003006; Ig_MHC.
InterPro, IPR003596; Ig_V.
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Best Local Similarity 53.74
Matches 65; Conservative
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P01747;
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P01768;
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NON TER
SEQÜENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIJINE-64182519; FubMed-6201362;
Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
"A V region determinant (idiotope) expressed at high frequency in B
Lymphocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523 (1984).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                      Lehman D.W., Putnam F.W.;
"Amino acid sequence of the variable region of a human mu chain:
location of a possible JH segment.";
Proc. Natl. Acad. Sci. U.S.A. 77:2239-3243 (1980).
-1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF
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                                                                                                                                                      PATIENT WITH MACKOGLOBULINEMIA.
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02021; M3HUAM.
GO, GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006557; P:immune response; NAS.
InterPro; IPR007110; IQ-like.
InterPro; IPR003506; IQ-MC.
InterPro; IPR003596; IQ-V.
                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF0047; ig; 1.
SMART; SM00406; IGv; 1.
PR05TE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
DOMAIN 1.112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 51.3%; Score 331.5; DB 1; Local Similarity 50.4%; Pred. No. 5.5e-27; les 62; Conservative 26; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13668 MW; A42D0F17D252F1C2
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01-JNN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IIG heavy chain V region AC38 205.12.
Mus musculus (Mouse).
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MEDLINE=81013859; PubMed=6774332;
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HSSP; P01789; 1MCP.
InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig-MIC.
InterPro; IPR003596; Ig-V.
PFam; PF00047; Ig; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
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"Heavy chain variable region contribution to the NPD family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1998).

-!- MISCELLAN-GOUS: THE B1-8 MU CHAIN MENA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL (NPB ANTIBODIES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                 HV07 MOUSE STANDARD, PRT, 139 AA.
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SBP-2003 (Rel. 42, Last annotation update)
16-SBP-2003 (Rel. 42, Last annotation update)
16 heavy chain V region B1-8/186-2 precursor.
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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1. J. Immunol. 128:302-307(1982).

2. I. MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOWA PROTEIN THAT ELIMS INULIN.

2. I. SIMILARITY: Contains 1 immunoglobulin-like domain.

3. PIR; C92811; AVMS06.

3. R. RISP; PO1789; JUCP.

3. R. InterPro; JFR003106; Ig_MHC.

4. InterPro; JFR003206; Ig_WHC.

5. R. InterPro; JFR003206; Ig_WHC.

6. R. InterPro; JFR003206; Ig_WHC.

7. R. RISP; PO1047; ig; 1.

8. RMART; SM00406; IGv; 1.

8. RMART; SM00406; IGv; 1.

8. RMART; PS50835; IG_LIKE; 1.

8. RMART; PS50835; IG_LIKE; 1.

9. RMART; PS50835; IG_LIKE; 1.

9. RMART; PS50835; IG_LIKE; 1.

9. RMART; PS50835; IG_LIKE; 1.

9. RMART; PS50835; IG_LIKE; 1.

9. RMART; PS50835; IG_LIKE; 1.

10. RMART; PS50835; IG_LIKE; 1.

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10. RMART; PS50835; IG_LIKE; 1.
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Johnson N., Slankaxd J., Paul L., Hood L.;
"The complete V domain amino acid sequences of two myeloma inulin-
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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51.2%; Score 330.5; DB 1; Length 53.3%; Pred. No. 6.7e-27; ive 21; Mismatches 32; Indels
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115 AA; 12810 MW; B67AD6638A121A5F CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Mus musculus (Mouse).
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BY SIMILARITY.
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P01801;
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                             PIR, A90809; MINSI8.
PDB; 1A6U; 27-MAX-98.
PDB; 1A6W; 15-UUL-98.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; IG-V.
Pfam; PF00407; ig; 1.
SMART; SMO0406; IGY; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
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D SEGMENT.
                                                                                                                                                                                         EMBL; J00529; AAA38170.1; -.
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139
139 AA;
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Matches 61; Conserv
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57 EPTYADDFKGRRAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYWGQGTLVT 116 

1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWI----NTYTG 1 BVKLEBSGGGLVQPGGSMKLSCVASGFTFSNYWMNWVRQSPEKGLEWVAEIRLKSNNYAT

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HV12_MC
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Best Local S
Matches 64
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P01756;
SEQUENCE.
MEDLINE=80078170; PubMed=6765983; Schilling J., Clevinger B., Davie
                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                    Mus musculus (Mouse)
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Biochemistry 21:5415-5424(1982).
-i- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN
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MEDLINE=83075344; PubMed=6816276;
MENLINE=83075344; PubMed=6816276;
MENLINE=83., Fuhrman J.S., Schilling J.W., Rogers J.,
                                                                                                                                       NCRI_TaxID=10090;
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PROSITE; PS50835; IG LIKE; 1.

Immuzoglobulin V region; Glycoprotein.

DOMAIN 1 116

IG-LIKE.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
1g heavy chain V region MOPC 104E.
Mus musculus (Mouse).
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SMART; SM00406; IG
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HSSP; P01789; 1MCP.
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Mammalia; Eutheria; Rodentia;
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Similarity 52:0%;
64; Conservative 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NQKFKGKATLTVDKSSSTAXMQLNSLTSEDSAVYYCARDYDWY---
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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Davie J.M., Hood L.;
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Pred. No. 2.4e
21; Mismatches
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N-LINKED (GLCNAC. .
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Sciurognathi; Muridae; Murinae; Mus
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Vrana M., Rudikoff S., Potter M.;
Vrana M., Rudikoff S., Potter M.;
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Nature 283:35-40(1980)

-I- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO HID DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF MHICH OCCUR IN THE DAND J SEGMENTS.

-I- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
                                                                                                                                                                                                                                                                                                                                                                                                 -1- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA BINDS INULIN.
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Best Local:
HV01_MOUSE STANDARD;
p01745;
21-JUL-1986 (Rel. 01, Created)
                                                                     TSTOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
NON_TER
SEQUENCE
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HV33_N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Immunol. 128:302-307(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HV33 MOUSE STANDARD; PRT; 115 AA. P01802; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 15 heavy chain V-III region W3082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASSP; PO1810; 2PBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BINDS INULIN.
-!- SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; D92811; AVMS82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Johnson N., Slankard J., Paul L., "The complete V domain amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=82099361; PubMed=6798111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                    115 A
                                                                                                                                                                                                                                                             59 TYADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGRAYWGQGTLYTVS
                                                                                                                                                                                                                                61 HYAESVKGRFTISRDDSKSSVYLRMNNLRPEDTGIYYCT---
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                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                         A 119
                                                                                                                                                                                                                                                                                                           EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWI--NTYTGEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVKLEBSGGGLVQPGGSMKLSCVASGFTFSNYWWWWVRQSPEKGLEWVABIRLKSHNYAT 60
                                                                                                                                                    115
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22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12887 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 323; DB 1;
Pred. No. 3.8e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG-LIKE.
BY SIMILARITY.
                                                PRT;
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No. 2.9e-26;
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Best Local :
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HV15_MOUSE
                            "Simultaneous expression of immunoglobulin mu an
by a cloned B-cell lymphoma: a single copy of th
by two adjacent CH genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982)
                                                                                                                                      MEDLINE=82222262; PubM
Knapp M.R., Liu C.-P.,
Blattner F.R.;
                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region BCL1 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG LIKE;
Immunoglobulin V region.
DOMAIN
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON TER
SEQUENCE
                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P01759;
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15-SEP-2003 (Rel. 42, Last annotation update)
19 heavy chain V region MPC 11.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Nucleic Acids Res. 8:4839-4840(1980).
-!- MISCELLANEOUS: THIS SECUENCE WAS TRANSLATED FROM AN
-FROM A MYELOMA THAT SECRETES IGGSB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; i.
SMART; SM00406; IGv;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam: PP00047: ig. 1
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HSSP; P01810; 2FBJ.
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                  SIMILARITY:
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Acad. Sci. U.S.A. 79:2996-3000(1982).
ITY: Contains 1 immunoglobulin-like domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                        PubMed=6806821; .-P., Newell N.,
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Pred. No. 6.4e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG-LIKE
                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                Ward R.B., Tucker P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136
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                                                                                 delta heavy chains 
VH gene is shared
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Best Local S
Matches 59
                                                                                                                                                                                                                                                                                                         P03930;
23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation updat
77 heavy chain V region TEPC 1017 precursor
                                                                                                                                                                                                                       MEDLINE=84248078; PubMed=6429663; MEDLINE=84248078; PubMed=6429663; Medline=84248078; Pichards J.
                                                                Interruc, 19; 1.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
SMART; PS50835; IG LIKE; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                DOMAIN
DOMAIN
                                                                                                                  HSSP, P01810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003396; Ig_v.
                                                                                                                                                                              "Illegitimate recombination generates a class switch delta in an IgD-secreting plasmacytoma."; Proc. Natl. Acad. Sci. U.S.A. 81;4164-4168(1984).
                                                                                                                                                                                                                                                                                                                                                                                        HV48
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                                                              SIGNAL
                                                                                                                                                                    PIR; A02033; HVMST7.
                                                                                                                                                                                                                    Tucker P.W.;
                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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                                                                        Signal
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IG HEAVY CHAIN V REGION TEPC 1 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 321;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG HEAVY CHAIN V REGION BCL1. IG-LIKE.
                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                              গে
                                                                                                                                                                                                                                                                                                                           precursor
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                                               CHAIN V REGION TEPC 1017.
                                                                                                                                                                                                                             Blattner F.R.,
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Best Local :
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21-JUL-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=77100368; PubMed=401950;
Adetugbo K., Milstein C., Secher D.S.;
"Molecular analysis of spontaneous somatic mutants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=81234548; Bothwell A.L.M., P
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                                                                                                                                            Immunoglobulin
NON_TER
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v.
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PDB; 1IGC; 03-JUN-95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 265:299-304(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Heavy chain variable antibodies: somatic mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain V reg
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                  EMBL; J00522; AAD15290.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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5 (Rel. 01, 13)
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138 AA;
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el. 42, Last annotation update)
V region MOPC 21 precursor (Fragment)
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COMPLEMENTARITY-DETERMINING-3.

FRAMEWORK-4.

BY SIMILARITY.
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DISULFID CONFLICT CONFLICT

HYAD -> DYAH DN -> ND (IN

(IN REF. 2). REF. 2).

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HV27_MOUSE
ID HV27_
AC P0179
AC P0179
DT 21-JU
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OC Eukar
OC Mamma
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Best Local S
Matches 63
                                                                                                                                                                                                                                                                                                                                                   InterPro; .... 19; 1.

Pfam; PP00047; 1Gy; 1.

SMART; SW00406; IGy; 1.

PROSITE; P850835; IG LIKE; 1.

Immunoglobulin V region.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 60; Conserva
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NON TER
SEQÜENCE
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BINDS INULIN.

-:- SIMILARITY: Contains 1 immunoglobulin-like domain.

PIR; A938L8; AVNSAB.

HSSP; P01810; 2FBJ.

InterPro; IPR007110; Ig-like.

InterPro; IPR003106; Ig MHC.

InterPro; IPR003596; Ig MHC.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H'27 MOUSE STANDARD; PRT; 113 AA. P01796; PRT; 113 AA. 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 15 heavy chain V-III region A4.
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CONFLICT
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE.
MEDLINE-78158406; PubMed=417344;
Vrana M., Rudikoff S., Potter M.;
"Sequence variation among heavy chains from inulin-binding myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins.";
Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                            / Match 49.4%; Score 319; DB 1; Length 113; Local Similarity 52.9%; Pred. No. 9.4e-26; hes 63; Conservative 18; Mismatches 30; Indels
                                                                   61 HYAESVKGRFTISRDDSKSSVYLOMNIRAEDTGIYYCT----TGFAYWGOGTLVTV 113
                                                                                                  59 TYADDEKGREAFSLETSASTAYLQINNLKNEDTATYFCALYGNSEKGFAYWGQGTLVTV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60; Conservative
                                                                                                                                                                   1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGIKWMGWI--NTYTGEP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSP-KGFAYWGQGTLVTVSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 DVQLVESGGGLVQDGGSRXLSCAASGFTFSSFGWHWVRQAPEKGLBWVAYISSGSSTLHY 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWYKQAPGKGLKWMGWINTYTGEPTY
                                                                                                                                               EVKLEESGGGLVQPGGSMKLSCVASGFTFSNYWWWWVRQSPEKGLEWVAEIRLKSHNYAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADTVKGRFISRDNPKNTLFLQMTSLRSEDTAMYYCARWGNYPYYAMDYWGQGTSVTVSS 136
                                                                                                                                                                                                                                                                                                            113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;
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12675 MW; 76658C121C598285 CRC64;
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120
136
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BY SIMILARITY.
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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(Without alignments)
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sp_organelle:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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sp human:*
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sp_mammal:*
sp_mhc:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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318.5	319	320.5	322.5	323	324	325.5	325.5	326	327	327.5	329.5	330	330	330.5	331	331.5	332	332.5	334.5	335	335	338	338	338.5	340	340	342.5	343
49.3	49.4	49.6	49.9	50.0	50.2	50.4	50.4	50.5	50.6	50.7	51.0	51.1	51.1	51.2	51.2	51.3	51.4	51.5	51.8	51.9	51.9	52.3	52.3	52.4	52.6	52.6	53.0	53.1
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## ALIGNMENTS

Qy 1 EVKLYESGPELKKPGETYKISCKASGYIFTNYGMNWYKQAPGKGLKWMGWINTYTGEPTY	Query Match 84.4%; Score 545.5; DB 11; Length 241; Best Local Similarity 86.6%; Pred. No. 1.5e-46; Matches 103; Conservative 6; Mismatches 9; Indels 1; Gaps	O221A6 ID 0921A6 ID 0921A6; AC 0921A6; AC 0921A6; DT 01-DEC-2001 (TrEMBLrel. 19, Created) DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) DT 01-DEC-2001 (TREMBLRel. 19, Last sequence update) DT 01-DEC-2001 (TREMBLRel. 19, Last sequence update) DT 01-DEC-2001 (TREMBLRel. 19, Last sequence update) DE Anti-CEA is Dutherlas; Rodentia; Sciurognathi; Muridae; Murinae; Mus. RX MCBI_TAXID=1090;	DECITION 1
	; Gaps 1;	Omi; Mus. Mus. -95 and	

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61

ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYWGQGTLVTVSA

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Strausberg R.;
Submitted (FEB-2001) to the EME
Submitted (FEB-2001) to the EME
EMBL; BC003495; AAH03495.1; -.
HSSP, P01810; 2FBJ; Ig-like.
InterPro; IPR0031006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMARY; SM00406; IGv; 1.
PROSITE; P850835; IG_LIKE; 4.
PROSITE; P850835; IG_LIKE; 4.
PROSITE; P850835; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 484 AA; 52567 MW;
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Q925S1;
01-DBC-2001
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Q991A6;
01-JUN-2001
01-JUN-2001
01-MAR-2003
"Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after irradiation in mice."; World J. Gastroenterol. 6;709-717(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-BALB/c;
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01-MAR-2003
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                                                                                                                                                                                                                                                      PubMed=11819679;
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Mus musculus (Mouse).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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Rodentia;
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9; Mismatches
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ASTAYLQINNLKNEDTATYFCALYGNSPKGFAYWGQGTLVTVSA 119

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Matches 90
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Pfam; pr00047; ig; 2.

Pfam; pr000405; IGv; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

PROSITE; PS50835; IG LIKE; 1.

PROSITE; PS50835; IG LIKE; 1.

PROSITE; PS50835; IG LIKE; 1.

PROSITE; PS50835; IG LIKE; 1.
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Q9JL79;
01-OCT-2000
01-OCT-2000
01-MAR-2003
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                           Malkiel S., Liao L., Cunningham M.W., Diamond B., "T-Cell-dependent antibody response to the dominant streptococcal polysaccharide, N-acetyl-glucosamine, with cardiac myosin.", Infect Tmm: ""
                                                                                                                                                                                                                                                                                                                                                      Infect. Immun. 68:5803-5808(2000).
EMBL; AF206027; AAF69325.1; -.
HSSP; P01772; 2FB4.
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SMART; SM00406; IGv;
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Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-myosin immunoglobulin heavy chain variable reg
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EMBL; AF240168; AAK43733.1, -

InterPro; IPR007110; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                             InterPro; IPR007110; Ig-like
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=A.CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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PS50835; IG_LIKE;
ETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTYADDFKGRFAFSLETS
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75.6%;
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                                                  Score 461; DB 11;
Pred. No. 1.5e-38;
3; Mismatches 10;
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Sciurognathi; Muridae;
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RESULT 6
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Best Local S
Matches 73
Clin. Immunol. Immunopathol. 8: MMEL; AF035020; AAD56256.1; -. HSSP; PO1810; 2FBJ. InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig MHC. InterPro; IPR003596; Ig_v.
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Submitted (SEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF307936; AAL09420.1; -.

Interpro, IPR007110; Ig-like.

Interpro, IPR0073596; Ig_MHC.

Interpro; IPR003596; Ig_WHC.
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Q9UL94;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
vyosin-reactive immunoglobulin heavy chain variable
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Q920E8;
01-DEC-2001
01-DEC-2001
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE=98277139; PubMed=9614934;

MUX., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                              "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                            Young D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Fragment)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Pterin-mimicking anti-idiotope heavy chain variable
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Mammalia; Eutheria;
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Rodentia;
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Niotope of Pterin-Mimicking Antibodies
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RESULT 8
Q9UL95
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PRELIMINARY;

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RESULT 7

Q9ULD

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AC Q9UL

DT 01-M

DT 01-M

DT 01-M

DT 01-M

OC ELM

OC Mamma

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Best Local S
Matches 68
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Best Local
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PR0STIE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_IKE; 1
NON_TER 1 1 1 19
NON_TER 119 119
SEQUENCE 119 AA; 13205 MP
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NON_TER
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9UL92 PRELIMINARY; PRT; 124 AA.
Q9UL92;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035022; AAD56258.1; -.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wu X., Liu B., Van
Young D.C.;
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SEQUENCE FROM N.A.
MEDULINE=98277139; PubMed=9614934;
Van der Merwe P.L.,
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TVSS 124
                                                                                                                                                                                   EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYMHWVRQAPGQGLEWMGIINPSGGSTSY
                                                                                                                                                                                                            EVKLVESGPELKKPGETVKISCKASGYIFTNYGWNWVKQAPGKGLKWMGWINTYTGEPTY
                                          TVSA 119
                                                                                        AQXFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGLYVVVPAAFSRFDYWGQGTLV
                                                                                                                                   ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCA--LYGNSPKGFA---YWGQGTLV
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124 AA;
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; 13205 MW;
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                                                                                                                                                                                                                                                                                                       58.3%;
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57.1%; Pred. No. 4.3e-30;
tive 22; Mismatches 29
                                                                                                                                                                                                                                                                                      24;
                                                                                                                                                                                                                                                                                                          Score 376.5;
Pred. No. 5.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PR0SITE; P850835; IG_LIKE; 1.
STRAIN=C57BL/G; TISSUE=Pancreas;

MEDLINE=21085660; PubMed=11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Pukuda S.,

Airawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9D8L4
Q9D8L4;
Q1-JUN-2001
01-JUN-2001
01-MAR-2003
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01-MAY-2000
01-MAY-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Butheria; Rodentia; NCBI_TaxID=10090;
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1810060009Rik protein
IGH-1 OR 1810060009RIK.
Mus musculus (Mouse)
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Young D.
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MEDLINE=98277139; PubMed=9614934;
Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                  SEQUENCE FROM
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HSSP; P01810; 2FBJ
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(TIEMBLrel. 13, Last sequence update)
(TIEMBLEL 23, Last annotation update)
Live immunoglobulin heavy chain variable region
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Primates;
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Last annotation updat
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Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                    Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
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Mismatches 29
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Matches 68
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Best Local :
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Q96QS0;
Q96QS0;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
O1-MAR-2003 (TrEMBLrel 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative matrix cell adhesion Homo sapiens (Human). Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., arriboldi M., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Mang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Mammalia; Eutheria;
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SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 1.

SEQUENCE 473 AA; 51699 MW;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001)
EMBL; AK007918; BAB25349
HSSP; P01842; 7FAB.
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                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                  CVQLVQSGAEVKXPGASVKVSCXASGXTFSNYXMMVVRQAPGQGFEMMGVINPSGGSARX
                                                                                                                                                                                    BVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKMMGWINTYTGEPTY
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                                                                                                                                                                                                                                                                                  Conservative
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Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                      55.2%; Score 356.5; DB 4; 52.3%; Pred. No. 6.8e-28; tive 22; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to the EMBL/GenBank/DDBJ
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, Mat-CAM 3).'
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O1-MAR-2002 (TIEMBLITE), 2

O1-MAR-2002 (TIEMBLITE), 2

O1-MAR-2003 (TIEMBLITE). 2
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MEDLINE=S6409289; PubMed=8814271;
MIOCH M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S Wloch M.K., Alexander A.L., Pippen and VH CDR3 sequence among "Differences in V kappa gene utilization and VH CDR3 sequence among anti-DNA from C3H-lpr mice and lupus mice with nephritis.";

- " Tmmunol. 26:2225-233 (1996).
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Q8VIJ1;
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Q1-MAR-2002
Q1-MAR-2003
SEQUENCE FROM N.A.

Zheng S., Shao X., Cao J., Geng L., Fang Y., D.

"Identification and characterization of SNC66,

down-regulated in colorectal cancer.";
                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Mammalia; Eutheria; Rodentia;
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IPR003006; Ig_MHC.
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(TrEMBLrel. 23, Last annotation update)
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Sciurognathi; Muridae; Murinae; Mus.
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Matches 67
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Best Local Similarity
Matches 65; Conserv
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP307937; AAL09421.1; -.
InterPro; IPR0037110; Ig-like.
InterPro; IPR003706; Ig_MHC.
InterPro; IPR003906; Ig_WHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q920E7 PRELIMINARY; PRT; 119 AA. Q920E7; Q920E7; Created)
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat)
Pterin-mimicking anti-idiotope heavy chain variab
                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF28366; AAL36987.1; -.
InterPro; IPR007110; Ig_1lke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Ffam; PF00047; Ig; 4.
SMART; SM00405; IGv; 1.
PROSITE; PS00290; IG_MHC; 1.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 497 AA; 53665 MW; F24D08DFA5A663E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia;
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                                                                                                      13
                                                                                                                                          61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYWGQGTLVTVSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 DFKGRFAPSLETSASTAYLQINNLKNEDTATYFCALYGN--SPKGFAY----WGQGTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 QLEQSGAEVTKPGASVKVSCKASGYTFIAYDINWVRQAPGQGLEWMGWMNPQTGNTEFAQ
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                                                                                                                                                                                                                             EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKMMGWINTYTGEPTY
                                                                                                   PDSVKGRFTISRDNAKNTLYLOMSSLKSEDTAMYXCARHGDYDVGFAYWGQGTLVTVSA
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119 AA;
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                                                                                                                                                                                                                                                                                                     54.6%; Score 353; DB 11;
54.6%; Pred. No. 1.1e-27;
tive 24; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.8%;
54.0%;
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Pred. No. 4.7e-27;
1; Mismatches 28
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                                                                                                                                                                                                                                                                                                                                                                                                                F6B904044381CA7C CRC64;
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chain variable
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C TISSUE-Breast tumor;

A Strausberg R.;

A Strausberg R.;

A Strausberg R.;

A Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

R EMBL; BC029188; AAH29188.1; -.

R InterPro; IPR003599; Ig_-1ike.

InterPro; IPR003597; Ig_-01.

InterPro; IPR003597; Ig_-01.

InterPro; IPR003597; Ig_-01.

InterPro; IPR003596; Ig_-W.

InterPro; IPR003596; Ig_-W.

R InterPro; IPR003596; Ig_-W.

SMAKT; SM00407; IG; 4.

SMART; SM00407; IGC1; 3.

SMART; SM00406; IGV; 1.
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Best Local S
Matches 67
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R MSD; MGI:96486; Igh-VU558.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR003006; Ig_MHC.

R InterPro; IPR003596; Ig_v.

R InterPro; IPR003596; Ig_v.

R Pfam; PP0047; ig; 4.

R PROSITE; PS00290; IGMC; 2.

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Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Q91WR1,
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 53.0 kDa protein.
1GH-VJ558 OR A1893585.
Mus musculus (Mouse).
Mus musculus (Mouse).
Mus musculus (Mouse).
Mus musculus (Mouse).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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PS50835; IG_LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.8%; Score 347.5; DB 11; ilarity 53.6%; Pred. No. 2.1e-26; Conservative 23; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1e-26;
ches 28; Indels
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Matches 63
                                                                                                                                                               PROSITE; PS00290; IG MHC; 2. SEQUENCE 480 AA; 51645 MW;
80 NEKFKGKATLTADKSSNTAYMHLSSLTSENSAVYFCA--RSKLGGFAYMGQGTLVTVSA 136
                  61 ADDFKGRPAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYMQQGTLYTVSA 119
                                                   63 ;
                                                                                                        h 53.7%; Score 347; DB 11;
Similarity 52.9%; Pred. No. 2.3e-26;
63; Conservative 26; Mismatches 28;
                                                                                                                                                               8690A63C669CDBED CRC64;
                                                                                                                                 Length 480;
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Search completed: November 7, 2003, 07:34:32 Job time : 42.343 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     Score
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        Match
                                                                                                                                                                                                                                                                                                         Query
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368.069 Million cell updates/sec
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3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:
5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:
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5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:
6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Anti-c-erbB-2 sing
Single chain antib
741F8 anti-c-erbB-
Single chain bindi
Anti-c-erbB-2 sFv'
                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                        Anti-FIX/FIXa anti
Chimeric 31.1 anti
KM10 Heavy Chain V
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117	141	160	442	183	123	183	366	365	667	466	505	503	503	499	252	252	183	183	183	183	183	183	183	183	183	183	119	118	115	138	140	140	139	139	139
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AAB84741	AAR47205	AA835101	AAB72230	AAW89536	AAB98664	AAP94778	AAW35132	AAW35131	AAR39573	AAR40750	AAU72875	AAU72874	AAU72873	AAU72872	AAB36825	AAB12562	AAB98087	AAW47518	AAW41068	AAW47511	AAW10240	AAW16341	AAW10586	AAP82939	AAP82938	AAP82936	AAB98666	AAR25414	AAB84740	AAR37717	AAR64257	AAR64232	ABU58898	0	AAW06217
ő	Human/murine IL-1		Humanised 323/A3 (	Anti-cancer antibo	Murine protein #1.	V region of the L6	R. pipiens recombi	R. pipiens recombi	Sequence of 741 sF	Sequence encoded b	Human NKG2D polype	3B10xP5-23 bispeci	ispeci	10xP4-14 bispec	rotein.	imer	cDNA clone		5		Variable region of	L6 antibody VH req	of C	regio		regio	Murine protein #3	Heavy chain variab		e 4ClO anti-		243 VH rec	antibody he	se KM10 heav	MAD KM10 heavy cha

## ALIGNMENTS

AAB20433;

AAB20433 standard; Protein; 242 AA.

RESULT 1
AAB20433
ID PAB2
XX AAB2
XX AAB2
XX AAT1
XX Pact
XX Fact
XX F Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse. WO200119992-A2 Region Protein Chimeric - Mus musculus. Chimeric - Synthetic. Peptide Region Protein Anti-FIX/FIXa antibody 193/AD3 scFv. 21-JUN-2001 (first entry) /label= VH 98..108 /label= CDR3 135..242 /label= VL Location/Qualifiers label= CDR: .20..134 label= Linker 231

22-MAR-2001.

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RESULT 2
AAE29158
ID AAE2
XX AAE2
XX AAE2
XX Chim
XX Chim
XX 31.1
XW heav
XX Unid
XX Unid
XX Unid
PN WO20
XX 26-S
XX 26-S
XX XX 15-M
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Best Local Sim
Matches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of a single chain Fv (scFv) derivative of antibody 193/AD3, comprising the heavy (VH) and light (VL) chain variable regions of 193/AD3 joined by an artificial, flexible linker 1950 peptide. The scFv was obtained by PCR amplification of cDNAs for 195/AD3 when the regions and cloning in vector pDAP2. 193/AD3 is 195/AD3 when the regions and cloning in vector pDAP2. 193/AD3 is 195/AD3 when the regions and cloning in vector pDAP2. 193/AD3 is 195/AD3 when the regions and cloning in vector pDAP2. 193/AD3 is 195/AD3 when the regions and cloning in vector pDAP2. 193/AD3 is 195/AD3 when the regions and cloning in vector pDAP2. 193/AD3 is 195/AD3 when the regions and cloning in vector pDAP2. 193/AD3 is 195/AD3 when the regions and cloning in vector pDAP2. 193/AD3 is 195/AD3 when the received in the proceeding activative. Administration leads to an increase in the proceeding activative frixa, even in the presence of increase in the proceeding activative frixa, even in the presence of FVIII or FVIII, and in the case of FVIII in the absence of FVIII or FVIII, and in the case of FVIII in the absence of FVIII or FVIII, and in the case of FVIII in the absence of FVIII or FVIII, and in the case of FVIII in the absence of FVIII or FVIII, and in the case of FVIII in the absence of FVIII or FVIII, and in the case of FVIII in the absence of FVIII or FVIII and derivatives are used in a 195/AD3 is 195/AD3 in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in the case of FVIII in 
                                                                                                                                                                                                                                                                                   31.1 antibody; pancreatic cancer; pancreatic carcinoma; antibody therapy;
                                                                                                                                                                                                                                                                                                                                       Chimeric 31.1 antibody heavy chain variable region
                         15-MAR-2001; 2001US-276284P
                                                                        15-MAR-2002; 2002WO-US09193.
                                                                                                                                                                    WO200274251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE29158 standard;
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N-PSDB; AAF30723.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKMMGWINTYTGEPTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein; 137
                                                                                                                                                                                                                                                                                                                                                                                          entry)
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Pred. No. 3.4e-46;
0; Mismatches 0;
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Best Local :
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                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding light and heavy chain variable regions of antibody 31.1, useful for expressing chimerized 31.1 antibodies for
                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Fig 4; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     treating pancreatic cancer or for diagnosing pancreatic carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-759857/82
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137 S 137
                          119 A 119
                                                                                                                                                                                   105;
                                                            80
                                                                            61 ADDFKGRFAFSLETSASTAYLQINNLKNBDTATYFC--ALYGNSPKGFAYWGQGTLVTVS
                                                                                                                     20 QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY
                                                                                                                                         1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY
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                                                         ADDEKGRFAFSLETSASTAYLQINNLKNEDTATYFCARAYYG---KYFDYWGQGTTLTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsang KY;
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                                                                                                                                                                                                  86.6%;
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                                                                                                                                                                                Score 559.5; DB
Pred. No. 3e-39;
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07-OCT-1993; 06-FEB-1992; 07-OCT-1993; 09-JUL-1996 US5534254-A. Peptide 74178; anti-c-erbB-2; monoclonal antibody; single chain Fv; construct; polypeptide linker; C-terminal amino acid sequenc in vivo imaging; drug targetting experiment; homodimer; increased; binding avidity; tissue retention time. Homo sapiens 741F8 anti-c-erbB-2 two single chain Fv construct. 25-MAR-2003 29-OCT-1996 AAW02278; AAW02278 standard; Protein; 250 AA. Peptide (updated) (first entry) 93US-0133804 92US-0831967 9305-0133804 Location/Qualifiers 122..135 246..250 note= 'label= linker "claimed C-terminal tail to facilitate crosslinking of two sFv polypeptides"

sequence;

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RESULT 4
AAW22961
ID AAW
XX AAW
XX AAW
XX O7-1
DT 25-1
DT 07-1
XX O7-1
XX Adel
KW Expi
KW Expi
KW Expi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The variable heavy (VH) and variable light (VL) genes of the 741F8 canti-c-erbB-2 monoclonal antibody (MAb), were isolated from the CCDNA of the parental 741F8 hybridoma line. A two single chain Fv CC (sFv) gene was constructed by connecting the VH and VL genes with a CDNA sequence endcoding a polypeptide linker. A synthetic DNA duplex cancering the C-terminal amino acid sequence, (G1)4-Cys was constructed, and the resulting 741F8 anti-c-erbB-2 two sFv inserted into an expression vector. The resulting gene, which encodes the Cresent sequence, was transformed into B. coil, and protein corression induced by the addn. of 1FVG to the culture medium. CC accepts in vivo imaging, and drug targetting experiments. The custom prod. is a honocimer, in which both fragments target the same antigen, therefore giving greater binding avidity and clonger tissue retention times, compared to individual sFv protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                         Adenovirus; ElA; transactivator; transcription activator; stimulate; expression vector; single-chain binding protein; VA1; enhance; PCR; translation; production; immortal; enkaryotic cell; scFv; primer; single-chain antibody fragment; imaging; tumour; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
07-JAN-1998
                             19-AUG-1997
                                                                                  US5658763-A
                                                                                                                                                                                                ovarian cancer;
                                                                                                                                                                                                                                                                                                                                                                Anti-c-exbB-2 single chain antibody 741F8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW29261 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Compans. contg. antigen-targetting antibody fragment comprising dimer of single-chain Fv fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEEFKGRFAFSLETSASTAYLQINNLKNEDTATYFCGRQFITYG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCA----LYGNSPKGFAYWGQSTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT36878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVKLVESGPELKKPGETVKISCKASGXIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTNTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                     (updated)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.4%;
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Pred. No. 2.3e-38;
5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ring
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 250;
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC This sequence is a single chain anti-c-erbB-2 antibody (scFv)

C derived from hybridoma 741P8. The protein product includes a C-terminal

CC tail [Gly4-Cys in some constructs. Single-chain antibodies can be

CC produced using a novel method which comprises culturing an immmortalised

CC eukaryotic cell having transfected DNA sequences (encoding the protein

CC effector vectors containing a non-native reporter DNA (encoding the scFv)

CC and viral sequences to promote transcription and translation (e.g. the

CC adenovirus EIA and VAI genes as shown in ANT91831 and AAT91834

CC respectively) are used. The scFv that is produced, when properly folded,

CC adenovirus EIA and the mono- or bi-functional binding activity. The method

CC has a structure with mono- or bi-functional binding activity. The method

CC is especially used to produce single-chain antibody fragments (scFv),

CC e.g. for imaging tumours or delivering therapeutic agents to them,

CC particularly breast and ovarian cancers that express the c-erbB-2

CC introjenter scFv are used in model studies and for treating digoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                         25-MAR-2003
09-OCT-1997
                                                                                                                                                                                      AAW22400;
                                                                                                                                                                                                                    AAW22400 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Producing single chain binding protein in immortalised eukaryotic cells - which comprise protein coding sequences, a transcription activator and translation promotion sequences, provides high expression at low copy number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dorai H, Oppermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT91837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-424235/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-1993;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                   119 VSA 121
                                                                                                                                                                                                                                                                                                                                 117 VSA 119
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                                                                                                                                                                                                                                                                                                                                                             AEEFKGRFAFSLETSASTAYLQINNLKNEDTATYFCGRQFITYG---
                                                                                                                                                                                                                                                                                                                                                                                 ADDFKGRFAFSLETSASTÄYLQINNLKNEDTATYFCA----LYGNSFKGFAYWGQGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                          EIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTNTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Column 29-32; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                     (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93US-0143498
95US-0463675
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                                                                                                                                                                                                                    Protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 552; DB 18;
Pred. No. 2.3e-38;
5; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 250;
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116 62

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Single chain antibody 741F8 protein sequence.

transcription activator; promoter; expression; adenovirus; EIA; I polymerase chain reaction; amplification; primer; herpes simplex thymidine kinase; vector; enhancer; translation; heterologous. Production; single-chain; binding protein; antibody; eukaryote; virus; transcription activator; promoter; expression; adenovirus; EIA; PCR;

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RESULT 6
AAW53168
ID AAW5
XX AAW5
AC AAW5
XY 16-J
XX 741F
XX ART1
KW C-ex
XX
XX Synt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to methods of increasing production of a single-chain binding protein, especially a single chain antibody, by generating enkaryotic cell lines containing DNA encoding either a viral transcription activator protein that acts on and stimulates a viral promoter controlling the expression of DNA encoding the cannot binding protein, such as the adenovirus Ad2 BIA protein encoded by the sequence AAT78873, or an RNA sequence able to promote translation of the RNA transcript from the heterologous gene, such as the adenoviral VAI gene (AAT78876).

The sequence presented here is the amino acid sequence of the active-c-rbB2 single chain antibody 741. The coding sequence was constructed by amplifying the variable heavy and light chain genes which were then cloned into a pUC vector. For secretion from mammalian chis more closed antibody 5202 (AAT78880) or from PacI (AAT78881).

CU (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 105; Conser
 Synthetic
                            Antigen imaging; single chain Fv; c-erbB-2; tumour; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                      741F8 anti-c-exbB-2 sFv' dimeric construct protein sequence.
                                                                                                        16-JUL-1998
                                                                                                                                     AAW53168;
                                                                                                                                                                AAW53168 standard; Protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Column 29-32; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Production of cell line for producing single-chain binding protein using construct containing DNA encoding viral transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT78879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-1993;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activator protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CREA-)
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                                                                                                                                                                                                                                                                        VSA 119
                                                                                                                                                                                                                                                                                                                             ADDFKGRFAFSLETSASTAYLQINNLKNBDTATTFCA----LYGNSPKGFAYWGQGTLVT 116
                                                                                                                                                                                                                                           VSA 121
                                                                                                                                                                                                                                                                                                     AEEFKGRFAFSLETSASTAYLQINNLKNEDTATYFCGRQFITYG---
                                                                                                                                                                                                                                                                                                                                                               EIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWININTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                   EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oppermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-0143498.
95US-0461184.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        85.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 552; DB 18;
Pred. No. 2.3e-38;
5; Mismatches 5;
                                           SFV:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 250;
                                                                                                                                                                                                                                                                                                     -GFANWGQGTLVT
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RESULT 7
AAW47012
ID AAW4
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AC AAW4
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AC AAW4
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AC AAW4
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                                                                                                                                                                                                                                                                                                                                                              Matches 105;
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                             This represents the protein sequence of a 741F8 sFv' (single chain Fv) C-terminal Gly4-Cys construct. This was constructed by connecting the Vh and VI genes with a DNA sequence encoding a 14 residue polypeptide linker. 741F8 is a monoclonal antibody useful in targeting c-erbB-2 antigen. This dimeric construct can be used in the methods of invention of imaging a preselected antigen expressed in a mammal. The methods are used in magnetic resonance imaging of c-erbB-2 or related antigens in cancer diagnosis. The biosynthetic constructs have enhanced properties as in vivo targetting agents in comparison with intact monoclonal antibodies or their Fab fragments. The dimeric constructs permit the in vivo targetting of an epitope on an antigen with greater apparent avidity, including greater tumour specificity, tumour localisation and cumour retention properties than that of the Fab fragment having the same
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06-FEB-1992;
05-JUN-1995;
                                          AAW47012;
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Peptide
                                                                AAW47012 standard; Protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Columns 25-28; 30pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fv fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-311318/27
N-PSDB; AAV21796.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Imaging of antigens
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(CREA-) CREATIVE BIOMOLECULES
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                                                                                                                                                             117 VSA 119
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                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                             ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCA----LYGNSPKGFAYWGQGTLVT
                                                                                                                                                                                                                                                               EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWNGWINTYTGEPTY
                                                                                                                                    VSA 121
                                                                                                                                                                                         AESFKGRFAFSLETSASTAYLQINNLKNEDTATYFCGRQFITYG----GFANWGQGTLVT
                                                                                                                                                                                                                                               EIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTNTGEPTY
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92US-0831967.
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122..135
note=_"linker peptide"
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                                                                                                                                                                                                                                                                                                                  85.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oppermann
                                                                                                                                                                                                                                                                                                  Score 552; DB 19;
Pred. No. 2.3e-38;
5; Mismatches 5;
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13-JUL-1998

(first entry)

116 62

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RESULT 8
AAW80422
ID AAW8
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AC AAW8
XX AAW1
DT 28-2
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Best Local
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                          Anti-c-erbB-2 sFv'; c-erbB-2; antigen; tumour cell; antibody 741F8; targeted delivery; antigen-expressing cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents single chain binding site molecule (SFV). The sequence was expressed to exemplify the invention, which is a method for the expression of poorly expressed genes in an immortalised eukaryotic cell. This cell contains transfected DNA sequences operatively integrated into its genome. The transfected DNA sequences encode a viral transcription promoter linked to a non-native reporter sequence encoding a single chain binding protein. The promoter is activated by a viral transcription activator protein. The cell allows the production on a commercial scale of proteins encoded by non-native hard to express
                                                                              Anti-c-erbB-2
                                                                                                              28-JAN-1999
                                                                                                                                             AAW80422;
                                                                                                                                                                         AAW80422 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Columns 31-32; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immortalised eukaryotic cell comprising transfected DNa sequences useful for enhanced production of proteins encoded by non native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dorai H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CREA-) CREATIVE BIOMOLECULES INC
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                                                                                                                                                                                                                                                                                                                                          61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCA----LYGNSPKGFAYWGQGTLYT
                                                                                                                                                                                                                                                                                                                                                                                            1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                   VSA 119
                                                                                                                                                                                                                                                                                                              ABEFKGRFAFSLETSASTAYLQINNLKNEDTATYFCGRQFITYG----GFANWGQGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          production; non-native gene; hard to express gene.
                                                                                                                                                                                                                                                                                                                                                                         BIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTNTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oppermann H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                             sFv'
                                                                                                            (first entry)
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                                                                             protein sequence
                                                                                                                                                                         Protein; 250
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Pred. No. 2.3e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 250;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents an anti-c-erbB-2 sFv'. C-erbB-2 is an antigen that is overexpressed on the surface of tumour cells. An antibody designated 741F78 binds c-erbB-2. Variable heavy and light sequences of antibody 741F8 are connected, together with a linker, to produce the present single chain Fv gene. Anti-c-erbB-2 sFv' exemplifies the invention. Dimers of the single chain Fv are used for targeted delivery of drugs or imaging agents (e.g. cytotoxins, prodrugs or 99m-technetium) to antigen-expressing cells, particularly for treatment or diagnosis of tumours (especially of ovary or breast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-OCT-1993;
06-FEB-1992;
05-JUN-1995;
                                                                               KM10 Heavy
                                                                                                                              25-MAR-2003
04-MAR-1993
                                                                                                                                                                                                             AAR09428;
                                                                                                                                                                                                                                                               AAR09428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding single-chain Fv fragment specific for antigens - and having C-terminal tail for crosslinking to form dimer with improved pharmacokinetic properties, used to deliver drugs and imaging agents, especially to tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-023541/02.
N-PSDB; AAV63397.
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(CREA-) CREATIVE BIOMOLECULES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 ABEFKGRFAFSLETSASTAYLQINNLKNEDTATYFCGRQFITYG----GFANWGQGTLVT
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ω
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                                                                                                                                                                                                                                                            standard; Protein; 139 AA
                                                                                                                                                                                                                                                                                                                                                                                             VSA
                                                                                                                                                                                                                                                                                                                                                                                                                                            VSA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTNTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVKLVESGÞELKKFGETVKISCKASGYIFTNYGMNWVKQAÞGKGLKWMGWINTYTGBFTY
                                                                          Chain V Region (mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 AA;
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                                                                                                                        (updated)
(first entry)
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92US-0831967.
95US-0461386.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.4%;
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Pred. No. 2.3e-38;
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62 60 N

Monoclonal antibody; chimera; light; heavy; chain; constant;

variable; antigen; diagnosis; cancer; tumour.

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RESULT 10
AAW06217
ID AAW066217
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Best Local Similarity
Matches 101; Conserv
                                                                   Chimeric antibody; monoclonal antibody; MB4; antibody engineering; tumour; antigen; colon carcinoma; stomach carcinoma; pancreas carcinoma; oesophagus carcinoma; cancer; diagnosis; therapy; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is used in the prodn. of a chimeric antibody mol. comprising two light chains and two heavy chains, each having a constant region (human) and a variable region (murine) having specificity to an antigen bound by murine monoclonal antibody (MAb) KM10. The chimeric antibodies can be used for any purpose for which the original murine MAbs can be used, with the advantage that they are more compatible with the human body. They are esp. used for the diagnosis and treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-1988;
19-JUN-1989;
21-JUL-1989;
                                                                                                                                                                                                                                         25-MAR-2003
13-FEB-1997
                                                                                                                                                                                       MAD KM10 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                AAW06217;
                                                                                                                                                                                                                                                                                                                                                        AAW06217 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                      Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; Page 123 + Fig 36; 173pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ08610
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13-SEP-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QIQLVQSGPELMKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKMMGWINTYTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKMMGWINTYTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDFKGRFAFSLETSVSTGHLQINNLKNEDTATYFCARWGGS-YGMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 AA;
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                                                                                                                                                                                                                                    (updated)
(first entry)
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89US-0367641.
89US-0382768.
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88US-0241744.
88US-0243739.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 548.5; DB 1
Pred. No. 2.5e-38;
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RESULT 11
AAW85064
ID AAW855
XX AAW85
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XX Heavy
KW Heavy
KW Chime
KW treat
XX Chime
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                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 101;
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The heavy chain variable region (AAW06217) of mouse monoclonal antibody KM10 is the product of a cDNA clone (AAF43442) isolated from a KM10 hybridoma cDNA library. Mea KM10 (IgG1) binds to an antigen that is expressed on the surface of human colon, stomach, pancreas and oesophagus carcinomas, but not on most normal adult issues. The heavy chain and light chain variable regions (see also AAW06218) of KM10 can be linked to human constant regions and expressed in transformed host cells. Novel mouse-human chimeric antibodies (see also AAW06209-16) can be produced that have specificity to human tumour antigens for use in the treatment and diamonate of human carcon.
                                                            Heavy chain variable region; murine antibody KM10; antibody ING-1; chimeric immunoglobulin; human tumour antigen; chimeric antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                 20-MAR-2003
16-APR-1999
                                                                                                                                                                       AAW85064;
                                                                                                                                                                                                AAW85064 standard; Protein; 139 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric mouse-human antibodies - recognise a human tumour antigen, used for the treatment and diagnosis of human cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUN-1989;
21-JUL-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-SEP-1988
                                                    treatment;
                                                                                                     Mouse KM10 heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis of human cancer. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Fig 36; 102pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                139 AA;
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(first entry)
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88US-0243739

88US-0253002

89US-0367641

89US-0382768

94US-0364001
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                                                                                                                                                                                                                                                                                                                                                                                       84.98;
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                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                        Score 548.5; DB 1
Pred. No. 2.5e-38;
7; Mismatches 10
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                                                                                                                                                                                                                                                                                                                                                                                                   DB 18;
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                                                                                                                                                                                                                                                                                                                                                                         10;
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US5843685-A Mus sp.

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ABUSAB ID ABUSA
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27-DEC-1994;
06-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents the heavy chain variable region of murine antibody KM10. The sequence was used to create chimeric mouse-human immunoglobulins which recognise the human tumour antigen bound by antibody ING-1 (produced by hybridoma cell line ATCC HB 9812). The chimeric antibodies also have an antigen-binding site that competitively inhibits the binding of antibody ING-1, and mediate complement-dependent cytolysis of target cells or antibody-dependent cellular cytotoxicity to target cells. The chimeric antibodies can be used for therapeutic purposes in the treatment of human cancer.
                                                                                       Mouse; human tumour antigen; anti-human tumour ING-1 antibody; cell line HB9812; immunoassay; tumour diagnosis; tumour therapy; cytostatic;
                                                                                                                                                     Mouse antibody heavy chain variable region #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric antibody specific for human tumour antigen - useful immunoassay, imaging or antitumour agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Better MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-1998.
              US6461824-B1.
                                                                                                                                                                                    16-APR-2003 (first entry)
                                                                                                                                                                                                                  ABU58898;
                                                                                                                                                                                                                                                ABU58898 standard; Protein; 139 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Fig 36; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAV71160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUN-1995;
                                                                        heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (XOMA ) XOMA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1999-044574/04.
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                                                                                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                                                                                                                                      20 QIQLVQSGPBLMKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKNMGWINTYTGEPTY 79
                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY 60
                                                                                                                                                                                                                                                                                                                                                ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYWGQGTLVTVSA 119
                                                                                                                                                                                                                                                                                                                          ADDFKGRFAFSLETSVSTGHLQINNLKNEDTATYFCARWGGS-YGMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chang CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88US-0243739.
88US-0253002.
89US-0367641.
89US-0382768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91US-0659401.
94US-0364001.
88US-0240624.
88US-0241744.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Horwitz AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 548.5; DB 2
Pred. No. 2.5e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                   immunoassay; imaging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lei S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 20; Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Robinson RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                       antigen-antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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The invention describes an antibody comprising a human constant region and a variable region having specificity for the human tumour antigen to bound by the ING-1 antibody, where the ING-1 is produced by cell line CC the ING-1 for the human tumour antigen. The antibody has the same affinity as CI immunoassay method for detecting an antigen in a sample by contacting a CC label-detectable antigen in the sample with the antibody, detecting the CC use in an imaging method for revealing the presence of the antigen; for CC use in an animal by contacting the antigen with the apart of the antigen; for CC uspected of containing the antigen, detectably with a part of the animal CC suspected of containing the antigen, detecting the label and relating the coarrying an antigen by contacting the antibody with a part of the animal CC carrying an antigen by contacting the cells with the antibody and CC diagnosis and therapy. The chimeric antibodies are useful in tumour CC diagnosis and therapy. The chimeric antibodies bind to the surface of the main tumour cells but do not bind detectably to normal cells, e.g., CC fibroblasts, endothelial cells or epithelial cells in the major organs. CC me high biological activity of the chimeric antibodies against human cells but do not bind detectably to normal cells, e.g., comply that these antibodies may mediate selectivity with normal tissues to comply that these antibodies may mediate selectivity with normal tissues to cantionate to clearance enhances the potential utility of these chimeric antibodies increases their resistance to creatable to chemeric antibodies increases their resistance to cantibodies, as well as their derivatives, in tumour diagnosis and contained to use diagnosis and contained to use diagnosis and contained to use diagnosis and contained to use diagnosis and contained to use of the contained antibody heavy chain cantibod en antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody for detecting antigen in animal or killing cells carrying antigen comprises human constant region and variable region having specificity for human tumor antigen bound by ING-1 antibody -
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Better MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-SEP-1989;
27-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-SEP-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-OCT-2002
                                         antigen-antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Fig 36; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (XOMA ) XOMA TECHNOLOGY LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L9-JUN-1989;
  139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Horwitz AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88US-0240624.
88US-0241744.
88US-0243739.
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89US-0367641.
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89WO-US03852.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lei S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chang CP
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Matches 101;
                                                61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYWGQGTLVTVSA 119
                                                                                                 20 QIQLVQSGPBLMKPGBTVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY 79
                                                                                                                               1 BYKIVESGPELKKPGETYKISCKASGYIFTNYGMNWYKQAPGKGLKHYGWINTYTGEPTY 60
ADDFKGRFAFSLETSVSTGHLQINNLKNEDTATYFCARWGGS-YGMDYWGQGTSVTVSS
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                  Score 548.5; DB 7
Pred. No. 2.5e-38;
7; Mismatches 10
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RESULT 13 AAR64232

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Query Match Best Local

Similarity

84.9%;

DB 24;

Length 139;

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RESULT 14
AAR64257
ID AAR64
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AC AAR64
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Best Local S
Matches 101
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27-JAN-1994;
09-FEB-1994;
29-MAR-1994;
            AAR64257;
                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                     L243 is a mouse MAb raised against human MHC class II. The nucleotide and amino acid sequences of L243 VL and VH regions given in AAQ80359/R64231 and AAQ80350/R64232, respectively. CDR-grafted humanized antibodies based on these sequences have
                                                                                                                                                                                                                                                                                                                                                             conditions
                                                                                                                                                                                                                                                                                                                                                                      New humanised anti-HLA DR antibodies treatment of immunological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanized antibody; antibody engineering; MHC class I; major histocompatibility region; HLA; monoclonal antibody; MAb; L243; immunological disease; transplantation; light chain; beavy chain; variable region; complementarity determining region
                                AAR64257 standard;
                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig. 2; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Athwal DS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9429451-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAb L243 VH region.
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-036480/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-DEC-1994.
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17-JUL-1995
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                                                                                                                                                                                                                                                                   (Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CLLT ) CELLTECH LTD
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                                                                                 140
                                                                                                     119
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                                                                                                                                                                                                                 Similarity
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                                                                                                                                                               QIQDVQSGPELKKPGETVKISCKASGFTFTNYGMNWVKQAPGKGLKWMGWINTYTREPTY
                                                                                                                                                                                                                                                                   g
                                                                                                    A 119
                                                                                                                                     ADDERGREAESLETSASTAYLQINNLKNEDTATYFCA--LYGNSPKGFAYWGQGTLVTVS 118
                                                                                                                                                                           EVKLVESGPELKKPGETVKISCKASGXIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                        ADDFKGRFAFSLETSASTAYLQINNLKNEDTAKYFCARDITAVVPTGFDYWGQGTTLTVS 139
                                                                                                                                                                                                                                              140 AA;
                                                                                                                                                                                                                                                                   25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (updated)
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94GB-0001597.
94GB-0002499.
94GB-0006222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94WO-GB01291.
                               Protein; 140 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                               84.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Emtage
                                                                                                                                                                                                                                                                                                                                                                    antibodies - used for diagnosis and diseases and transplantation related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140
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                                                                                                                                                                                                      Score 546; DB 16;
Pred. No. 4.1e-38;
8; Mismatches 10;
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                                                                                                                                                                                                                                                                                       sequences have
                                                                                                                                                                                                                          Length 140;
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RESULT 15
AAR37717
ID AAR37
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Query Match
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09-FEB-1994;
29-MAR-1994;
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31-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                cDNA for mouse anti-human MHC-III MAb L243 (ATCC HB 55) heavy chain variable region was cloned by PCR. Clone pB1702 was obtained that contained a VH insert having the sequence given in AAR00426; the deduced amino acid sequence is given in AAR04257. Altered antibodies have been prepared that retain immunosuppressive properties but show reduced binding to PCRI. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L243; heavy chain; VH; monoclonal antibody; MAb; MHC-II; major histocompatibility complex class II; immunosuppressive; variable region; Fc receptor I; FcRI; antibody engineering;
25-MAR-2003
30-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antibodies with altered ability to fix complement - having one or more amino acid residues in the N-terminal region of the constant chain heavy domain altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-036409/05.
N-PSDB; AAQ80426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer;
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                                      AAR37717;
                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig. 3; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-1994.
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                                                               AAR37717 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Athwal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CLLT ) CELLTECH LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunotherapy.
                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                    ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCA--LYGNSPKGFAYWGQGTLVTVS
                                                                                                                                                                                                                                  QIQLVQSGPELKKPGETYKISCKASGFTFTNYGMNWVKQAPGKGLKWMGWINTYTREPTY
                                                                                                                                                                                                                                                     EVKLYESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKMMGWINTYTGEPTY
                                                                                                                                                                                  ADDFKGRFAFSLETSASTAYLQINNLKNEDTAKYFCARDITAVVPTGFDYWGQGTTLTVS
                                                                                                                                                                                                                                                                                                                                         140 AA;
                                                                                                                                                                                                                                                                                       Conservative
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(first entry)
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94GB-0002499.
94GB-0006244.
94GB-0006222.
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                                                               Protein;
                                                                                                                                                                                                                                                                                                 84.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Emtage
                                                               138
                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                     Score 546; DB 16;
Pred. No. 4.1e-38;
8; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Morgan
                                                                                                                                                                                                                                                                                                             Length 140;
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                                                                                                                                                                                                               Query Match 84.2
Best Local Similarity 84.0
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                              The sequence is that of the 4Cl0 anti-idiotype Ab heavy chain V region which was used in the construction of a murine/human monoclonal anti-idiotype antibody (MAIA). The WAIA elicits an anti-ganglioside response and produces antibodies which induce cytotoxic destruction of cancer cells bearing the gangliosides. It can be used for treating cancers partic, melanomas. It can also be used as an immunomodulator to enhance anti-cancer immunity, suppress organ transplant rejection and suppress autoimmune disease. The MAIA can also be used in the diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric murine-human anti-idiotype monoclonal antibodies useful as immuno-modulators for treating and diagnosing cancers, and for suppressing organ transplant rejection and auto:immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 33; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-182538/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAIA; monoclonal antibody; hybridoma; organ transplant rejection; immuno-modulator; cancer; treatment; diagnosis; melanoma; anti-cancer immunity; enhancement; suppression.
                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hastings A, Irie RF, Morrison SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse 4Cl0 anti-idiotype Ab heavy chain V region.
                                                                                                                                                                                                                                                                                                                               (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA.
                                                                 80 TEEFKGRFAFSLETSANTAYLLINNLKNEETATYFCARGEGHAWGFAYWGQGTLVTVSA 138
                                                                                            20 QIQLVQSGPBLKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTNTGBPTY 79
                                                                                                                                                                       1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY 60
                                                                                                                                                                                                                                                                                              138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91US-0791934.
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                                                                                                                                                                                                                 84.2%; Score 544; DB 14; Length 138;
84.0%; Pred. No. 5.9e-38;
ative 8; Mismatches 11; Indels 0; Gaps
                     7, 2003, 07:26:59
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum Match
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                           Score
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Match
               November 7, 2003, 07:30:19; Search time 104.383 Seconds (without alignments)
195.799 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/US07
2: /cgn2_6/ptodata/2/pubpaa/PCT_
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/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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US-10-222-026A-35

US-10-268-883-8

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US-09-971-543-8

US-09-971-543-2

US-10-138-727A-26

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Sequence 19, Appl
Sequence 35, Appli
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US-09-887-853-2
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Patent No. US20020168375A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

COMPUTER READABLE FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/887,853

FILING DATE: 21-Jun-2001

CLASSIFICATION UNMBER: US/09/887,853

FILING DATE: 4Unknown>

PRIOR APPLICATION NUMBER: US/08/133,804

FILING DATE: 4Unknown>

APPLICATION NUMBER: US/08/133,804

FILING DATE: 4Unknown>

APPLICATION NUMBER: 34,637

REFERENCE/DOCKET NUMBER: 2054/22

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-248-7407

TELEPHONE: 617-248-7407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwit
STREET: Exchange Place,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins
Imaging
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
    TELEFAX: 617-248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oppermann, Hermann
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Place, 53 State Street
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US-09-977-283A-15
US-10-138-727A-11
US-10-1310-719-30
US-10-1310-719-30
US-10-1310-727A-41
US-09-965-099-11
US-09-965-099-11
US-10-051-852-71
US-10-051-852-71
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US-10-051-852-71
US-10-1310-727A-21
US-10-1310-727A-21
US-10-1310-727A-22
US-10-1310-727A-23
US-10-1310-719-33
US-10-1310-719-33
US-10-310-719-33
US-10-310-719-33
US-10-310-727A-19
US-10-310-727A-19
US-10-310-727A-19
US-10-310-7310-73
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OTHER INFORMATION: Antibody
US-10-422-049-19
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CURRENT FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: US/09/267,281
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 08/456,418
PRIOR FILING DATE: 1995-06-01
PRIOR APPLICATION NUMBER: 08/373,882
PRIOR FILING DATE: 1995-01-17
PRIOR FILING DATE: 1995-01-17
PRIOR APPLICATION NUMBER: 07/920,378
PRIOR FILING DATE: 1995-01-17
PRIOR FILING DATE: 1995-01-17
PRIOR APPLICATION NUMBER: 07/920,378
PRIOR FILING DATE: 1995-09-28
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN PAIR
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Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/10422049 Publication No. US20030199679A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 19
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APPLICANT: Athwal, Dilject Singh
APPLICANT: Emtage, John Spencer
APPLICANT: Bodmer, Mark William
TITLE OF INVENTION: Recombinant Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: CARPO063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 118
TYPE: PRT
ORGANISM: Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
118 S 118
                                                             119 A 119
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                                                                                                                                                          62 DDFKGREAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGF---AYWGQGTLYTVS 118
                                                                                                                       62 DDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCA----RKEGFYAMDYWGQGTSVTVS
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                                                                                                                                                                                                                                                                                     63 ABBFKGRFAFSLETSASTAYLQINNLKNEDTATYFCGRQFITYG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                84.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 543.5; DB 12;
Pred. No. 8e-41;
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Pred. No. 2.9e-41;
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APPLICANT: Wirsching, Peter
APPLICANT: Lerner, Richard A.
APPLICANT: Gao, Changshou
TITLE OF INVENTION: METHODS FOR DISPLAY OF HETERODIMERIC
TITLE OF INVENTION: METHODS FOR DISPLAY OF HETERODIMERIC
TITLE OF INVENTION: COMPOSITIONS, VECTORS AND COMBINATORIAL LIBRARIES
FILE REFERENCE: TSRI 693.0 D1
CURRENT APPLICATION NUMBER: US/10/222,026A
CURRENT PILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: US 09/318,786
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 160
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                                                                                                                                                   ; ORGANISM: Mouse US-10-268-883-9
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US-10-268-883-9
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US-10-222-026A-35
                                                                Query Match
Best Local Similarity
Matches 100; Conserv
                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Tso, J. Yun
APPLICANT: Green, Jennifer Macphate
APPLICANT: Green, Jennifer Macphate
TITLE OF INVENTION: Anti-HLA-DR Antibodies and the Methods of Using Thereof
FILS REFERENCE: 05882.0062.NPUS01
CURRENT APPLICATION NUMBER: US/10/268,883
CURRENT FILING DATE: 2003-03-26
CURRENT FILING DATE: 2003-03-26
                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/10268883
Publication No. US20030138862A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: USSN 60/329,178
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: USSN 60/331,965
PRIOR FILING DATE: 2001-11-21
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                               LENGTH: 118
TYPE: PRT
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ORGANISM: Artificial Sequence
FEATURE:
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1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDFRGRFAFSLATSASTAYLQIINLKNEDTATYFCETY-DSPLG-DYWGQGTTVTVSS 119
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                                                           Conservative
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                                                                              82.4%;
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85.7%;
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                                                         Score 532.5; DB 12;
Pred. No. 7.5e-40;
6; Mismatches 9;
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Pred. No. 4.9e-40;
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                                                                                                   DB 12;
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                                                                                                   Length
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1 QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMAWINTYNGEPTY

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US-09-887-853-6
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; ORGANISM: Mouse
US-10-268-883-8
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Patent No. US20020168375A1
GENERAL INFORMATION:
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SEQ ID NO 8
LENGTH: 137
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APPLICANT: Tso, J. Yun
APPLICANT: Green, Jennifer Macphate
TITLE OF INVENTION: Anti-HLA-DR Antibodies and the Methods of Using Thereof
FILE REFERENCE: 0582.0062.NPUS01
FULE REFERENCE: 0582.0062.NPUS01
CURRENT APPLICATION NUMBER: US/10/268,883
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: USSN 60/329,178
PRIOR FILING DATE: 2001-10-10
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Publication No. US20030138862A1
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Best Local Similarity 82.0%;
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PRIOR FILING DATE: 2001-11-21
NUMBER OF SEQ ID NOS: 16
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault/Patent Department STREET: Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                                   Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Huston, James S.
                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 SS 137
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                                                                                                                                        CITY: Boston
STATE: Massachusetts
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                    ZIP: 02109
                                                                                                                         COUNTRY: USA
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Houston, L. L.
                                                                                                                                                                                                                                                                    Imaging
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Sequence 8, Application US/09971543

Patent No. US20020146846A1

GENERAL INFORMATION;
APPLICANT: PLUCKTHUN, ANDREAS

APPLICANT: HONEGGER, ANNEWARIE

APPLICANT: HOLUGA, JORG

TITLE OF INVENTION: INMUNOSLOBULING OR INMUNOGLOBULIN FRAGMENTS, AND

TITLE OF INVENTION: INMUNOSLOBULING OR INMUNOGLOBULIN FRAGMENTS, AND

TITLE OF INVENTION: STABILIZED ANTI-EGP-2 SCFV FRAGMENT

FILE REFERENCE: PLUCK-3 CON

CURRENT APPLICATION NUMBER: US/09/971,543

CURRENT FILING DATE: 2001-10-04

PRIOR APPLICATION NUMBER: US/09/971,543

FRIOR FILING DATE: 2000-04-10
                                                                                                                                                                                                                                                                                         GRGANISM: Mus sp. US-09-971-543-8
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SEQ ID NO 8
                                                                                                                                                                                        Matches 100;
                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                LENGTH: 116
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FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/887,853
FILING DATE: 21-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ADDFKGRPAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGPAYWGQGTLVTVSA 119
61 ADDFKGRFAFSLETSASAAYLQINNLKNEDTATYFCARF--AIKG-DYWGQGTTLTVSS 116
                          61 ADDFKERFAFSLETSATTAHLQINNLRNEDSATYFCA----RRFGFAYWGQGTLVSVSA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98;
                                                                                            1 QVQLQQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGRGLKWMGWINTYTGESTY 60
                                                                                                                                        1 SVKLVESGPBLKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVKLVESGPELXKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 BIQLVQSGFELKKPGETVKISCKASGYTFANYGMMMKQAPGKGLKWMGWINTYTGQSTY 60
                                                                                                                                                                                                             b 82.0%;
Similarity 84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.0%; Score 530; DB 10; Length 243;
82.4%; Pred. No. 2.5e-39;
tive 10; Mismatches 7; Indels
                                                                                                                                                                                        8
                                                                                                                                                                                                             Score 529.5; DB 10;
Pred. No. 1.3e-39;
                                                                                                                                                                                        Mismatches
                                                                                                                                                                                        00
                                                                                                                                                                                     Indel8
                                                                                                                                                                                                                                     Length 116;
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Sequence 2, Application US/09971543

Patent No. US20020146846A1

GENERAL INFORMATION:
APPLICANT: PLUCKTHUN, ANDREAS
APPLICANT: HONEGGER, ANNEMARIE
APPLICANT: HONEGGER, ANNEMARIE
APPLICANT: HONEGGER, ANNEMARIE
APPLICANT: HONEGGER, ANNEMARIE
APPLICANT: HILLUDA, JORG
ITITLE OF INVENTION: INMUNOSLOBULINS OR IMMUNOSLOBULIN FRAGMENTS, AND
ITITLE OF INVENTION: STABILIZED ANTI-EGP-2 SCFV FRAGMENTS, AND
ITITLE OF INVENTION: STABILIZED ANTI-EGP-2 SCFV FRAGMENT
FILE REFERENCE: PLUCK-3 CON
CURRENT PILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: US/09/971,543
CURRENT FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: ET/FP00/03176
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 12
SOPTWARE PATENTIN Ver. 2.1
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US-10-127-890-124
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; ORGANISM: Mus sp.
US-09-971-543-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 124, Application US/10127890 Publication No. US20030166196A1 GENERAL INFORMATION:
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LENGTH: 253
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Best Local Similarity
                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunottxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Better, Marc D.
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 QVQLQQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGRGLKWMGWINTYTGESTY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYWGQGTLVTVSA 119
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APPLICATION NUMBER: US/08/646,360 FILING DATE: 13-MAY-1996 APPLICATION NUMBER: PCT/US94/05348 FILING DATE: 12-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDEKGREAFSLETSASAAYLQINNLKNEDTATYECARF--AIKG-DYWGQGTTLTVSS 253
                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                           CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Pred. No. 2.9e-39;
8; Mismatches 8
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Sequence 2, Application US/10138727A

Publication No. US20030157054A1

GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Gillies, Stephen
APPLICANT: Qian, Susan
ITITE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/10/138,727A
CURRENT APPLICATION NUMBER: US 60/288,564
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR APPLICATION STEP: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.0
SEQ ID NO
SEQ ID NO
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SEQ ID NO
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                                                                                                                                                                                                                                                                            Query Match 81.5%; Score 526.5; DB 1
Best Local Similarity 81.5%; Pred. No. 2.5e-39;
Matches 97; Conservative 11; Mismatches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: KS VH mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICholae, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELECHONE: 312/707-8889
TELECAX: 312/707-9155
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 124:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51
61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSFKGFAYMGGGTLVTVSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYWGQGTLVTVSA 119
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                                                                                                                                                                                            1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.8%;
83.2%;
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                                                                                                                                                                                                                                                                                    Indels
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ADDFKGRFVFSLETSASTAFLQLNNLRSEDTATYFCVRF--ISKG-DYWGQGTSVTVSS 116

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61 ADDFKGRFAFSLETSASTAYLQINNLKNEDMATYFCATTTLITYYFDYWGQGTTLTVSS 119

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US-10-268-883-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: KS VH mouse US-10-138-727A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
US-10-138-727A-26
                                                                                                                                                                                                                                              ; ORGANISM: Mouse 
US-10-268-883-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10268883 Publication No. US20030138862A1 GENERAL INFORMATION:
                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lo, Kin-Ming
APPLICANT: Qian, Susan
TITLE OF INVENTION: Recombinant Tumor Specific Antibody and Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/10/138,727A
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US 60/288,564
ERIOR PLICATION NUMBER: US 60/288,564
REIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: USSN 60/329,178
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: USSN 60/331,965
PRIOR FILING DATE: 2001-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: T80, J. Yun
APPLICANT: Green, Jennifer Macphate
TITLE OF INVENTION: Anti-HLA-DR Antibodies and the Methods of Using Thereof
FILE REFERENCE: 05882.0062.NPUS01
CURRENT APPLICATION NUMBER: US/10/268,883
CURRENT FILING DATE: 2003-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gillies, Stephen APPLICANT: Lo, Kin-Ming APPLICANT: Qian, Susan
                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                           TYPE: PRT
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61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSFKGFAYWGGGTLYTVSA 119
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                                                                   1 QIQLVQSGPELKKPGETVKISCKASKYTFTNYGMNWVKQAPGKVLRWMGWINTYTGEPTY 60
                                                                                                           1 EVKLVESGPELKKPGETVKISCKASGYIFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTY 60
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Pred. No. 2.8e-39;
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RESULT 13
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                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tso, J. Yun
APPLICANT: Green, Jennifer Macphate
APPLICANT: Green, Jennifer Macphate
TITLE OF INVENTION: Anti-HLA-DR AntiDodies and the Methods of Using Thereof
FILE REFERENCE: 05882.0062.NPUS01
CURRENT APPLICATION NUMBER: US/10/268,883
CURRENT FILING DATE: 2003-03-26
CURRENT FILING DATE: 2003-03-26
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TITLE OF INVENTION: ANTI-HLA-DR ANTIBODIES AND THE METHODS OF USE THEREOF
FILE REPERENCE: 05882.0062.NPUS01
CURRENT APPLICATION NUMBER: US/10/269,010
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: USSN 60/329,178
PRIOR PILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: USSN 60/329,178
PRIOR PILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: USSN 60/331,965
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PRIOR PILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: USSN 60/331,965
PRIOR FILING DATE: 2001-11-21
NUMBER OF SEQ ID NOS: 16
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NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
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                                       61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYWGQGTLVTVSA 119
                                                                                           20 QIQLVQSGPELKKPGETVKISCKASKYTFTNYGMNWVKQAPGKVLRWMGWINTYTGEPTY 79
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ADDFKGRFAFSLETSASTAYLQINNLKNEDMATYFCATTTLITYYFDYWGQGTTLTVSS
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Pred. No. 2.8e-39;
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US-09-977-283A-13

Sequence 13, Application US/09977283A

Publication No. US20030031664A1

GENERAL INFORMATION:

APPLICANT: Reed, Guy L.

FILE REFERENCE: 0609-4320003

CURRENT FILING DATE: 2001-10-16

PRIOR APPLICATION NUMBER: US/09/977,283A

CURRENT FILING DATE: 2001-10-16

PRIOR APPLICATION NUMBER: 08/934,000

PRIOR PILING DATE: 1997-09-19

PRIOR PILING DATE: 1997-09-19

INMBER OF SEQ ID NOS: 81

SOFTWARE: PATENTIAL DATE: 1996-09-20

NUMBER OF SEQ ID NOS: 81

SOFTWARE: PATENTIAL VERSION 3.1

SEQ ID NO 13

FEATURE:

ORGANISM: Artificial Sequence

FEATURE:

ORGANISM: Artificial Sequence

FEATURE:

ORGANISM: ARTIFICIAL Alpha-2 Antiplasmin Antibody

NAME/KEY: MISC FEATURE

LOCATION: (-18). (-18)

NAME/KEY: MISC FEATURE

LOCATION: (-18). (-18)

OTHER INFORMATION: May be either Asp or Ala

NAME/KEY: MISC FEATURE

LOCATION: (-14). (-14)

OTHER INFORMATION: May be either Asp or Thr
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Search completed: November 7, 2003, 08:16:50 Job time : 104.383 secs
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                                                                                                    20 QIQLVQSGPELKKPGETVKISCKASGYTFTKYGMNWVKQAPGKGLKWMGWINTNSGEPTY 79
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Maximum Match 10
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Maximum DB seq length: 2000000000
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-569-147-76
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US-08-902-486-9
US-08-975-811-53
US-08-875-811-55
US-08-483-749A-24
US-08-461-838-6
US-08-461-838-6
US-08-461-386-6
US-08-461-386-6
US-08-461-386-10
US-08-461-386-124
US-08-488-113B-124
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US-08-447-788A-28
US-08-4477-531B-28
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US-08-461-184-8

US-08-463-675-8

US-08-464-589-8

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	79.7	79.7	79.7	79.7	80.5	80.7	81.0	81.0	81.1	81.3	81.3	81.3	81.3	81.3	81.4	81.8	81.8	81.8
	121 4	121 4	121	121 3	138	118 '	284	136	119	138 :	118 :	118 :	118 :	118 :	278	118	118	118
ALIGNMENTS	4 US-09-344-050-111	4 US-09-344-050-7	3 US-08-783-853A-111	3 US-08-783-853A-7	3 US-08-933-983-15	4 US-09-406-532-21	3 US-09-184-658-40	3 US-09-184-658-32	1 US-08-491-845-2	3 US-08-933-983-13	2 US-08-082-842A-88	2 US-08-477-531B-66	1 US-08-472-788A-88	1 US-08-107-669D-66	3 US-09-184-658-47	4 US-09-610-838-124	3 US-09-136-389-124	3 US-08-839-765-124
		Sequence 7, Appli									Sequence 88, Appl		Sequence 88, Appl					Sequence 124, App

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TELEPA: 617-240-,...
TELEPA: 617-240-,...
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: linear
                                                                                                                                            ; MOLECULE TYPE: protein US-08-133-804-2
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US-08-133-804-2
                                                                         Best Local Sin
Matches 105;
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                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachusetts
COUNTRY: USA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Biosynthetic Binding Proteins
TITLE OF INVENTION: Baging
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Teath
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Excha
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3 EIQLVQSGPELKKPGETVKISCKASGYTPTNYGMYWYKQAPGKGLKWMGWINTNTGEPTY
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                                                                                          Similarity
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85.4%;
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                                                                   Score 552; DB 1; I
Pred. No. 2.2e-43;
5; Mismatches 5;
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RESULT 3
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US-08-461-184-8
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Best Local Similarity 85.4
Matches 105; Conservative
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INFORMATION FOR SEQ ID NO: 8:
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PRIOR APPLICATION NUMBER: US/08/143
APPLICATION NUMBER: US/08/143
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRPO
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,184
FILING DATE:
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APPLICANT: OPPERMANN, HERMANN
TITLE OF INVENTION: MECHODS AND COMPOSITIONS FOR HIGH PROTEIN
TITLE OF INVENTION: PRODUCTION FROM NON-NATIVE DNA
                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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ZIP: 07148
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                                                                                                                                                                                                                                                                                                                                                                : 250 amino acids
amino acid
GV: linear
                                                               VSA 121
                                                                                                                          AEEFKGRFAFSLETSASTAYLQINNLKNEDTATYFCGRQFITYG--
                                                                                                                                                                                        BIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTNTGEPTY
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Pred. No. 2.2e-43;
5; Mismatches 5
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Sequence 8, Application US/08464
Patent No. 5733782
GENERAL INFORMATION:
APPLICANT: DORAL HAIMANTI
APPLICANT: OPPERMANN, HERMAN
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: PRODUCTI
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Best Local Similarity 85...
105; Conservative
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Patent No. 5658763
GENERAL INFORMATION:
APPLICANT: DORAL, HAIMANTI
APPLICANT: OPPERMANN, HERMANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/463,67
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMER: 08/143,498
FILING DATE: 25-OCT-1993
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                            NUMBER OF SEQUENCES: 1
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LENGTH: 250 amino acid
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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                               DDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 34,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                            8, Application US/08464589
5. 5733782
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SEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
: 45 SOUTH STREET
HOPKINTON
                                                                                                                                                                                                                                                                                                                                  ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCA----LYGNSPKGFAYWGQGTLVT 116
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45 SOUTH STREET
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                                                                            PRODUCTION
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                                                                       AND COMPOSITIONS FOR HIGH PROTEIN
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COUNTRY:

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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                               APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: KELLEY, ROBIN D
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 08/143,498
FILING DATE: 25-OCT-1993
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TYPE: amino acid
TOPOLOGY: linear
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FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                           CITY: Boston
STATE: Massac
                                                                                                                                                                                                                                ADDRESSEE: Testa, Hurwitz & Thibeault/Patent Department STREET: Exchange Place, 53 State Street
APPLICATION NUMBER: US/08/461,838
                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 VSA 121
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5753204
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                                                                                                                                                                                         Massachusetts
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Pred. No. 2.2e-43;
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                                                         TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 2:
                                                                                                            CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acids
TYPE: amino acid
TOPOLLOGY: line...
                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,386
FILING DATE:
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NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,6
REFERENCE/DOCKET NUMBER:
            SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Huston, James S. APPLICANT: Oppermann, Hermann APPLICANT: Houston, L. L. APPLICANT: Ring, David B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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TELEPHONE: 617-248-7477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Biosynthetic Binding Proteins For TITLE OF INVENTION: Imaging
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                       TELEPHONE: 617-248-7100
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                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                       Massachusetts
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Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                             617-248-7477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hurwitz & Thibeault/Patent Department
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TOPOLOGY:

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                                                         Matches
                                                                                          Query Match
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                                                                                                                                                                                              TELEFAX: (617) 248-710
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acid
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/356,78
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                 NAME: Pitcher, Edmund R.
REGISTON NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
STREET: Exchange Place, 53 State Street
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APPLICANT: Oppermar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
TITLE OF INVENTION: Marker
                                                       Local Similarity
nes 105; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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amino acid
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EVKLVESGPELKKPGETYKISCKASGYIPTNYGMNWVXQAPGKGLKWMGWINTYTGEPTY 60
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- NO: 16:
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Pred. No. 2.2e-43;
5; Mismatches 5
                                                                                                                                                                                                                                                                                                        CRP-053
                                                     Score 552; DB 2;
Pred. No. 5.7e-43;
5; Mismatches 5
                                                                                        Length 622
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RESULT 9
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US-08-569-147-76
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                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (215) 568-343:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/569,147
FILING DATE: 25-March-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION UNMBER: 35,719
REFERENCE/DOCKET NUMBER: CARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 140 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Woodcook Washburn Kurtz Mac
ADDRESSEE: No. 6180377ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                  140 S 140
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                                                                                                                                                                                                                                                                           84.5%;
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                                                                                                                                                                                                                                                                           Score 546; DB 3;
Pred. No. 4.1e-43;
                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                            Length 140;
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US-08-279-772A-6

Sequence 6, Application US/08279772A Patent No. 6080560

GENERAL INFORMATION:

Russell, David R

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RESULT 10
US-08-902-486-9
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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NAME: Seay, Nicholas J.
REGISTON NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 11-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,772A
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                           APPLICANT: Russel, David R.
APPLICANT: Fuller, James T.
TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND
TITLE OF INVENTION: PROTEIN TOXINS IN PLANT CELLS
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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ADDRESSEB: Quarles and Brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Fuller, James T
TITLE OF INVENTION: Method for Producing Antibodies in Plant
TITLE OF INVENTION: Cells
                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                COUNTRY: US
ZIP: 53701-2113
                                                                                                           STATE:
                                                                                                                               CITY: Madison
                                                                                                                                              ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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   amino acid
   GY: linear
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RESULT 11
US-08-875-811-53
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LENGTH: 252 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence by Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 84.1%;
Best Local Similarity 84.3%;
Matches 102; Conservative
APPLICATION NUMBER: WO PCT
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                  COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FBB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
                                                                                                                                                                                                                                                                               ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rybak, Susanna M. APPLICANT: Newton, Dianne L. APPLICANT: Boque, Lluis APPLICANT: Wlodawer, Alexand TITLE OF INVENTION: Recombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/902,486
                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 ADDEKGREAFSLETSAYTAYLQINNIKANEDMATYECARESYGNS-RYADWGQGTTLTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53, Application US/08875811
>: 6045793
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                                                                                                                                                                                                                                                                                                                                                 USA
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VBNTION: Recombinant Ribonuclease Proteins
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                                            US 60/011,800
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Pred. No. 1.3e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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/ MOLECULE TYPE: protein
US-08-875-811-55
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US-08-875-811-55
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// MOLECULE TYPE: protein
US-08-875-811-53
                                                                                                                                                                                                                NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 0152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPEAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 55:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55, App. Sequence 55,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHON: (**15) **576-0200
                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rybak, Susanna M. APPLICANT: Newton, Dianne L. APPLICANT: Boque, Lluis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
STATE: California
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                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 QVKLQQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTYTGESTY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                            i: 366 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYWGQGTLVTVSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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Pred. No. 4.5e~42;
5; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
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APPLICANT: Wirsching, Peter
APPLICANT: Wirsching, Peter
APPLICANT: Wirsching, Peter
APPLICANT: Lerner, Richard A
APPLICANT: Lerner, Richard A
APPLICANT: Lerner, Richard N
TITLE OF INVENTION: FILAMENTOUS PHAGE USING PVII AND PII, COMPOSITIONS,
TITLE OF INVENTION: FILAMENTOUS PHAGE USING PVII AND PII, COMPOSITIONS,
TITLE OF INVENTION: VECTORS AND COMBINATORIAL LIBRARIES
TITLE OF INVENTION: VECTORS AND COMBINATORIAL LIBRARIES
CURRENT APPLICATION NUMBER: US/09/318,786
CURRENT APPLICATION NUMBER: US/09/318,786
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 35
LENGTH: 160
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-08-483-749A-24
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US-09-318-786-35
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                                                                                                                                                                                                                                                                                                                        Sequence 24, Application US/08483749A Patent No. 6054561 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 83.0%;
Best Local Similarity 85.7%;
Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 35,
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
COUNTRY: USA
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                    NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY -
                                                                                                                                                                                                                                              APPLICANT: RING, DAVID B.
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
                                                                                                                                  STREET: LWATTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCALYGNSPKGFAYWGQGTLVTVSA 119
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Pred. No. 3.9e-42;
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Pred. No. 4.5e-42;
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US-08-133-804-6
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REFERENCE/DOCKET NUMBER: 0508
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2585
TELEPHONE: (510) 655-542
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE; amino acids
TYPE; amino acids
TYPE; amino acids
TYPE; amino acids
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Patent No. 5534254
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Best Local :
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TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617.248-7477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/133,804
FILING DATE:
CLASSIFICATION: 424
CTARSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Blosynthetic Binding Proteins For
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,749A
FILING DATE: 07-UN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SAVEREDIE, PAUL B.
REGISTRATION NUMBER: 36,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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JS-08-133-804-6

US-08-133-804-6

Query Match
Best Local Similarity 82.4%; Pred. No. 2.2e-41;
Matches 98; Conservative 10; Mismatches 7; Indels 4; Gaps

Over 1 EVILVESGPELKEPGETVKISCKASGYIFINYGMNWVKQAPGKGLKWMGWINIYTGEPTY 60

I EIQLUGSGPELKEPGETVKISCKASGYIFANYGMNWMKQAPGKGLKWMGWINIYTGQETY 60

Over 1 EIQLUGSGPELKEPGETVKISCKASGYIFANYGMNWMKQAPGKGLKWMGWINIYTGQETY 60

Over 1 EIQLUGSGPELKEPGETVKISCKASGYIFANYGMNWMKQAPGKGLKWMGWINIYTGQETY 60

Over 1 EIQLUGSGPELKEPGETVKISCKASGYIFANYGMNWMKQAPGKGLKWMGWINIYTGQETY 60

Over 1 EIQLUGSGPELKEPGETVKISCKASGYIFANYGMNWMKQAPGKGLKWMGWINIYTGQETLUTUSA 119

Over 1 EIGLUGSGPELKEPGETVKISCKASGYIFANYGMNWMKQAPGKGFAYMGQGTLUTUSA 119

Over 1 EIGLUGSGPELKEPGETVKISCKASGYIFANYGMNWMKQAPGKGLKWMGWINIYTGQETLUTUSA 119

Over 1 EIGLUGSGPELKEPGETVKISCKASGYIFANYGMNWMKAAPGKGLUTUSA 119

Over 1 EIGLUGSGPELKEPGETVKISCKASGYIFANYGMNWMKAAPGAFAYMGQGTLUTUSA 119

OVER 1 EIGLUGSGPELKEPGE
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Search completed: November 7, 2003, 07:30:07 Job time: 18.4766 secs

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Match
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572
1 DIQMTQSPKFLLVSAGDRVT......QQDYGSPFTFGGGTKLEIKR 108
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         Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Query Match 85.1%; Score 487; DB 2; Length 127; Best Local Similarity 87.7%; Pred. No. 4.3e-37;	A;Accession: 804577 A;Molecule type: mRNA A;Residues: 1-127 <kof> A;Residues: 1-127 <kof> A;Cross-references: EMBL:X14622; NID:952400; PIDN:CAA32775.1; PID:952401 A;Cross-references: EMBL:X14622; NID:952400; PIDN:CAA32775.1; PID:952401 C;Superfemily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;1-20/Domain: signal sequence #status predicted <sig> F;21-127/Product: Ig kappa chain V region (fragment) #status predicted <mat> F;36-110/Domain: immunoglobulin homology <imm></imm></mat></sig></kof></kof>	R;Kofler, R.; Duchosal, M.A.; Dixon, F.J.  Bubmitted to the EMBL Data Library, March 1989  A;Description: Complexity, polymorphism and connectivity of murine V(kappa)  A;Reference number: S04577	RESULT 2 \$04577 \$194577 Ig kappa chain precursor V region (MRL-RF28L) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Species: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000 C;Accession- \$64577	Qy 62 FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPFTFGGGTKLEIKR 108	Qy 2 IQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAMYQQKPGQSPKLLMYYASNRYTGVPDR 61	Query Match 89.2%; Score 510.5; DB 2; Length 225; Best Local Similarity 92.5%; Pred. No. 5.9e-39; Matches 99; Conservative 4; Migmatches 3; Indels 1; Gaps	submitted to the EMBL Data Library, February 1993 A;Reference number: \$37483 A;Accession: \$37484 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-225 < DUC> A;Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin	use (fragment) ulus (house mouse) #sequence_revision 06-Jan-19	ALIGNMENTS	391 68.4 134 2 PC1214  390 68.2 127 2 \$40367  389.5 68.1 107 2 \$36275  389.5 68.1 113 2 PT0407  389.5 68.1 113 2 PT0356  389.5 68.1 118 2 PT0356  389.5 68.1 118 2 ST0356  389.5 68.1 118 2 ST0356  389.5 118 2 ST0356  389.5 118 2 ST0356  389.5 118 2 ST0356  389.5 118 2 ST0356  389.5 118 2 ST0356  389.5 118 2 ST0356  389.5 118 2 ST0356	19 kappa chain 11 Ig kappa chain 12 Ig kappa chain 13 Ig kappa chain 14 Ig kappa chain 15 Ig kappa chain 16 Ig kappa chain 17 Ig kappa chain 17 Ig kappa chain 17 Ig kappa chain 17 Ig kappa chain	393 68.7 98 2 PH1073 Ig light chain
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R;Boyd, R.T.; Goldrick, M.M.; Gottlieb, P.D.
Proc. Matl. Acad. Sci. U.S.A. 83, 9134-9138, 1986
A;Title: Structural differences in a single gene encoding the V-k;A;Reference number: A94141; MUID:87067464; PMID:3097643
A;Reference number: DNA...
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C;Keywords:
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A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin W region; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-115/Product: Ig kappa chain V region Ser-b #status predicted
F;36-110/Domain: immunoglobulin homology <IWM>
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A;Cross-references: GB:M14360; NID:g197464; PIDN:AAA39034.1; PID:g197465
A;Experimental source: strain BALB/C
C;Genetics:
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C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revisic
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                                  IQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAMYQQKPGQSPKLLMYYASNRYTGVPDR 61
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Pred. No. 1.9e-36;
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7.2e-36;
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A; Residues: 1-71 <KEL>
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82.4%;
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and their pH-reactivity profiles.
A;Reference number: A53285; MUID:92017897; PMID:1922102
A;Accession: D53285
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A;Title: Molecular characterization of monoclonal anti-steroid antibodies:
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A;Residues: 30-149 <SMI>
A;Residues: 30-149 <SMI>
A;Residues: 310-149 <SMI
A;Residues: 310-149 <SMI
A;Residues: 310-149 <SMI
A;Residues: 310-149 <SMI
A;Residues: 310-149 <SMI
A;Residues: 410-149 <Ambinoment: The amidation states of residue of typical kappa chains.
42 corresponds to the amino-terminal residue of typical kappa chains.
6;Complex: An immunoglobulin heterotetramer subunit consists of two identical lighth disulfide bonds. In some cases, such as IgA and IgM, the subunits associate c;Superfamily: immunoglobulin v region; immunoglobulin homology
6;Keywords: duplication; heterotetramer; immunoglobulin
F;1-29/Domain: signal sequence #status predicted <SIG-
F;30-149/Product: Ig kappa chain v region (MPCII) #status experimental <MAT>
F;57-31/Domain: immunoglobulin homology <IMM>
F;67-131/Domain: immunoglobulin homology <IMM>
F;64-130/Nicolfide bonds: #status experimental <MAT>
F;67-131/Domain: immunoglobulin homology <IMM>
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A;Title: The variability, arrangement, and rearrangement A;Reference number: A90753; MUID:80176554; PMID:6245773 A;Accession: A90753
A;Ressidues: 41-149 < RAB>
                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain V and J regions, monoclonal antibody SCET.M8.1 - C;Species: Mus musculus (house mouse)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change
C;Accession: D53285
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A;Title: Sequence of the full-length immunoglobulin kappa-chain
A;Reference number: A90298; MUID:78186617; PMID:418775
A;Contents: myeloma protein MPC11
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protein
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Pred. No. 4e-35;
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A; Residues: 1-107 < IZU>
A; Cross-references: EMBL:X70097; NID:g288262; C; Superfamily; immunoglobulin V region; immunoglobulin C; Keywords: heterotetramer; immunoglobulin F; 16-90/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
S32192
                                                                                                                                                                                                                                                                      19 kappa chain V region - mouse (fragment)
C;Species: Mus musculius (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change
C;Accession: S32192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: PQ0265
R;Lohman, K.L.; Carrillo, M.A.; Kennedy, R.C.
Gene 105, 283-284, 1991
A;Title: Sequence analysis of the variable region of a mouse
A;Reference number: PQ0265; MUID:92039046; PMID:1937027
                                                                                                                             A; Molecule type: mRNA
                                                                                                                                                   submitted to the EMBL Data Library, A;Reference number: S32185 A;Accession: S32192 A;Status: preliminary
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A; Residues: 1-119 < LOH>
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A;Cross-references: GB:D12737; NID:g220597; PIDN:BAA02229.1; PID:g220598
A;Cross-references: GB:D12737; NID:g220597; PIDN:BAA02229.1; PID:g220598
A;Note: sequence extracted from NCBI backbone (NCBIN:63304, NCBIP:63309)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;101-109/Region: complementarity-determining 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig kappa chain V region (MC1) - mouse (fragment) C;Species: Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Comment: This protein recognizes a restricted idiotype associated with antibodies superfamily: immunoglobulin V region; immunoglobulin homology;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-102/Domain: immunoglobulin homology <IMM>
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82.1%;
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Pred. No. 3.1e-34;
6; Mismatches 14
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Pred. No. 2.3e-34;
7; Mismatches 12
                                                                                                                                                                                                                       February 1993
                                                    immunoglobulin
                                                                        PIDN:CAA49701.1; PID:g288263
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IQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPDR

Query Match Best Local : Matches 8:

82;

Conservative

Similarity

75.9%; 87.2%;

Score 434; DB 2; Pred. No. 2.3e-32; 5; Mismatches 7;

Length 115;

Indels

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Gaps

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A;Introns: 17/1
C;Keywords: heterotetramer; immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                             C;Accession: A25924
R;Boyd, R.T.; Goldrick, M.M.; Gottlieb, P.D.
Proc. Natl. Acad. Sci. U.S.A. 83, 9134-9138, 1986
A;Title: Structural differences in a single gene encoding A;Reference number: A94141; MUID:87067464; PMID:3097643
                                                                                                                                                                                                                                                                                                                                   Ig kappa chain precursor V region (Ser-a) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
P;36-110/Domain: immunoglobulin homology < IMM>
                                                                                                                                     A;Cross-references: GB:M14361; NID:g197466; PIDN:AAA39035.1; PID:g197467
A;Experimental source: strain C.C58
                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-115 < BOY>
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$32191
                                                                                                                            C;Genetics:
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F;16-90/Domain:
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A;Cross-references: EMBL:X70095; NID:g288260; PIDN:CAA49700.1; PID:g288261
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number:
A;Accession: S32191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, A;Reference number: S32185
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                ;1-20/Domain: signal sequence #status predicted <SIG>;21-115/Product: Ig kappa chain V region Ser-a #status
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Best Local Similarity
Matches 87; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPD 60
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80.4%;
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81.3%;
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Pred. No. 2.2e-33;
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Pred. No. 7.8e-34;
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                   predicted <MAT>
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A;Cross-references: EMBL:X05877; NID:g52195; PIDN:CAA29301.1; PID:g52196 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;45-119/Domain: immunoglobulin homology <IMM> F;138-152/Domain: C region (C-kappa) (fragment) #status predicted <CRE> F;138-152/Domain: C region (C-kappa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: strain BALB/c A;Note: the sequence shown here is from the V kappa region of an C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-91/Domain: immunoglobulin homology <IMM>
RESULT
PL0204
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A;Title: Improved RNA sequencing method to determine immunoglobulin A;Reference number: S30751; MUID:87260030; PMID:3601683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig kappa chain precursor V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: 1-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca
J. Exp. Med. 169, 519-533, 1989
A;Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are
A;Reference number: PLO080; MUID:89094248; PMID:2492056
A;Accession: PL0083
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A; Residues: 1-152 < GRA>
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A; Residues: 1-108 < MEE>
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                                                                                                                                                                                              DIQMTQSPKELLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPD
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                                                                                                                                                            DIVMTQSHRFMSTSVGDRVSITCKASQDVTTAVSWYQQKPGQSPKLLIFWASTRHTGVPD
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                                                                           RFTGSGSGTDYTLTTSSVQAEDLALYYCQQHYSTPLTFGAGTKLELKR 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RFTGSGSGTVDFTFTISSVQAEDQAVYYCQQHYTTPPTFGGGTKLGIK 108
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Pred. No. 3
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R/Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A,Title: Variable region primary structures of monoclonal A,Reference number: PL0198; MUID:90309768; PMID:2114528
                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X78108; NID:g460824; PIDN:CAA54998.1; PID:g460825
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;26-100/Domain: immunorlobulin
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S42466
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                                                                                                                                                                                                                                                                                                                                                                                                            R;Shiyanov, P.A.; Bespalov, I.A.; Terletskaya, submitted to the EMBL Data Library, March 1994 A;Reference number: $42466 A;Accession: $42466
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S42466
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C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
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A; Residues: 1-108 < SMI>
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A; Accession: PL0204
                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
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Similarity 75.0%;
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                        RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIK 107
                                                                              DÍVMTQSHKFMSTSVGDRVSÍTCKÁSÓDVGTAVÁMÝQQKÞGQSÞKILIYMASTRHTGVPD
                                                                                                                         DIQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPD
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RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPYTFGGGTKLEIK 117
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76.6%;
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Pred. No. 5:3e-31;
6; Mismatches 19
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Pred. No. 4.9e-31;
9; Mismatches 18
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Ig kappa chain V region (anti-haloperidol antibody A) - mouse (;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 21-JaC;Accession: A28195
R;Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4663, 1988
A;Title: Haloperidol binding to monoclonal antibodies. Hypervariable A;Reference number: A28195; MUID:88153717; PMID:3267217

21-Jan-2000

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Title:
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Maximum Match 10
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PIR; A90823; KVMS11.
HSSP; P80362; 1WTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig\_MHC.
InterPro; IPR003596; Ig\_V.
Pfam; PP00047; ig; 1.
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Immunoglobulin V region; Signal; Repeat.

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                     Pfam; PF00047; ig; 1.
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Immunoglobulin V region; Signal; 3D-structure.
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MEDLINE=73053310; PubMed=4638343;
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MEDIJINE-82059477; PubMed-6170937;

Hamlyn P.H., Gait M.J., Milstein C.;

Hamlyn P.H., Gait M.J., Mimmunoglobulin mRNA using specific priming 
"Complete sequence of an immunoglobulin mRNA using specific priming 
and the dideoxynucleotide method of RNA sequencing.";

Nucleic Acids Res. 9:4485-4494(1981).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                       Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                          EMBL; Z00022; CAA77317.1; ...
PIR; A01904; K4HUJI.
HSSP; P80362; 1WTL.
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                                                                                    SIGNAL :
                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 13:6515-6529(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=86041853; PubMed=2997712; Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1988 (Rel. 05, Created)
01-JAN-1988 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-IV region JI precursor.
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                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          "Subgroup IV of human immunoglobulin K light chains is encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                        Zachau H.G.
                                                                                                                                                                                     GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding act
GO:0006955; P:immune response; NA
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Pred. No. 1
                                              IG KAPPA CHAIN V-IV REGION JI FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
 COMPLEMENTARITY-DETERMINING-3
            COMPLEMENTARITY-DETERMINING-2 FRAMEWORK-3.
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COMPLEMENTARITY-DETERMINING-3
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                                    FRAMEWORK-2
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RESULT 4

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Best Local (
  Best Local Similarity
                     Query Match
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GO; GO:0003823; F:antigen bindl
GO; GO:0006955; P:immune respot
InterPro; IPR0077110; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGV; 1.
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PDB; 1EEU;
PDB; 1EFQ;
PDB; 1EK3;
PDB; 1LVE;
PDB; 3LVE;
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-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Creat 01-OCT-1996 (Rel. 34, Last 15-SEP-2003 (Rel. 42, Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The primary structure of a monoclonic immunoglobulin-L-chain subgroup IV of the kappa type (Bence-Jones protein Len)."; Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
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Schneider M., Hilschmann N.;
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Eukaryota; Metazoa;
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P01625;
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GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding activity; NAS.
GO:0006955; P:immune response; NAS.
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                                                                                                                                                                                                                                          region; Bence-Jones protein; 3D-structure 23 FRAMEWORK-1.
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annotation
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Pred. No. 8.4e-35;
Score 391;
Pred. No. 8
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BY SIMILARITY.
                                                                                                                                                                              COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                    FRAMEWORK-
                                                                                                                                        FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
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  8e-35;
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                   Length 114;
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RESULT 5

KY4C HOMA

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GO; G
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                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
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GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-APR-1988 (Rel. 07, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
Ig kappa chain V-IV region B17 precursor.
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SMART; SM00406; IG;
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Marsh P., Mills F., Gould H.;
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1 DIQMTQSPKFLLVSAGDRVTITCKASQSV-----SNDVAWYQQKPGQSPKLLMYYASNR
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Pred. No. 2.
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FRAMEMORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEMORK-4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                        IG KAPPA CHAIN V-IV REGION B17. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2.
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21-JUL-1986 (Rel. 01, Last sequ
15-JUL-1999 (Rel. 38, Last anno
16 kappa chain V-I region Lay.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DOMAIN
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:000823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Capra J.D., Klapper D.G.;
"Complete amino acid sequence of the variable domains of IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
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SMART; SM00406; IGv; 1.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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 £80362;
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MISCELLANBOUS: THE SECOND AND THIRD HYDERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN, WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.

MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.

(A01871; KHULY.
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                                                              RESGSGSGTETETISSIQPEDIATYYCQQYNNWPPTFGQGTKVEVKR
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38, Last annotation update)
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Pred. No. 2.6e-34;
3; Mismatches 21
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BY SIMILARIT
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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COMPLEMENTARITY-DETERMINING-3
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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01-NOV-1995
28-FEB-2003
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Stevens F.J., Westholm F.A., Panagiotopoulos N.,
Popp R.A., Solomon A.;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ig kappa chain V-I region WAT.
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66.1%; Score 378; DB 1; 1
66.7%; Pred. No. 1.8e-33;
cive 15; Mismatches 21;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PR00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
  - KV1N HUMAN

P01606;

21-JUL-1986

21-JUL-1986

15-JUL-1999
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation updat
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-!- MISCELLANEOUS: THE C REGION OF THIS ON MISCELLANEOUS: THIS IS A BENCE-JONES
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Watanabe S., Hilschmann
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GO:0003823; F:antigen binding activity;
GO:0006955; P:immune response; NAS.
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E; PS50835; IG LIKE; 1.

FRAMEWORK-1

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FRAMEWORK-2

COMPLEMENTARITY-DE

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FRAMEWORK-2.

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COMPLEMENTARITY-DE

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FRAMEWORK-3.

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Pred. No. 3e-33;
1; Mismatches
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING-2.
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21-JUL-1986 (
15-JUL-1999 (
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Mammalia; Eutheria;
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Interra; Ir...035>.
InterPro; IPR0035>.
InterPro; IPR0037; ig; 1.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IG LIKE; 1
TTE; PS50835; IG LIKE; 1
23
                                                                                             SEQUENCE FROM N.A.

MEDLINE=81241357; PubMed=6788890;
Kwan S.-P., Rudikoff S., Seidman
"Nucleic acid and protein sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chains.";
Science 169:56-59(1970).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3)
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'
This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the SMBL
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=70201507; PubMed=5447531;
Kohler H., Shimizu A., Paul C., Putnam F.W.;
"Macroglobulin structure: variable sequence of light and heavy
                                                        J. Exp. Med. 153:1366-1370(1981).
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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G0:0005576; C:extracellular; NAS.
G0:0003823; F:anntigen binding activity; NAS.
G0:0006955; P:immune response; NAS.
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ain V-I region S107A.
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                                                                                               protein sequences
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Primates;
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56.5%;
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BY SIMILARTTY
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Pred. No. 3e-33;
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COMPLEMENTARITY-DETERMINING-1.

FRAMEWORK-2.

COMPLEMENTARITY-DETERMINING-2.

FRAMEWORK-3.
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                                                                                           Leder P., Scharff M.D.; phosphocholine-binding
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KV3D_HUMAI
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Best Local 5
Matches 74
                          PIR; A01895; K3HUTI.
HSSP; P80352; IWTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding activ
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_WHC.
InterPro; IPR003596; Ig_v.
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NON_TER
SEQUENCE
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Suter L., Barnikol H.U., Watanabe S., Hilschmann N.

"Rule of antibody structure. The primary structure inmunoglobulin L-chain of kappa-type, subgroup 3 (B Ti). IV. The complete amino acid sequence and its sthe mechanism of antibody production.";

HODDE-Seyler's Z. Physiol. Chem. 353:189-208(1972).

-i- MISCELLANBOUS: THE C REGION OF THIS CHAIN HAS TO MISCELLANBOUS: THIS IS A BENCE-JONES PROTEIN.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Pfam; PF00047; i
SMART; SM00406;
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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RESULT 12
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Best Local &
Matches 70
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GO; GO:0003823; F:antigen bindi
GO; GO:0006955; P:immune respon
InterPro; IPR007110; Ig-like
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00396; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
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13-AUG-1987
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the Buropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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Mammalia; Eutheria;
                                                                                                                                                                                               SIGNAL
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PIR; A01883; K1HUWK.
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(Rel. 05, Last sequence update)
(Rel. 38, Last annotation update)
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Primates;
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Pred. No. 1.
                                                                                                                 IG KAPPA CHAIN V-I REGION WALK
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                             FRAMEWORK-3.
COMPLEMENTARITY
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Catarrhini; Hominidae;
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RESULT 14
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ID KV3H_HUMAN
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DOMAIN
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15-JUL-1999 (Rel. 38, Last
Ig kappa chain V-I region
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges."; J. Biol. Chem. 244:3550-3560(1969).

-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

-I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
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Mammalia; Eutheria; Primates;
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21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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E; PS50835; IG LIKE; 1.
globulin V region; Benc
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Pred. No. 2.1e-3
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIK5; 1.
                                                  KV1P HUMAN
P01608;
21-JUL-1986
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20-MAR-1987
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HSSP; P80362; IWTL
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GO; GO:0006955; P:immune resp
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region CLL precursor (Rheumatoid factor).
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Ig kappa cnam var and Homo sapiens (Human).
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Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
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                            21-JUL-1986
15-JUL-1999
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GO:0003823; F:antigen binding activity;
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Pred. No. 2.
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BY SIMILARITY
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COMPLEMENTARITY-DETERMINING-3.
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HSSP; P80362; INTL.
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GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR00306; Ig_MHC.
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(In) Franck F., Shugar D. (eds.);
Gamma globulins: structure and function, pp.57-74, Academic Press,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and Cum.) ^{\prime\prime};
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[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 AA;
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1: sp_archea:*
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          Query
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Copyright (c) 1993 - 2003 Compugen Ltd.
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	268	276	290	290.5	298	299.5	300	301.5	301.5	303.5	304	305	309.5	312	314.5	318.5	320	323	323.5	325.5	327	329	330.5	331	331.5	332.5	333	335	338
			50.7			52.4	52.4	52.7	52.7	53.1	53,1	53.3	54.1	54.5	55.0	55.7	55.9	56.5	56.6	56.9	57.2	57.5	57.8	57.9	58.0	58.1	58,2	58.6	59.1
	109	97	127	241	234	239	101	112	106	134	114	103	235	234	239	112	298	107	104	112	109	116	114	214	239	109	234	111	233
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	Q9N0W5	Q9JL76	Q925S9	Q921A6	Q8R028	Q8K0F8	Q9JL78	Q8K1F0	Q9U410	Q8VDD0	Q9UL80	Q9JL80	Q91W12	042A80	QSTCDO	Q8K1F2	Q9QYF0	Q9JL84	Q9JL82	Q8K1F3	Q920E6	Q96PF6	Q8K1F1	Q9R1A5	Q8NEK0	98TD60	Q8R062	Q920E9	6SM160
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### ALIGNMENTS

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Query Match 88.6%; Score 507; DB 11; Length 99; Best Local Similarity 97.0%; Pred. No. 4.8e-48; Matches 96; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	with cardiac myosin"; Infect. Immun. 68:5803-5808(2000). EMBL; AF206032; AAF69330.1; HSSP; P80362; IWTL. InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_WHC. InterPro; IPR003596; Ig_V. Pfam; PF00047; ig; 1. SMART; SM00406; IGV; 1. SMART; SM00406; IGV; 1. PROSITE; PS5035; IG_LIKE; 1. NON_TER 1		SUL JL7

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Matches 78; Conserv
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Q8VIJO;
01-MAR-2002
                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa
variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                             Q96SA9;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                      SEQUENCE FROM N.A.

MEDILINE=98375893; PubMed=9712075;

Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;

Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gil "Differences in V kappa gene utilization and VH CDR3 sequer anti-DNA from C3H-lpr mice and lupus mice with nephritis.", Eur. J. Immunol. 26:2225-2233(1996).
EMBL; U59155; AAB02917.1; -.
                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C3H/HeJ-lpr/lpr;
MEDLINE=96409289; PubMed=8814271;
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  antibody V region genes.";
                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                    Homo sapiens (Human)
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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108 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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.; 11859 MW;
                                                                                                                                                                                       Chordata;
Primates;
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Pred. No. 3.8e-36;
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Catarrhini; Hominidae;
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Young D.C.;
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Mammalia; Eutheria;
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01-MAY-2000 (TrEMBLrel. 23, Last amotation update)
01-MAR-2003 (TrEMBLrel. 23, Last amotation update)
Myosin-reactive immunoglobulin light chain variable
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EMBL; U96396; AAB68785.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
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IPRO03596; Ig_v.
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Primates;
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Catarrhini; Hominidae;
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PROSITE; PS50835.
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; Van der Merwe P.L.,
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Sukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                             InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
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EMBL; AP035037; AAD56273.1; -.
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
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Mammalia; Eutheria;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable
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01-MAY-2000 (TYEMBLrel. 13, Last sequence update)
01-MAR-2003 (TYEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable
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   PROSITE; PS50835; IG_LIKE;
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Pred. No. 1.3e-33;
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Myosin-reactive immunoglobulin light chain variable
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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HSSP; P01607; 1REI
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InterPro; IPR003596; Ig_v.
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 23, Last smootation update)
rive immunoglobulin light chain variable
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Primates;
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 370.5; DB pred. No. Se-33;
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HSSP; P80362; 1MTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IRR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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Q9UL85;
01-MAY-2000
01-MAY-2000
01-MAR-2003
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Eukaryota; Metazoa;
Mammalia; Butheria;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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HSSP; P80362; 1WTL
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Myosin-reactive immunoglobulin kappa chain variab
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Mammalia; Eutheria;
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MEDLINE=98277139;
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PS50835; IG_LIKE; 1.
                                                                                                                                                                                      M00406; ĬĠV; 1.
PS50835; IG_LIKE;
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109 AA;
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n der Merwe P.L.,
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n der Merwe P.L.,
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Primates;
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11761 MW;
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Primates;
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65.1%;
  64.1%; So 64.2%; Po tive 19;
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  Score 366.5;
Pred. No. 1.4e
19; Mismatches
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Pred. No. 5.1e-33;
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Catarrhini; Hominidae;
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Catarrhini; Hominidae;
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Best Local (
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01-MAR-2003 (TTEMBLrel. 23, Las
Hypothetical 26.2 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metarra
                                                                                                                                                                                                                           SEQUENCE
Chen P.,
"Cloning
genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC019760; AAH19760.1; -: Interpro; IPR003006; Ig_MHC. Interpro; IPR003596; Ig_v. Pfam; PF00047; Ig; 2. SMART; SM00406; IGv; 1.
                                                                                                                                                                                                   genes of
J. Cell.
                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa;
Mammalia; Eutheria;
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   human
Ti 4 C
                              SEQUENCE FROM N.A.

Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B.,
"Construction and sequencing of the single-chain
human TNF-alpha specific monoclonal antibody.";
Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).
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, Deng J.B., Wang ;
g and sequencing of
f an anti-hTNF-a mc
Mol. Immunol. 12:
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238 AA; 2
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Rodentia;
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                                                                                                                                                                                                   ng Z.L., Han H., Su C.Z.
g of the light chain frag
a monoclonal antibody.";
12:21-26(1996).
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Last ann
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Pred. No. 3.7e-32;
4; Mismatches 21;
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Sciurognathi; Muridae; Murinae; Mus
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Sciurognathi; Muridae;
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antibody
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; Murinae; Mus
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Best Local S
Matches 68
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Best Local S
Matches 70
                                                                                                                                                         Clin. Immunol. Immunopathol. 87:184-192(1998).

EMBL; AP035031; ADD56267.1; -.

HSSP; P80362; IWTL.

InterPro; IPR0037110; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.

Pfam; P90047; ig; 1.

SMART; SM00406; IGv; 1.

PNON TER 108 108

108 108
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Chen P., Deng J.B., Wang Z.I

Submitted (MAY-2000) to the

EMBL; AF262753; AAG23804.1;

HSSP; P80362; 1MTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9UL83 PRELIMINARY; PRT; 108 AA.
Q9UL83; Q1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable
(Fragment).
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

NON TER 107 107

SEQUENCE 107 AA; 11784 MW;
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=98277139; PubMed=9614934;

MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                         Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                 fetus."
                                                                                                                                                                                                                                                                                                            Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                             Similarity
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                                              VPDRFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKL 104
RESGSGSGTEFTLTISSLQFEDFAVYYCQHYNNWPFTFGPGTKVDIKR
                       RETGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPFTFGGGTKLEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VPDRFMGSGSGTDFTLTISSVQTEDLADYFCQQHYRTPFTFGSGTKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MTQSPSSLAMSVGQKVTMSCKSSQSVLNSNTQKNYLAMYQKKPGQSPELLVYFASTRESG
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108 AA;
                                                                                                Conservative
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                                                                                                                                            108
11834 MW; 9F9C5A92EBA96EEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang Z.L., Han H., Yao L.B., Su C.Z ) to the EMBL/GenBank/DDBJ databases
                                                                                             62.8%; Sc
63.0%; Pr
tive 19;
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Pred. No. 7.1e-32;
3; Mismatches 18
                                                                                                           Score 359; DB 4;
Pred. No. 9.3e-32;
                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                 Mismatches
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                                                                                                                       DB 4; Length 108;
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ID Q91WF
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DT 01-DE
DT 01-DE
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Q8NEK1
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                              Strauberg R.;

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ dat

RMBL; BC015292; AAH12592.1; -

R InterPro; IPR003006; Ig_MHC.

R InterPro; IPR001865; Ribosomal_S2.

R Pfam; PF00047; ig; 2.

R Pfam; PF00047; ig; 1.

R Pfam; PS00290; IG_MHC; 1.

DR PROSITE; PS00290; IG_MHC; 1.

DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.

RMART; PS00962; RIBOSOMAL_S2_1; 1.

RMYDOThetical protein.

SQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2
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Best Local S
Matches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-2002) to the EMBL/GenBank/DDBJ dat
EMBL; BC030813; AAH30813.1; -.

Interpro; IPR003597; Ig-like.

Interpro; IPR003597; Ig-c1.

Interpro; IPR003597; Ig-c1.

Interpro; IPR003596; Ig-w.

Pfam; PF00047; Ig-c2.

Pfam; PF00047; IG-c1; 1.

SMART; SM00407; IG-c1; 1.

SMART; SM00407; IG-LIKE; 2.

PROSITE; PS50835; IG-LIKE; 2.

PROSITE; PS50835; IG-LIKE; 2.

PROSITE; PS50835; IG-LIKE; 2.

PROSITE; PS50835; IG-LIKE; 2.

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PROSITE; PS50835; IG-LIKE; 2.

PROSITE; PS50835; IG-LIKE; 2.

PROSITE; PS50835; IG-LIKE; 2.
Query Match
Best Local Similarity
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Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25.9 kDa protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-OCT-2002 (TrEMBLrel. 22,
01-MRR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIVMTQSPATLSVSPGERATLSCRASQSVTSNLAWYQQTPGQSPRLVIYGASSRASGVPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESGSGSGTEFTLTISSLQSEDFAVYYCQQYNKWPHTFGQGTKLDIKR
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61.0%;
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Last sequence update)
Last annotation update)
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Pred. No. 3.le-31;
1; Mismatches 19
Score 349; DB 1
Pred. No. 3e-30;
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                                                    B0D0B0E6EB7812D2
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                DB 11;
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RESULT 15
Q99M37
ID Q99M3
AC Q99M3
AC Q99M3
DT 01-JU
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Search completed: November 7, 2003, 07:34:33 Job time : 36.7155 secs
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Best Local S
Matches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Strausberg R.;
Submitted (JAK-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JAK-2001) to the EMBL/GenBank/DDBJ databases.
R HSSP; F00679; 2FBJ;
R HSSP; P01679; 2FBJ;
R InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_v.
R InterPro; IPR003596; Ig_v.
R InterPro; IPR003596; Ig_v.
R FNART; SM00406; IGv; 1.
R PROSITE; PS00035; IG_ILKE; 2.
R PROSITE; PS00035; IG_ILKE; 2.
R PROSITE; PS00035; IG_MHC; 1.
R PROSITE; PS00039; IG_MHC; 1.
R PROSITE; PS00039; IG_MHC; 1.
R PROSITE; PS00039; IG_MHC; 1.
R PROSITE; PS00039; IG_MHC; 1.
R PROSITE; PS00039; IG_MHC; 1.
R PROSITE; PS00039; IG_MHC; 1.
R PROSITE; PS00039; IG_MHC; 1.
R PROSITE; PS00039; IG_MHC; 1.
R PROSITE; PS00039; IG_MHC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q99M37
Q99M37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLiel. 17, Created)
01-JUN-2001 (TrEMBLiel. 17, Last sequence update)
01-JUN-2001 (TrEMBLiel. 23, Last annotation update)
01-MAR-2003 (TrEMBLiel. 23, Last annotation update)
Hypothetical 26.3 kDa protein.
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 60.6%; Score 346.5; DB 11; Length 238;
Local Similarity 61.9%; Pred. No. 5.7e-30;
hes 70; Conservative 15; Mismatches 23; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                      56 TGVPDRFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPFTFGGGTKLEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 RFSGSGSGTDYSLTÍSNLEQEDIÁTYFCQQGNTPPFTFGSGTKLEVKR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RFTGSGYGTDFTFTISTVQABDLAVYFCQQDYGSPPTFGGGTKLBIKR 108
                                                                                                                                                                 80 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGSGTXLEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Mismatches 28; Indels
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Database
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein - protein search, using sw model
                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                            Score
        100.0
92.5
92.3
91.4
91.4
91.4
91.4
91.4
                                                                                                                                                                                                                                                                                                 US-09-661-992B-82_COPY_135_242
572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 November 7, 2003, 07:21:17; Search time 46.5741 Seconds (without alignments) 368.069 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Geneseq 19Jun03:*
1: /SIDS1/gcgdata/g
2: /SIDS1/gcgdata/g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1107863 seqs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maximum Match 100%
                                                                                                                                                                                                                                                                                          /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIQMTQSPKFLLVSAGDRVT.....QQDYGSPPTFGGGTKLEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
                                                                                                                                                          Length
        1066
                                                                                                                                                            DB
                                                                                                                                                            A
      AAR58750
AAY23985
AAY01034
                                                  AAB20433
AAR70828
AAB29157
AAR39818
AAR39567
AAR39537
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Anti-FIX/FIXa anti
MAb 4197X light ch
Chimeric 31.1 anti
HP1/2 Vk. Homo sa
Sequence of the va
HP1/2 Vk. Synthet
Anti-VLA4 Ab HP1/2
Antibody HP1/2 lig
Anti VLA-4 antibod
                                                                                                                                                        Description
 ARESULT 1
AABA0433
ID AABA
XX AABA043
XX AABA
XX AAC
XX AAC
XX Fact
XX Fact
XX Fact
XX Fact
XX Haen
OS Chin
OS Chin
COS Chin
FT Prot
FT Regi
FT Regi
FT Regi
XX FT Regi
XX WO21
XX WO21
XX WO21
XX WO21
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                              WO200119992-A2.
                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB20433 standard; Protein; 242 AA.
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461	461	461	463	466	466	466	466	466	474	474	478.5	479	479	481	490	497	497	497	497	498	502	502	502	502	502	502	505	507	511	512	518	$\mathbf{r}$	523	523	523
80.6	80.6	80.6	•	81.5	•	٠		81.5			٠	83.7	83.7	84.1		86.9	•			87.1		87.8	87.8	87.8	87.8	87.8	88.3	œ	•			Ō			91.4
128	128	128	128	129	128	128	128	128	105	105	225	128	124	107	672	488	488	488	488	107	595	592	243	243	243	243	126	107	206	107	554	246	106	106	106
16	15	15	15	16	20	19	19	15	18	17	14	15	15	18	24	24	24	22	ა 0	18	20	22	22	20	20	20	20	13	20	13	16	5	24	22	20
AAR70254	AAR59933	AAR55209	AAR55211	AAR70256	AAY01036	AAW31691	AAW72435	AAR58752	AAW19018	AAW00832	AAR40385	AAR59935	AAR59943	AAW35377	ABP58454	ABU07262	ABU07253	AAB83836	AAW86004	AAW35376	AAW86003	AAB83838	AAB83835	AAW86002	AAY27407	AAY42294	AAY17494	AAR25411	AAY39452	AAR25413	AAR70827	AAR58612	ABU08539	AAB73463	AAW96742
nsplanted V-	Į.	HP1/2	ised H	-VLA-4	4			XUMDX	ın Fasi	<b>}</b> +•	oclonal antibo	ĸ	**		eered super	expressed		acid sequer	1	nce	5 <b>T4</b> Bi		tcid seque	ine an	2	5T4 sec	chain	Light chain variab	ody AB	Light chain variab	,	binding inhi	S)	e anti-	Light chain variab

### ALIGNMENTS

Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse. Region Chimeric - Mus musculus. Chimeric - Synthetic. Anti-FIX/FIXa antibody 193/AD3 scFv. Protein Peptide Protein 21-JUN-2001 AAB20433; (first entry) /label= VH 98..108 Location/Qualifiers 'label= VL .20..134 'label= Linker label= CDR3

'label= CDR3

Result No.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of a single chain FV (scFV) derivative of antibody 193/AD3, comprising the heavy (VH) and light (VL) chain or variable regions of 193/AD3 joined by an artificial, flexible linker peptide. The scFV was obtained by PCR amplification of cDNAs for comprising the vector pDAP2. 193/AD3 is an example of anti-human Factor IX (FIX)/activated Factor IX (FIX) and their derivatives, and example of anti-human Factor IX (FIX)/activated Factor IX (FIX) and contivatives, and their derivatives, contributies of the invention. Anti-FIX/FIX and their derivatives, concluding scFv and CDR3 fragments, have Factor VIIIa (FVIIIa) cofactor activity or FIXa activating activity. Administration leads to an increase in the proceagulant activity of FIXa, even in the presence of foreign and their presence continuous in the case of FVIII or FVIII or FVIII and inhibitors. The antibodies and derivatives are used in a claimed pharmaceutical composition for treating patients with blood compulation disorders, especially haemophilia A and haemorrhagic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 108; Consert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
                                                               Key
Region
                                                                                                                                               Immunotoxin; heavy chain; light chain; variable region; antibody; ricin-A; cytostatic; cataract; lens opacification; epithelial cell; pHB19; 4197X; monoclonal antibody; MAb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Fig 14; 138pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-2000; 2000WO-EP08936
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31-AUG-1995
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               Region
                                                                                                                  Synthetic
                                                                                                                                                                                                                  MAb 4197X light chain variable region.
                                                                                                                                                                                                                                                                                                     AAR70828;
                                                                                                                                                                                                                                                                                                                                     AAR70828 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                      195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 DIQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPD
                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIKR 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAMYQQKPGQSPKLLMYYASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 572; DB 22; Llarity 100.0%; Pred. No. 3.1e-39; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                (updated)
(first entry)
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                                                                                   Location/Qualifiers
                 /note= "complementarity determining region
80..86
/label= CDR2
                                             label= CDR1
                                                                                                                                                                                                                                                                                                                                      154
                                                                                                                                                                                                                                                                                                                                      B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 242;
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                                                                                                                                                                                                                                                                                                                                                                                                                        242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194
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ARESULT 3
ARE29157
ID 9A82
XX AAE2
XX 27-J
XX Chim
XX 31.1
XW 1igh
XX Unid
XX Unid
XX Unid
XX Wep
FT Pept
FT Pept
FT Prot
XX WO20
PD 26-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        An immunotoxin (given in AAR70827) comprises the heavy (VH) and light chain (VL) variable regions of anti-lens epithelium IgG3 MAb 4197X linked to ricin-A. CDMAs encoding the VL and VH regions of 4197X (AAQ85387-88, respectively) were obtained from hybridoma mRNA, amplified by PCR, and engineered for inclusion in the immunotoxin construct (AAQ85386).
                                                                                                                                    31.1 antibody; pancreatic cancer; light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New single chain immuno:toxin - binds specifically to epithelial cells, for inhibiting development of sec. cataracts after extra:capsular cataract extraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gould RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-FEB-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                             27-JAN-2003
                                                                                                                                                                                                                    AAE29157;
                                                                                                                                                                                                                                          AAE29157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig.3; 68pp; English.
                                                                                                                Unidentified.
                                                                                                                                                                     Chimeric 31.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HOUS-) HOUSTON BIOTECHNOLOGY INC.
                        WO200274251-A2
                                                        Protein
                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1995-082036/11.
                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                              31
                                                                                                                                                                                                                                                                                                                                                                                           100;
                                                                                                                                                                                                                                                                                                                                                                   N
                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                         standard; Protein; 128
                                                                                                                                                                                                                                                                                                 FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYSSPYSFGGGTKLEIKR 137
                                                                                                                                                                                                                                                                                                                FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIKR
                                                                                                                                                                                                                                                                                                                                             IVMTQTFKFLLVSAGDRVTTTCKASQSVNNOVAWXQQKFGQSFKLLIYYASNRYTGVPDR
                                                                                                                                                                                                                                                                                                                                                                    IQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kelleher
                                                                                                                                                                                                                                                                                                                                                                                                                                      154 AA;
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                            (first entry)
                                                                                                                                                                      antibody light chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= CD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "complementarity determining region"
                                                                                         Location/Qualifiers
                                                                 /label= Signal-peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pq,
                                                                                                                                                                                                                                                                                                                                                                                                    92.5%;
                                            "31.1 antibody light chain
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5.4e-36;
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                                                                                                                                                carcinoma; antibody therapy;
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                                            variable region"
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Best Local S
Matches 100
Use of anti-VLA-4 antibodies e.g. HP1/2, HP2/1, HP2/4, L25
P4C2 antibodies - for inhibiting late phase response to all
                                                                                                                                                                                                                                                                                                                                                                                                                            WO9313798-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibody; allergen; light chain; asthma; VLA-4; very late antigen; hypersensitivity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              light and heavy chain variable regions of the antibody 31.1. Seques of the invention are useful in expressing chimerised 31.1 antibodic which can be used for treating pancreatic cancer or for diagnosing pancreatic carcinoma. They are also used in antibody therapy. The pancreatic carcinoma is chimeric 31.1 antibody light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding light and heavy chain variable regions of antibody 31.1, useful for expressing chimerized 31.1 antibodies for treating pancreatic cancer or for diagnosing pancreatic carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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11-JAN-1994
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DB; AAQ47059.
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(first entry)
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93.5%;
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Pred. No. 6.5e
3; Mismatches
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  response to allergens
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Best Local
Anti-VLA-4 antibody = anti-very late antigen-4 antibody. One anti-
VLA-4 monoclonal antibody is designated HPI/2 (obtained from Biogen
Inc. Cambridge, MA). The variable regions of the heavy and light
chains of the anti-VLA-4 antibody HPI/2 were cloned, sequenced and
expressed in combination with constant regions of human,
immunoglobulin heavy and light chains. Such a chimeric HPI/2
antibody is similar in specificity and potency to the murine HPI/2
antibody, and may be useful in methods for treating ulcerative
                                                                                                                                                                                                                                                                                                     Treatment of inflammatory bowel disease - using anti-very antigen-4 antibody, polypeptide or other molecule recognia anti-very late antigen-4, reducing acute inflammation in ulcerative colitis, Crohn's disease, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asthma is treated by admin. of an anti-VLA (very late antigen)-4 antibody, esp. monoclonal antibody HP1/2. The antibody is able to bind to the alpha 4 subunit of VLA-4 so as to (a) inhibit late phase response to an allergen to which the subject is hypersensitive or (b) decrease airway hypersensitivity after allergen challenge. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence of the variable region of the light monoclonal antibody HPI/2 (HPI/2 V kappa).
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08-FEB-1994
                                                                                                                                                                                                                                                       Disclosure; Page 26; 35pp; English.
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Best Local S
Matches 99
                                                                               non-human complementarity determining regions at VH positions 31-35 (CDR1), 50-65 (CDR2) and 95-102 (CDR3). It may further comprise non-human residues at framework positions 27-30, 75, 77-79 or 66-67, or 69-71 and 69-71, or 84-85, or 38 and 40 or 24. The VL of the rAb has non-human CDRs at positions 24-34 (CDR1), 50-56 (CDR2) and 89-97 (CDR3). It may allso have non-human residues at framework positions 60 and 67. The non-human CDRs are pref. derived from the HP1/2 murine monoclonal antibody. HP1/2 is a member of Kabat V with no unusual residues. The rAb can be used to treat inflammation in mammals, esp. asthma or inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanised; human; mouse; recombinant; antibody; anti-VLA4; heavy; light; variable; framework; rAb; monoclonal; CDR; HP1/2; asthma; CDR; complementarity determining region; inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              colitis, Crohn
bowel disease.
                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the HP1/2 antibody kappa chain variable region (Vk). This protein sequence was used in the production of a humanised recombinant anti-VLA4 antibody (rAb). The humanised rAb comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant and humanised anti-VLA4 antibodies - contgnon-human CDRs in their light and heavy chains, used to (non-) specific inflammation, e.g. asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carr FJ,
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07-MAR-1995
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Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 78; 140pp; English.
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                                                                                                                                                                                                                                                                                                                                    Chimeric HP1/2 antibody comprises the variable regions of
and light chains of mouse anti-VLA4 Ab HP1/2 and constant
human heavy and light chains. CDNA encoding the HP1/2 VH
kappa sequences are given in AAQ67343-44, and the encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treatment and prevention of insulin dependent diabetes - administering monoclonal antibodies specified for the int VLA4 blocking interactions with VCAM-1 and fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric antibody; HP1/2; integrin; VLA4; very late antigen-4; heavy chain; light chain; constant region; variable region; antibody engineering; VCAM-1; fibronectin; monocional antibody;
                                                                                                                                                                                                                                              Sequence
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21-MAR-1995
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                                                                                                                                                                                                                                                                                                                    kappa sequences are
AAR58749-50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 54; 73pp; English.
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N-PSDB; AAQ67344.
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FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEI 106
                                                                                      IQMTQSPKFILVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPDR
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Pred. No. 1.4e-35;
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Pred. No. 1.4e-35;
3; Mismatches 3;
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FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYSSPYTFGGGTKLEI 106

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RESULT 9
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12-FEB-1992;
02-FEB-1993;
11-AUG-1994;
18-JAN-1995;
                                                                                                                                                                                                                                                                                     The present sequence represents the light chain variable region of the murine anti-human very late antigen-4 (VLA-4) monoclonal antibody HP1/2. The protein can be used in the method of the invention. The specification describes methods for treating inflammatory bowel disease with a composition comprising an antibody, or its fragments, able to bind to the Bi or B2 epitope of the alpha 4 subunit of VLA-4. The method is useful for treating ulcerative colitis and Crohn's disease.
04-JUN-1999
                        AAY01034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Light chain variable region; very late antigen-4; VLA-4; antibody HP1/2; inflammatory bowel disease; B1 epitope; B2 epitope; alpha 4 subunit; ulcerative colitis; Crohn's disease.
                                               AAY01034 standard;
                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Columns 25-26; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             Treating inflammatory bowel disease with VLA-4 blockers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burkly LC, Lobb RR
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22-SEP-1999
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                                                                                                                                                                    IQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAMYQQKBQQSPKLLMYYASNRYTGVPDR 61
                                                                                                                               FTGSGYGTDFTFTISTVQABDLAVYFCQQDYGSPPTFGGGTKLBI 106
                                                                                                                                                    IVMTQTPKFLLVSAGDRVTITCKASQSVTNDVAWYQQKPGQSPKLLIYYASNRYTGVPDR
                                                                                                                                                                                                                                                       106 AA;
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94US-0284603.
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92US-0835139.
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                                             Protein;
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94.3%;
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09-FEB-1993;
09-FEB-1994;
                                     Light chain variable region; antibody HPI/2; alpha 4 beta 1 integrin very late antigen-4; VIA-4; chronic allergen-induced asthma; VIA4-leukocyte migration; leukocyte infiltration; signal transduction inhibition.
                                                                                                                                             20-MAR-2003
16-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is the anti VLA-4 antibody HP1/2 VK chain. The invention relates to a method for the treatment of insulin-dependent type I diabetes, comprising administering to a prediabetic mammal (or on showing partial beta-cell destruction) one or more compositions of an antibody that binds to the alpha 4 subunit of VLA-4 (very late antigen-4), its antigen-binding fragments, or a soluble VCAM-1 (vascular cell adhesion molecule-1) polypeptide that binds to the alpha 4 subunit of VLA-4. The treatment is used to prevent development of
                                                                                                                Light chain
                                                                                                                                                                                      AAW96742;
                                                                                                                                                                                                                  AAW96742 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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N-PSDB; AAX27914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIA-4; antibody; anti VIA-4 antibody HP1/2; VH chain; alpha 4 subunit; insulin-dependent type I diabetes; very late antigen-4; soluble VCAM-1; vascular cell adhesion molecule-1; insulin-dependent diabetes; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating insulin-dependent diabetes by blocking VLA-4
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                                                                                                                                                                                                                                                                                                                  FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEI 106
                                                                                                                                                                                                                                                                                                                                          IVMTQTPKFLLVSAGDRVTITCKASQSVTNDVAWYQQXPGQSPXLLIYYASNRYTGVPDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 AA;
                                                                                                               variable region of antibody HP1/2.
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(first entry)
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93US-0029330.
94US-0001456.
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Pred. No. 1.4e-35;
3; Mismatches 3;
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RESULT 11
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13-JAN-1992;
12-JAN-1993;
12-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents the light chain variable region of antibody HP1/2. This antibody binds alpha 4 beta 1 integrin very late antigen 4 (VLA-4). The antibody can be used in methods to treat chronic allergen-induced asthma. Inhibition of VLA-1 eukocyte migration prevents secondary effects of leukocyte infiltration (release of toxins, inducers of soluble inflammatory cell mediators or chemotactic agents) and inhibition of signal transduction causing release of such mediators and chemotactic agents.
                                                                                        Integrin antagonist; VLA-4 antagonist; alpha-4-beta-1 integrin; very late antigen; monoclonal antibody HP1/2; mouse; murine; kidney disease; chronic renal failure; end-stage renal disease; chronic diabetic nephropathy; diabetic glomerulopathy; diabetic renal hypertrophy; hypertensive nephrosclerosis; hypertensive glomerulosclerosis; chronic glomerulonephritis; hereditary nephritis; renal dysplasia; nephrotropic; light chain variable region; VL.
                                                            ds snw
                                                                                                                                                                                                                                   Murine anti-VLA-4 monoclonal antibody HP1/2 VL
                                                                                                                                                                                                                                                                02-JUL-2001
                                                                                                                                                                                                                                                                                                                             AAB73463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating allergic asthma with very late antigen-4 binding agent - to inhibit late phase response and decrease airway hypersensitivity
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 22-MAR-2901
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                                                                                                                                                                                                                                                                                                                             standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IVMTQTPKFLLVSAGDRVTITCKASQSVTNDVAWYQQKPGQSPKLLIYYASNRYTGVPDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQXPGQSPKLLMYYASNRYTGVPDR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                (first
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94US-0256631.
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92US-0821768.
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                                                                                                                                                                                                                                                                                                                             Protein; 106
                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 523; DB 20;
Pred. No. 1.4e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 106;
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                                                                                                                                                                                                                                                                                                     RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method for treating a mammal with, cor at risk of developing, chronic renal failure, involving the administration of at least one integrin antagonist. The integrin companists that may be used in the method include antagonists of alpha-4-subunit containing integrins or antagonists of alpha-1-subunit containing integrins or antagonists are antibodies specific for VLA-1 (very late antigen-1, alpha-1-beta-1 integrin) or VLA-4 (alpha-4-beta-1 integrin) which inhibit the interaction of the contegrin and its cognate ligand (collagen I, collagen IV, and laminin in the case of VLA-1, and fibronectin and VCAM-1 in the case of VLA-4).

The method of the invention may be used to treat chronic renal failure, collager renal disease, chronic diabetic nephropathy, diabetic collager collager in the case of VLA-4, and disease, chronic diabetic nephropathy, diabetic collager stage renal disease, chronic glomerulopathy, diabetic collager stage renal dysplasia. The present sequence represents the light collapse to renal dysplasia. The present sequence represents the light collapse to the case of VLA-4 (alpha-xegion (VL) of the murine anti-VLA-4 monoclonal antibody collapse to the case of vLA-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                              Mouse; antibody; VLA-4; alpha4betal integrin; VCAM-1; IBD; vascular call adhesion molecule-1; inflammatory bowel disease; vascular colitis; Crohn's disease; chronic inflammatory disorder; antiulcer; antiinflammatory; VCAM 2D IgG; kappa chain variable region.
                                                Mus musculus.
                                                                                                                                                                 Mouse anti-VLA-4 antibody HP1/2 kappa chain variable region
                                                                                                                                                                                                   02-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; Page -; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mammal
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(UNLO ) IMPERIAL COLLEGE SCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is not given in the specification, ven in US5932214, columns 25-26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a mammal in, or at a risk of developing, chronic renal involves administering at least one integrin antagonist to the
                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                       FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEI 106
                                                                                                                                                                                                                                                                                                                                                                                                                     IQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAMYQQKPGQSPKLLMYYASNRYTGVPDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 AA;
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Pred. No. 1.4e-35;
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15-OCT-1997;
02-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to treating inflammatory bowel disease (IBD), comprising administering to a mammal suffering from IBD a composition comprising a vascular cell adhesion molecule (VCAM)-1)/immunoglobulin G (IgG) fusion protein in an amount effective to provide relief to the mammal. Antibodies against VLA-4 (alpha4betal integrin, a binding partner for VCAM-1) may also be effective in treating IBD. The method is useful for treating inflammatory bowel disease in a mammal, preferably a human suffering from ulcerative colitis or Crohn's disease (both are chronic inflammatory diseases). The composition is administered during an acute flare-up of the inflammatory bowel disease. The fusion protein is termed VCAM 2D IgG and comprises 2 N-terminal domains of VCAM-1 fused to the bresent sequence represents the kappa chain variable regions of a mouse monoclonal antibody HPI/2 which recognises VLA-4 and may be of
                             EP617126-A2
                                                                                                                                                    Human interleukin-6 binding inhibitor;
                                                                                                                                                                                              Il-6 binding
                                                                                                                                                                                                                                                      25-MAR-2003
28-APR-1995
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18-JAN-1995;
                                                                          Homo sapiens
                                                                                                                         septic shock;
                                                                                                                                                                                                                                                                                                                                                                                AAR58612 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use as a treatment for IBD.
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(first entry)
                                                                                                                         multiple myeloma; ss
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93WO-US00924.
94US-0284603.
95US-0373857.
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93US-
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Pred. No. 1.4e
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1.4e-35;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ70612 codes for human interleukin-6 binding inhibitor, the polypeptide described in AAR56612. This polypeptide hibits the binding of human II-6 to its receptor, and can therefore be useful in the treatment of a variety of autoimmune diseases; specifically in the treatment of rhounatoid arthritis, septic shock due to bacterial infection and multiple myeloma. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptide inhibiting its receptor - useful or aggravated by IL-6
               Domain
                                                  Domain
                                                                                                                  Domain
                                                                                                                                                     Peptide
                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                       pHB19; 4197X;
                                                                                                                                                                                                                                                                          Anti-cataract
                                                                                                                                                                                                                                                                                                   25-MAR-2003
31-AUG-1995
                                                                                                                                                                                                                                                                                                                                          AAR70827;
                                                                                                                                                                                                                                                                                                                                                                  AAR70827 standard; Protein; 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-FEB-1994;
                                                                          Peptide
                                                                                                                                                                                                                                    ricin-A;
                                                                                                                                                                                                                                               Immunotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 18; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hamuro J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-SEP-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AJIN ) AJINOMOTO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                62 RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYRSPFTFGSGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                     xin; heavy chain; light chain; variable region; antibody;
cytostatic; cataract; lens opacification; epithelial cell;
197X; monoclonal antibody; MAb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DILLTQSPKTLLVSAGDRYTITCKASQSVSTDVSWYQQKPGQSPKLLIYYASNRYTGVPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakazawa H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                (updated)
(first entry)
                                                                                                                                                                                                                                                                          immunotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93JP-0028173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94EP-0102346.
                                                                                                                /note= "
28..145
                                                                                                                                                                   Location/Qualifiers
'label= RICIN-A
                        /note= "MAb 419X
                                     'label= LIGHT
                                                           /label= LINKER
                                                                                      /note= "MAb
                                                                                                    'label= HEAVY
                                                                                                                                          /label= Sig_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.7%;
                                                                                                                           = Sig_peptide
"phoA signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              binding of human interleukin-6 (IL-6) to for treating auto:immune disease induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shimamura
                                                                                      4197X heavy chain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 519; DB 15;
Pred. No. 6.6e-35;
3; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                    B
                       light chain"
                                                                                                                             sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
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ID ARRES
XX ARRES
XX 25-MA
DT 11-JA
XX Light
XX Monoc
XW Monoc
XW Shock
XW Shock
XW Shock
XW Multi
XX Chime
XX WO921
XX O9-JU
PD 09-JU
PD 21-DE
PR 21-DE
PR 21-DE
PR 21-DE
PR 21-DE
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Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The immunotoxin given in AAR70827 comprises the heavy and light chain variable regions of anti-lens epithelium IgG3 MAb 4197X linked to ricin-A and a hexa-histidine tag. The DNA construct encoding the immunotoxin was expressed from pHB19 in E. coli.
(Updated on 25-MAR-2003 to correct PN field.)
              21-DEC-1990;
03-MAY-1991;
                                                                                                                                                monoclonal antibody; humanised; chimeric; CDR; neoplastic therapy; shock; antilymphocyte therapy; endotoxin shock; septic shock; sepsis; cardiovascular shock; tumour necrosis factor alpha; multi-organ failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New single chain immuno:toxin - binds specifically to epithelial cells, for inhibiting development of sec. cataracts after extra:capsular cataract extraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gould RM,
                                                                                                                            Chimeric.
                                                                                                                                                                                                               Light chain variable domain of MAb
                                                                                                                                                                                                                                       25-MAR-2003
11-JAN-1993
                                                                                                                                                                                                                                                                             AAR25413;
                                                                                                                                                                                                                                                                                                    AAR25413 standard; Protein; 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig.4; 68pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9503828-A1
                                                20-DEC-1991;
                                                                          09-JUL-1992
                                                                                                   WO9211383-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HOUS-) HOUSTON BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-FEB-1995.
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                                                                                                                                                                                                                                                                                                                                                                  229
                                                                                                                                                                                                                                                                                                                                                                                                                169 IVMTQTPKFLLVSAGDRVTITCKASQSVNNDVAWYQQKPGQSPKLSIYYASNRYTGVPDR
                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                IQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPDR
                                                                                                                                                                                                                                                                                                                                                                 FTGSGYGTDETFTISTVQAEDLAVYFCQQDYSSPYSFGGGTKLBIK 274
                                                                                                                                                                                                                                                                                                                                                                                         FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kelleher PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    554 AA;
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                                                                                                                                                                                                                                       (updated)
(first en
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              90WO-GB02017.
91GB-0009645.
                                                  91WO-GB02300.
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/label= TAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "hexa-histidine tail"
                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wallace TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 518; DB 16;
Pred. No. 1.7e-34;
4; Mismatches 4;
                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                               hTNF3 to TNFalpha epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wood MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 554;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                         Query Match
Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                                                                          Recombinant antibody specific for human TNF-alpha - for treatment of shock and immuno:regulatory and inflammatory disorders, also used in diagnosis
                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                 antibody to an epitope of human tumour necrosis factor. The sequence shows 21 differences compared with CB6 (R225411,2) - in the light chain at positions 50, 96, and in the framework at 1, 19, 40, 45, 46, 76, 103, and 106, and in the heavy chain in the CDR at 52, 60 and 95, and in the framework at 1, 10, 38, 40, 67, 73, 87,
                                                                                                                                                                                                                                                                                                                                                            Claim 2; Fig 4; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1992-250102/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adair JR,
                                                                                                                                                                                                                                                                                                                                This sequence is that of the light chain variable domain of a chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CLLT ) CELLTECH LTD
                                                                                                                                                                                                                     (Updated on 25-MAR-2003 to correct PN field.)
61
                           61 RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIK 107
                                                                                                                         94;
                                                                              1 DIQMTQSPKFLLVSAGDRVTITCXASQSVSNDVAWYQQXPGQSPKLLMYYASNRYTGVPD
                                                            1 NIVMTQTPKFLLVSAGDRITITCKASQSVSNDVAWYQQKPGQSPRLLIYYVSNRYTGVPD
                                                                                                                                          Similarity
RFTGSGYGTDFTFTINTVQAEDLAYYFCQQDYSSPYTFGGGTRLEVK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Athwal DS,
                                                                                                                                                                                      107 AA;
                                                                                                                           Conservative
                                                                                                                                        89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bodmer MW,
                                                                                                                         8
                                                                                                                                        Score 512; DB 13;
Pred. No. 1.1e-34;
                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Emtage JS;
                                                                                                                      5.
                                                                                                                                                       Length 107;
                                                                                                                            Indels
                                                                                                                           0
                                                                                                                         Gaps
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Search completed: November 7, 2003, 07:27:00 Job time: 47.5741 secs

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Result
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
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  110
112
113
114
                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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19: /cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.pep:*
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Match
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572
1 DIQMTQSPKFLLVSAGDRVT......
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Gapop 10.0 , Gapext 0.5
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195.799 Million cell updates/sec
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US-10-05-496-2
US-10-052-978-4
US-10-252-978-4
US-10-422-049-17
US-10-423-049-13
US-10-428-662-71
US-10-428-662-67
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US-10-428-662-31
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                                                                                                                                                                                                                                                                                                                    Description
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421	421	421	421	421	421	421	422.5	422.5	422.5	422.5	422.5	422.5	423	423	423	424	424	425	427	427	430	431	435	437	439	439	439	439	442
73.6	73.6	73.6	73.6					73.9		73.9	73.9	73.9	74.0	74.0	74.0	74.1	74.1	74.3	74.7	74.7	75.2	75.3	76.0	76.4	76.7	76.7	76.7	76.7	77.3
126	126	126	126	126	126	126	234	234	234	213	213	213	127	107	106	133	133	107	127	107	109	107	250	331	131	131	131	107	333
16	<u>1</u> 5	12	11	11	ø	w	12	12	12	7,2	12	12	10	10	ø	11	11	15	10	10	9	11	10	15	16	11	11	11	15
US-10-218-253-106	US-10-315-125-6	US-10-428-085-6	US-09-509-098-12	US-09-269-921-106	US-09-355-925-6	US-09-760-723-6	US-10-286-132A-24	US-10-275-180A-24	US-10-281-479A-24	US-10-286-132A-76	US-10-275-180A-76	US-10-281-479A-76	US-09-956-206A-65	US-09-956-206A-81	US-09-824-286-4	US-09-874-141-51	US-09-874-141-45	US-10-268-501-1	US-09-956-206A-49	US-09-956-206A-79	US-09-811-123-4	US-09-509-098-134	-09-887-853-		US-10-218-253-104	-09-509-096-	US-09-269-921-104	US-09-509-098-130	US-10-059-261-61
100			Sequence 12, Appl	ø	_			24,	24,		76,	76,		œ	Sequence 4, Appli	ģ	45	Ļ	Sequence 49, Appl	e 79	4	13,		160	ó		104,	,	Sequence 61, Appl

## ALIGNMENTS

```
APPLICANT: LOBD, ROY R.
APPLICANT: Carr, Frank J.
APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
ITILE OF INVENTION: RECOMBLINANT ANTI-VLA4 ANTIBODY MOLECULES
FILE REFERENCE: 10274-007001
CURRENT APPLICATION NUMBER: US/10/428,662
CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: US/08/454,899G
PRIOR APPLICATION NUMBER: US 08/004,798
PRIOR APPLICATION NUMBER: US 08/004,798
PRIOR FILING DATE: 1993-01-12
PRIOR APPLICATION NUMBER: PCT/US94/00266
PRIOR FILING DATE: 1993-01-07
NUMBER OF SEQ ID NOS: 109
SOPTWARE: FastSEQ for Windows Version 4.0
SEQUIFI: 106
TYPE: DOT
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                                                                                                                                                                                                                                       ; OTHER INFORMATION: light chain variable region US-10-428-662-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/10428662
Publication No. US20030185819A1
                                                                                                                                                          Matches
                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                   FEATURE:
62 FTGSGYGTDETFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEI 106
                                                                                                                                                      99;
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                                                                                          IQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAMYQQKPGQSPKLLMYYASNRYTGVPDR
                                                               IVMTQTPKETLUSAGDRUTITCKASQSVTNDVAMYQQXPGQSPKLLIYYASNRYTGVPDR
                                                                                                                                                      Conservative
                                                                                                                                                 91.4%; Score 523; DB 12; 94.3%; Pred. No. 9.4e-44; ative 3; Mismatches 3
                                                                                                                                                                                          Length 106;
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62

FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYSSPYTFGGGTKLEI 106

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APPLICANT: Biogen, Inc.
APPLICANT: Biogen, Inc.
APPLICANT: Imperial College of Science, Technology and Medicine
ITILE OF INVENTION: Therapies for Chronic Renal Failure
ITILE OF INVENTION: Using One or More Integrin Antagonists
ITILE OF INVENTION: Using One or More Integrin Antagonists
ITILE OF INVENTION: UNUMBER: US/10/095,496
CURRENT APPLICATION NUMBER: ECT/US00/25140
PRIOR APPLICATION NUMBER: ECT/US00/25140
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/153,826
PRIOR APPLICATION NUMBER: 60/153,826
PRIOR APPLICATION NUMBER: 60/153,826
PRIOR APPLICATION NUMBER: 60/153,826
PRIOR APPLICATION NUMBER: 60/153,826
PRIOR APPLICATION NUMBER: 60/153,826
PRIOR APPLICATION NUMBER: 60/153,826
PRIOR APPLICATION NUMBER: 60/153,826
PRIOR FILING DATE: 1999-09-14
SOFTWARE: FastSEQ for Windows Version 4.0
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; OTHER INFORMATION: HP1/2 light chain variable region US-10-095-496-2
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                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/252,978
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: US/09/157,452
PRIOR FILING DATE: 1998-09-21
PRIOR PRICATION NUMBER: US 08/950,660
PRIOR PRICATION NUMBER: US 08/950,660
PRIOR PILING DATE: 1997-10-15
PRIOR PILING DATE: 1995-01-16
PRIOR PILING DATE: 1995-01-18
PRIOR PILING DATE: 1995-01-18
PRIOR APPLICATION NUMBER: US 08/284,603
PRIOR PILING DATE: 1994-08-11
PRIOR APPLICATION NUMBER: PCT/US93/00924
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10252978 Publication No. US20030095969A1 GENERAL INFORMATION:
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Publication No. US20030007969A1
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                 SOFTWARE: PASTSEQ for Windows Version 3.0 SEQ ID NO 4
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APPLICANT: Allen, Ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LOBD, ROY R.
APPLICANT: BURKLY, LINGA C.
TITLE OF INVENTION: TREATMENT FOR INFLAMMATORY BOWEL DISEASE
FILE REFERENCE: 10274-004003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                          PRIOR FILING DATE: 1992-02-12
NUMBER OF SEQ ID NOS: 16
                                                                                                                             PRIOR APPLICATION NUMBER: US 07/835,139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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106
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Pusey, Charles
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Pred. No. 9.4e-44;
3; Mismatches 3
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APPLICANT: Athwal, Diljeet Singh
APPLICANT: Entage, John Spencer
APPLICANT: Bodmer, Mark William
TITLE OF INVENTION: Recombinant Antibodies Specific For TNF-Alpha
FILE REFERENCE: CARPO063
CURRENT FILLING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: US/10/422,049
CURRENT FILLING DATE: 1995-03-04-22
PRIOR APPLICATION NUMBER: US/09/267,281
PRIOR FILING DATE: 1995-03-12
PRIOR APPLICATION NUMBER: 08/456,418
PRIOR APPLICATION NUMBER: 08/373,882
PRIOR APPLICATION NUMBER: 08/373,882
PRIOR APPLICATION NUMBER: 08/373,882
PRIOR APPLICATION NUMBER: 08/373,882
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US-10-422-049-13
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                                                                                                                                                                                              Sequence 13, Application US/10422049 Publication No. US20030199679A1 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                            APPLICANT: Adair, John Robert
APPLICANT: Athwal, Dilject Singh
APPLICANT: Emtage, John Spencer
APPLICANT: Boddmer, Mark William
TITLE OF INVENTION: Recombinant Antibodies Specific For TNF-Alpha
FILE REFERENCE: CARPO063
CURRENT APPLICATION NUMBER: US/10/422,049
CURRENT FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: US/09/267,281
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Adair,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 07/920,378
PRIOR FILING DATE: 1992-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 10
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Pred. No. 9.4e-44;
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Pred. No. 1.1e-42;
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PRIOR FILING DATE: 1995-06-01
PRIOR PPLICATION NUMBER: 08/373,882
PRIOR FILING DATE: 1995-01-17
PRIOR APPLICATION NUMBER: 07/920,378
PRIOR APPLICATION NUMBER: 07/920,378
PRIOR FILING DATE: 1992-09-28
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/10283838 Publication No. US20030092894A1 GENERAL INFORMATION:
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ORGANISM: Murine
                                                                                                         TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,838

FILING DATE: 30-Oct-2002

CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/695,692
FILING DATE: August 12, 1996
APPLICATION UNUMBER: 9601245-5
FILING DATE: March 29, 1996
ATTORNEY/AGENT INFORMATION:
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                     NAME: Krieger, Paul E.
REGISTRATION NUMBER: 25,886
REFERENCE/DOCKET NUMBER: 41:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
Johan Hansson, Terje Kalland, Lars
Abrahmsen and Goran Forsberg
TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                              LENGTH: 107 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pravel, Hewitt, Kimball & Krieger STREET: 1177 West Loop South, 10th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTGSGYGTDFTFTITTVQAEDLAVYFCQQDYSSPWTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IVMTQTPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKSGQSPKVLIYHVSNRYTGVPDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 507; DB 12;
Pred. No. 3.4e-42;
                                                                                                                                                                                                                          41986/1
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GENERAL INFORMATION:

APPLICANT: Lobb, Roy R.

APPLICANT: Carr, Frank J.

APPLICANT: Tempest, Philip R.

ITILS OF INVENTION: RECOMBINANT ANTI-VLA4 ANTIBODY MOLECULES

FILE REFERENCE: 10274-007001

CURRENT APPLICATION NUMBER: US/10/428,662

CURRENT APPLICATION NUMBER: US/08/454,899G

PRIOR APPLICATION NUMBER: US/08/454,899G

PRIOR APPLICATION NUMBER: US/08/454,899G

PRIOR FILING DATE: 1995-05-31

PRIOR PILING DATE: 1995-05-31

PRIOR APPLICATION NUMBER: US 08/004,798

PRIOR APPLICATION NUMBER: US 08/004,798

PRIOR APPLICATION NUMBER: US 08/004,798

PRIOR FILING DATE: 1993-01-12

PRIOR FILING DATE: 1994-01-07

NUMBER OF SEQ ID NOS: 109

**COPTMANDER: US 08/004/00266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(672)
; OTHER INFORMATION: Conjugate protein
US-09-900-766-1
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US-10-428-662-71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FORSBERG, GORAN
APPLICANT: ERLANDSON, EVA
APPLICANT: ANTONSON, PER
APPLICANT: WALSE, BJORN
TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
FILE REFERENCE: P02188US0;10104199
CURRENT APPLICATION NUMBER: US/09/900,766
CURRENT FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 672
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                                                                                                                                                                                                                                                                                                                                                   Sequence 71, Application US/10428662
Publication No. US20030185819A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09900766 Publication No. US20030039655A1
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Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIKR 108
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87.9%;
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Pred. No. 2.6e-41;
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Pred. No. 1.1e-39;
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US-10-428-662-63
Sequence 63, Application US/10428662
Publication No. US20030185819A1
GENERAL INFORMATION:
APPLICANT: Lobb, Roy R.
APPLICANT: Carr, Frank J.
APPLICANT: Tempest, Philip R.
TITLE OF INVENTION: RECOMBINANT ANTI-VLA4 ANTIBODY MOLECULES
FILE REFERENCE: 10274-007001
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Publication No. US20030185819A1
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LENGTH: 124
                                                                                                                                                                                                                                                                                                                                               Query Match
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CURRENT APPLICATION NUMBER: US/10/428,662
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                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
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                                                                                                                                                                                                            RFTGSGYGIDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIKR 108
                                                                                                                                                                                                                                                                           DIQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPD 60
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                                                                                                                                                                                            RFSGSGYGTDFTFTISSLQPEDIATYYCQQDYSSPYTFGQGTKVEIKR 127
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85.7%;
                                                                                                                                                                                                                                                                                                                 83.7%; Score 479; DB 12;
81.5%; Pred. No. 2.2e-39;
tive 10; Mismatches 10
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Pred. No. 2.1e-39;
7; Mismatches 8;
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CURRENT APPLICATION NUMBER: US/10/428,662
CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: US/08/454,899G
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/004,798
PRIOR FILING DATE: 1993-01-12
PRIOR PILING DATE: 1993-01-07
PRIOR FILING DATE: 1994-01-07
NUMBER: PCT/US94/00266
PRIOR FILING DATE: 1994-01-07
NUMBER: OF SEQ ID NOS: 109
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 128
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US-10-428-662-31
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APPLICANT: Lobb, Roy R.
APPLICANT: Carr, Frank J.
APPLICANT: Tempest, Philip R.
TITLE OF INVENTION: RECOMBINANT ANTI-VLA4
FILE REFERENCE: 10274-007001
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 63
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PRIOR APPLICATION NUMBER: US/08/454,899G
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/004,798
PRIOR FILING DATE: 1993-01-12
PRIOR APPLICATION NUMBER: PCT/US94/00266
PRIOR FILING DATE: 1994-01-07
NUMBER OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF THE SECRET OF 
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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                                                                   61 RETGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIKR 108
                                                                                                                                                                                  1 DIQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                 85;
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RFSGSGSGTDFTFTISSLQPEDIATYYCQQDYSSPYTFGQGTKVEIKR
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78.7%;
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80.4%; Pred. No. 4.1e-38;
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                                                                                                                                                                                                                                                                                         Score 461; DB 12;
Pred. No. 1.3e-37;
1; Mismatches 12;
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RESULT 12 US-10-422-049-18

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; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Antibody
US-10-422-049-18
                                                                                                                                CÜRRENT APPLICATION NUMBER: US/10/010,729
CÜRRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/730,473
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: 09/580,787
PRIOR APPLICATION NUMBER: 09/580,787
PRIOR FILING DATE: 2000-05-30
PRIOR PILING DATE: 1090-05-28
PRIOR APPLICATION NUMBER: 09/322,862
PRIOR PILING DATE: 1999-05-28
PRIOR PILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: 08/692,084
PRIOR APPLICATION NUMBER: 08/692,084
PRIOR FILING DATE: 1996-08-08
PRIOR FILING DATE: 1996-08-08
PRIOR FILING DATE: 1996-08-08
PRIOR FILING DATE: 1996-08-08
PRIOR FILING DATE: 1996-08-08
PRIOR FILING DATE: 1996-08-08
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CURRENT APPLICATION NUMBER: US/10/422,049
CURRENT FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: US/09/267,281
PRIOR PILING DATE: 1999-03-12
PRIOR PPLICATION NUMBER: 08/456,418
PRIOR FILING DATE: 1995-06-01
PRIOR FILING DATE: 1995-06-01
PRIOR APPLICATION NUMBER: 08/373,882
PRIOR APPLICATION NUMBER: 07/920,378
PRIOR FILING DATE: 1995-01-17
PRIOR APPLICATION NUMBER: 07/920,378
PRIOR FILING DATE: 1992-09-28
NUMBER OF SECTION NUMBER: 07/920,378
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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Publication No. US20030185827A1
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Best Local :
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                                                    PRIOR APPLICATION NUMBER: 08/236,520
PRIOR FILING DATE: 1994-04-29
NUMBER OF SEQ ID NOS: 80
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Publication No. US20030199679A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J
APPLICANT: Pease, Larry R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Therapeutic Uses TITLE OF INVENTION: System FILE REPERSNCS: 1199-1-005CIP2
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APPLICANT: Bodmer, Mark William
TITLE OF INVENTION: Recombinant Antibodies Specific For TNF-Alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
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APPLICANT: Athwa
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ORGANISM: Artificial Sequence
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76.9%;
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RESULT 15
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; ORGANISM: Mus musculus
US-10-010-729-72
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SEQ ID NO 14
LENGTH: 108
                                                                                                                                          Sequence 36, Application US/08779784
Publication No. US20020164325A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/10422049 Publication No. US20030199679A1 GENERAL INFORMATION:
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Best Local :
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APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Miller, David J.
APPLICANT: Metalura, Kunihiko
TITLE OF INVENTION: REMOMOTION
TITLE OF INVENTION: REMYELINA
NUMBER OF SEQUENCES: 37
                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 07/920,378
PRIOR FILING DATE: 1992-09-28
NUMBER OF SEQ ID NOS: 20
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PRIOR FILING DATE: 1995-01-17
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PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 08/456,418
PRIOR FILING DATE: 1995-06-01
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CURRENT FILING DATE: 2003-04-22
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APPLICANT: Emtage, John Spencer
APPLICANT: Bodmer, Wark William
TITLE OF INVENTION: Recombinant Antibodies Specific For TNF-Alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Adair, APPLICANT: Athwa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Humanized OTHER INFORMATION: Antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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    Kunihiko
PROMOTION OF CENTRAL NERVOUS SYSTEM
REMYELINATION USING MONOCLONAL AUTOANTIBODIES
37
                                                                                                                                                                                                                                                                                                                                                                                                                                       77.3%; Score 442; DB 12; 75.9%; Pred. No. 7.5e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                    11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 445; DB 12;
Pred. No. 4.6e-36;
7: Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 108;
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; MOLECULE TYPE: pro
; HYEOTHETICAL: NO
; FRAGMENT TYPE: N-t
; ORIGINAL SOURCE:
; ORGANISM: Mus mu
US-08-779-784-36
Search completed: November Job time : 95.7343 secs
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REGISTRATICN NUMBER: 26,742
REGISTRATICN NUMBER: 1199-1-001 CIPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5804
TELEPHONE: 201-343-1684
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acids
TYPE: amino acid
CTPENDITURES: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,784
FILING DATE: 07-DATA:
APPLICATION HUMBER: US/08/779,784
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/520
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
PRIOR APPLICATION DATA:
APPLICATION BY ACENT INFORMATION:
NAME: JS-APR-1994
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                      Query Match 77.3%; Score 442; DB 8; Length 128; Best Local Similarity 78.7%; Pred. No. 8.9e-36; Matches 85; Conservative 8; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single TOPOLOGY: linear
                                                                                            21 DIVMTQSHKFMSTSVGDRVSITCKASQDVSTAVAWYQQKPGQSPKLLIYSASYRYTGVPD 80
                                                                                                                                                                                                                     1 DIQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLMYYASNRYTGVPD 60
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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
      Query
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/cgm2_6/ptodata/1/iaa/6A_COMB.pep:*
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/cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-08-840-713-35
US-08-840-713-37
US-08-840-713-37
US-08-235-838-14
US-08-465-473B-14
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US-08-950-660-4
US-09-157-452B-4
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PCT-US93-00924-4
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419	419	420.5	420.5	421	423	423	423	427	427	427	427	432	432	435	435	435	435
73.3	73.3	73.5	73.5	73.6	74.0	74.0	74.0	74.7	74.7	74.7	74.7	75.5	75.5	76.0	76.0	76.0	76.0
107	107	124	124	126	127	107	106	127	126	126	107	241	241	250	250	250	250
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US-08-925-339-1	US-08-554-840-1	US-08-466-163B-4	US-08-466-151-4	US-09-355-925-6	US-08-525-539A-65	US-08-525-539A-81	US-09-189-129-4	US-08-525-539A-49	US-08-479-285-28	US-08-822-028-28	US-08-525-539A-79	US-08-465-473B-5	US-08-235-838-5	US-08-461-386-2	US-08-461-838-2	US-08-464-589-8	US-08-463-675-8
Sequence 1,	Sequence 1,	Sequence 4,	Sequence 4,	Sequence 6,	Seguence 65,	Sequence 81,	Sequence 4,	Sequence 49,	Seguence 28,	Sequence 28,	Sequence 79,	Sequence 5,	Sequence 5,	Sequence 2,	Seguence 2,	Sequence 8,	Sequence 8,
Appli	Appli	Appli	Appli	Appli	Appl	Appl	Appli	Appl	App1	Appl	Appl	Appli	Appli	Appli	Appli	Appli	Appli

### ALIGNMENTS

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Sequence 4, Application US/08822830B
PAtent No. 5871734
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lobb, Roy R.; Burkly, Linda C.
TITLE OF INVENTION: Treatment for Asthma wi
TITLE OF INVENTION: Agents
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEB: LAHIVE & COCKFIELD, LLP
TRIEFAX: (617) 72 O: 4:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
US-08-822-830B-4
                                                                                                                                                                                                                                                  PILING DATE: 12-JAN-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/821,768

FILING DATE: 13-JAN 1992

ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis (FLM)
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BGP-0211
TELECOMMUNICATION INFORMATION:
TELEPONE, (471)27-7440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/822,830B
                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                 (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treatment for Asthma with VLA-4 Blocking
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                                                               ; MOLECULE TYPE:
US-08-950-660-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-950-660-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08950660 Patent No. 5932214
 Query Match
Best Local Similarity
Matches 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,660
                                                                                                                                                                                      NAME: Myers, Louis (PLM)
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US93/0092.
FILING DATE: 02-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/835,139
APPLICATION NUMBER: US 07/835,139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKPIELD
                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                 FILING DATE: 12-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/373,857
FILING DATE: 18-JAN-1995
KIOR APPLICATION DATA:
                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
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                                                                                                                           ENGTH:
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OR SEQ ID NO: 4:
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Pred. No. 1.3e-46;
              Score 523; DB 2;
Pred. No. 1.3e-46;
   Mismatches
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CURRENT FILING DATE: 1998-09-21
PRIOR APPLICATION NUMBER: US 08/950,660
PRIOR FILING DATE: 1997-10-15
PRIOR FILING DATE: 1997-10-15
PRIOR FILING DATE: 1995-01-18
PRIOR FILING DATE: 1995-01-18
PRIOR APPLICATION NUMBER: US 08/284,603
PRIOR APPLICATION NUMBER: US 08/284,603
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-02
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APPLICANT: LODD, ROY R.
APPLICANT: Burkly, Linda C.
TITLE OF INVENTION: TREATMENT FOR INFLAMMATORY BOWEL DISEASE
FILE REFERENCE: 10274-004003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4
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GENERAL INFORMATION:
APPLICANT: Lobb,
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Best Local
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PRIOR FILING DATE: 1992-02-12
NUMBER OF SEQ ID NOS: 16
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ORGANISM: Mus musculus
                                                                                                  COUNTRY: US
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00030
                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                           APPLICANT: Lobb, Roy
TITLE OF INVENTION: 1
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CITY: Chicago
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FILING DATE:
                                                                                                                                                                                                       STATE:
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Pred. No. 1.3e-46;
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                                                                                      Query Match
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GENERAL INFORMATION:
APPLICANT: Lobb, Roy R.
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Best Local Similarity
Matches 99; Conserv
                                                       Matches
                                                                                                                                                                                     TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
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INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES: 4
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LENGTH: 106 amino acids
TYPE: AMINO ACID
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NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 92,308-A; D003 CIP PCT
                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 312-715-1000
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MEDIUM TYPE: Floppy
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NAME: McNicholas, Janet M.
                                                                       Local
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CLASSIFICATION:
                                                                                                                                                          TOPOLOGY:
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REFERENCE/DOCKET NUMBER: 92,307-A; D002 CIP PCT
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                                                                       Similarity
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IQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAMYQQKPGQSPKLLMYYASNRYTGVPDR 61
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10 South Wacker Drive, Suite 3000
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                                                                    Score 523; DB 5;
Pred. No. 1.3e-46;
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Pred. No. 1.3e-46;
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US-08-695-692B-6
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US-08-197-834-7
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Sequence 6, Application US/08695692B Patent No. 6514498
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Best Local Similarity
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 7
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 028173/.
FILING DATE: 17-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5639455man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,834
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: IMMU
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CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: P.C. STREET: 1755 S.
                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                        8
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                                                                                                                                                                                                                                                                                                                                                                         l: 246 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virginia
X: U.S.A.
                                                                                                                           RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIK 107
                                                                                                      RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYRSPFTFGSGTKLEIK 108
                                                                                                                                                                            DILLTQSPKFLLVSAGDRVTITCKASQSVSTDVSWYQQKPGQSPKLLIYYASNRYTGVPD
                                                                                                                                                                                                      DIQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAMYQQKPGQSPKLLMYYASNRYTGVPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTXLEI 106
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NAKAZAWA, HARUMI
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                  90.7%;
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                                                                                                                                                                                                                                                                  Score 519; DB 1
Pred. No. 9e-46;
                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version #1.25
                                                                                                                                                                                                                                                                                   DB 1; Length 246;
                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                               Gaps
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GENERAL INFORMATION:
APPLICANT: Per An
APPLICANT: Johan

Per Antonsson, Per Bjork, Mikael Dohlsten, Johan Hansson, Terje Kalland, Lars

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                                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Appli
Patent No. 6068841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/695,692B
FLING DATE: August 12, 1996
CLASSIFICATION: 530
DRIOR APPLICATION DATA:
OR APPLICATION DATA:
                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: SEINO, Ken-ichiro
APPLICANT: KANGAKI, No. 6068841uhiko
APPLICANT: YAGITA, Hideo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TYPE: cv. liacid
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 9601245-5
FILING DATE: MAYCH 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Krieger, Paul E.
REGISTRATION NUMBER: 25,886
REFERENCE/DOCKET NUMBER: 4198
                                                                                                                                                                                                        APPLICANT: OKUMURA, KO
APPLICANT: NAKATA, MOTOMI
TITLE OF INVENTION: THERA
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Abrahmsen and Goran Forsberg
TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
TITLE OF INVENTION: AND THEIR USE
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 713-850-0909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                CITY: Alexandria
STATE: Virginia
COUNTRY: USA
                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
STREET: 1177 West Loop South, 10th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 77027-9095
                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIQMTQSPKFLLVSAGDRVTITCKASQSVSNDVAMYQQKPGQSPKLLMYYASNRYTGVPD 60
                                                                 22314
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                                                                                                                                                                                                                                                                                                                                                                                              Application US/09065059
                                                                                                                                           99 Canal Center Plaza
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                                                                                                                                                                 McDermott, Will & Emery
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Pred. No. 5e-44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 107;
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RESULT 9
US-08-463-128-10
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COMPUTER: ILM PC COMPATIBLE
COMPUTER: ILM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,128
FILING DATE: 05-UNN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11060
FILING DATE: 11-11-1993
APPLICATION NUMBER: US 07/977,702
FILING DATE: 11-11-1993
APPLICATION NUMBER: US 07/977,702
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B173CIP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/08463128
Patent No. 5695755
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local S
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INFORMATION FOR SEQ ID NO:
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NAME: BUCCA Ph.D., Daniel
REGISTRATION NUMBER: P-42,368
REFERENCE/DOCKET NUMBER: 5035
                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acid
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SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/09/065,059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Papayannopoulou, Thalia (USA only)
APPLICANT: Board of Regents, U.
APPLICANT: Washington (except USA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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Y: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1251 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                   Floppy disk
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Pred. No. 1.4e-41;
6; Mismatches 10
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US-08-463-298-10
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US-08-463-298-10
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                                                                                                                                                                                                                                                                                                                      SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/463,298
FILING DATE: 05-UNN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11060
FILING DATE: 11-NOV-1993
APPLICATION NUMBER: US 07/977,702
FILING DATE: 11-NOV-1993
APPLICATION NUMBER: US 07/977,702
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08463298
Patent No. 5824304
GENERAL INFORMATION:
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Best Local Similarity 80.4%;
Matches 86; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 128 amino Type
                                                                                                                                                                                                                   TELEFAX: (212) 596-9090 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B173CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEPAX: (212) 596-9090
FORMATTON: (212) 596-9090
                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Papayannopoulou, Thalia APPLICANT: Board of Regents, U, APPLICANT: Washington (except USA) TITLE OF INVENTION: PERIPHERALIZAT TITLE OF INVENTION: CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE.
                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 FTGSGYGTDFTFTISTVQABDLAVYFCQQDYGSPPTFGGGTKLEIKR 108
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                             Similarity
                                                                                                                                                    amino acid
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1251 Avenue of the Americas
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Papayannopoulou, Thalia (USA only)
                        81.5%; Score 466; DB 2;
80.4%; Pred. No. 1.2e-40;
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      10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Mismatches
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                                          Length 128;
    Indels
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Gaps
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                                                                                                                                                          Query Match 81.5%; Score 466; DB 2; Best Local Similarity 80.4%; Pred. No. 1.2e-40; Matches 86; Conservative 10; Mismatches 11
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                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/463,128
FILING DATE: 05-UUN-1995
APPLICATION NUMBER: PCT/US93/11060
FILING DATE: 11-11-1993
APPLICATION NUMBER: US 07/977,702
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 8173CIP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 109000
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                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Board of Regents, U.
APPLICANT: Washington (except USA)
TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM
TITLE OF INVENTION: CELLS
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                          LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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81
                            62 FTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIKR 108
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                                                                          TVMTQSPSSLSASVGDRVTITCKASQSVTNDVAWYQQKPGKAPKLLIYYASNRYTGVPDR
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1251 Avenue of the Americas
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                                                                                                                                                          11; Indels
                                                                                                                                                                                               Length 128;
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US-08-463-128-6

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RESULT 13
US-08-463-298-6
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Patent No. 5824304
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
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                                                                        APPLICANT: Papayannopoulou, Thalia (USA only)
APPLICANT: Board of Regents, U.
APPLICANT: Washington (except USA)
TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC
TITLE OF INVENTION: CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11060
FILING DATE: 11-11-1993
APPLICATION NUMBER: US 07/977,702
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARD: Datasty PC-DOS/MS-DOS
                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B173CIP
TELECOMMUNICATION INFORMATION:
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APPLICANT: Board of Regents, U.
APPLICANT: Washington (except USA)
                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/463,128 FILING DATE: 05-JUN-1995 CLASSIFICATION: 424
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                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                      61 RFTGSGYGTDFTFTTSTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIKR 108
                                                                                                                                                                           INFORMATION:
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3: c/o FISH & NBAVE
1251 Avenue of the Americas
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1251 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 461; DB 1; Length 128;
Pred. No. 3.7e-40;
L1; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6,
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APPLICANT: Papayannopoulou, Thalia (USA only)
APPLICANT: Board of Regents, U.
APPLICANT: Washington (except USA)
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                                                                                                                                                                                                                                                                                           APPLICANT: Washington ()
TITLE OF INVENTION: PER.
TITLE OF INVENTION: CELL
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA
                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,339A
                                                                                                                                          MEDIUM TYPE: Floppy
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REGISTRATION NUMBER: 27,794
REFERENCE/DOCKST NUMBER: B173CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
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FILING DATE: 11-NOV-1993
APPLICATION NUMBER: US 07/977,702
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: 13-NOV-1992
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PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: PatentIn Dalante
                   FILING DATE:
CLASSIFICATI
                                                                                                                                                                                                                                                          STREET:
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TYPE: amino acid
TOPOLOGY: linear
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                         STATE:
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                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIKR 108
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5843438
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                                                                                                                                                                                               New York
Y: U.S.A.
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Y: U.S.A.
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1251 Avenue of the Americas
                     TION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                 10
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Pred. No. 3.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 128;
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US-07-934-373C-5
                                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/934,373C

FILING DATB: 21-Aug-1992

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/05126

FILING DATB: 15-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/05126

FILING DATB: 15-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/715272

FILING DATE: 14-JUN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/07934373C
Patent No. 5821337
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INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/463,128
FILING DATE: 05-UN-1995
APPLICATION NUMBER: PCT/US93/11060
FILING DATE: 11-11-1993
APPLICATION NUMBER: US 07/977,702
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B173CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: POT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/25-1994
TELEPAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 80.6%; Score 461; DB 2; Length 128;
Local Similarity 78.7%; Pred. No. 3.7e-40;
nes 85; Conservative 11; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: South San
STATE: Californi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYGSPPTFGGGTKLEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 DIQLTQSPSSLSASVGDRVTITCKASQSVTNDVAMYQQKPGKAPKLLIYYASNRYTGVPS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIQMTQSFKFLLVSAGDRVTITCKASQSVSNDVAMYQQKFGQSFKLLMYYASNRYTGVFD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Genentech, Inc.
1 DNA Way
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                                                                            P0709P2
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Search completed: November 7, 2003, 07:30:08
Job time : 16.8611 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18; Search time 15.6702 Seconds (without alignments)
742.581 Million cell updates/sec

Title: US-09-661-992B-84_COPY_1_121

Perfect score: 643
Sequence: 1 EVQLVESGGGLVKPGGSLKL...........HGYGSSFDYWGQGTTLTVSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database: PIR 76:\*
1: pirl:\*

Minimum DB seq length: 0
Maximum DB seq length: 200000000

base : PIR\_76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	თ	ហ	4.	ω	2	μ.	No.	Result
495.5	497.5	498	498.5	500.5	501.5	503.5	504.5	504.5	504.5	506	507	507.5	508	508	508	509.5	512.5	515.5	518	524	528.5	529.5	530.5	531	535.5	542	546.5	557	Score	
77.1	77.4		77.5	77.8	78.0	78.3	78.5	78.5	•	٠	78.8			79.0	79.0	•		•	80.6	•	82.2	•	•	82.6	•	•	85.0		Match	Query
121	112	124	121	121	548	121	139	121	119	138	120	123	124	119	119	254	123	119	120	120	121	118	121	120	118	152	119	122	Length	
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Ig heavy chain V r	•	•	heavy	neavy	epsilo	neavy	heavy	heavy	neavy	heavy	heavy	Ig heavy chain, V	heavy chain V	Ig heavy chain V r	ti-pept		•	•	Ig heavy chain V r	Ig heavy chain V r	•	•	chain V	heavy chain V	heavy chain V	heavy chain pr	heavy chain V	상	Description	

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473.5	474.5	476	477	482	483.5	484	485	485	485.5	487.5	488	488.5	490	490	492
73.6	73.8	74.0	74.2	75.0	75.2	75.3	75.4	75.4	75.5	75.8	75.9	76.0	76.2	76.2	76.5
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PH1531	\$26468	HVMS96	E27889	S31107	S26327	C34903	PL0252	PH1007	PL0248	PH1537	S20641	PH1010	A43413	C36005	PL0249
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# ALIGNMENTS

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RESULT 2 F27888 I heavy C;Specie C;Date: C;Date: C;Catcon, EMBO J. A;Refere A;Refere A;Refere A;Residu A;Residu A;Roperi A;Note:	Qy Db Qy Db Qy Db	RESULT 1 E27888 Ig heavy C;Specia C;Date: C;Access R;Caton, EMBO J A;Title: A;Refere A;Refere A;Recess A;Molecu A;Residu A;Resperi A;Residu A;Reyeri A;Reyeri C;Cyumen C;Suyerf C;Keywor F;15-98; Best L
y chain V region (H158-89H4) - mouse ies: Mus musculus (house mouse): 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change ssion: F27888 rs. A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W 5, 1577-1587, 1986 e: Structural and functional implications of a restricted rence number: A91043; MUID:86300658; PMID:2427335 ssion: F27888 cule type: DNA dues: 1-119 CCAT> rimental source: strain Balb/c : this sequence was determined from the germline gene	107; Conservative 8; Mismatches 5; Indels 2;  1 EVQLVESGGLVKPGGSLKLSCAASGFTFSTYTWSWVRQTPEKRLEWVATISSGG:  :	ry chain V region (H35-C6) - mouse  des: Mus musculus (house mouse)  : 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change ssion: 827888  n, A.J; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  5, 1577-1587, 1986  : Structural and functional implications of a restricted seace number; A91043; MVID:86300658; PMID:2427335  ssion: 827888  cule type: DNA dues: 1-122 <cat>  rimental source: strain Balb/c  rithis sequence was determined from the germline gene ent: This schain was isolated from a hybridoma protein that rfamily: immunoglobulin V region; immunoglobulin homology ords: heterotetramer; immunoglobulin homology ords: heterotetramer; immunoglobulin homology ords: heterotetramer; immunoglobulin bomology S/Domain: immunoglobulin V region; immunoglobulin homology Watch  96.68; Score 557; DB 2; Length 122 Local Similarity 87.7%; pred. No. 1.5e-41;</cat>
16-Aug-1996 antibody respons	Gaps 2;	16-Aug-1996 antibody respons t binds influenza

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Ig heavy chain precursor V region (MAK33) - mouse (C;Species: Mus musculus (house mouse) (C;Species: Mus musculus (house mouse) (C;Date: 05-Jun-1988 #sequence revision 05-Jun-1988 #text_change 23-Jul-1999 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: B26471; S70410 (C;Accession: 
Ig heavy chain V region (anti-cyclosporin B) - mouse (fragment) c;Species: Mus musculus (house mouse) C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 16-A C;Accession: PH0097
R;Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.;
                                                                                                                                                                                  RESULT
PH0097
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;1-19/Domain: signal sequence #status predicted F;20-152/Product: Ig heavy chain V region MAK33 #status predicted
F;34-117/Domain: immunoglobulin homology <IMMs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Boundaries of somatic mutation in A;Reference number: S70410, MUID:91079775; A;Accession: S70410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M16163; NID:g195405; R;Lebecque, S.G.; Gearhart, P.J. J. Exp. Med. 172, 1717-1727, 1990
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Best Local S
Matches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: EMBL:X53776; NID:g52475; PIDN:CAA37792.1; PID:g52476;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCFR-GETYYDYAMDYWGQGTSVTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDSVKGRFTISRDNAKNNLYLQMSSLKSEDTAMYYCARDKAYYGNYGDAMDYWGQGTSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVQGVESGGGLVKPGGSLKLSCAASGFTFSDYYMYWVRQTPEKRLEWVATISDGGSYTYY
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Pred. No. 3.7e-40;
5; Mismatches 12
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RESULT 5
S55536
Ig heavy chain V region pe20 - mouse (fragment)
Ig heavy chain V region pe20 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Sate: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: $55536
C;Accession: $55536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-120 <BOE>
A;Cross-references: EMBL:X82589; NID:g854304; PIDN:CAA57925.1; PID:g854305
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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F;31-35/Region: complementarity-determining 1
F;50-66/Region: complementarity-determining 2
F;99-105/Region: complementarity-determining 3
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A; Residues: 1-118 <SCH>
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A;Title: Analysis of the structural diversity of monoclonal antibodies
A;Reference number: PH0087; MUID:91042649; PMID:2122240
A;Accession: PH0097
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A;Accession: $55536
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J. Mol. Biol. 247, 932-946, 1995
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Pred. No. 2.6e-39;
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antibody respons

16-Aug-1996

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Ig heavy chain V region (H37-45) - mouse C;Species: Mus musculus (house mouse) C;Date: 15-Dec;1988 #sequence_revision 15-Dec-1988 #text_change C;Accession: I27887
B;Caton; A.J: Brownlee, G.G.; Staudt, L.M.; Gerhard, W. EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted
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A; Residues: 1-118 <SCH>
C; Superfamily: immunoglobulin V region; immuno
C; Keywords: heterotetramer; immunoglobulin
C; Keywords: immunoglobulin homology <IMN>
F; 15-98 / Domain: immunoglobulin homology <IMN>
F; 15-96 (Region: complementarity-determining 1
F; 50-66 / Region: complementarity-determining 2
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A;Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.
A;Reference number: PH0087; MUID:91042649; PMID:2122240
A;Accession: PH0096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain V region (anti-cyclosporin A) .
C;Species: Mus musculus (house mouse)
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A;Molecule type: DNA
A;Residues: 1-121 <CAT>
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Structural and functional implications of a restricted antibody response
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ilarity 83.5%;
Conservative 1
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Pred. No. 3.4e-39;
0; Mismatches 5
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Pred. No. 2.9e-39;
9; Mismatches 8
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Ig heavy chain V region pe24 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #te
C;Accession: $55539
R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
                  A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibod: utations in the variable region genes.
A;Reference number: $55528; MUID:95239763; PMID:7536850
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A;Reference number: 855528; MUID:95239763; PMID:7536850
A;Accession: 855537
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C;Species: Mus museculus (house mouse)
C;Species: Nus museculus (house mouse)
C;Date: 27-Oct-195 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: S55537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: immunoglobulin V region; immuno
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
A; Accession: S55539
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A; Residues: 1-120 <BOE>
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J. Mol. Biol. 247, 932-946, 1995
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A;Accession: 127887
A;Molecule type: DNA
A;Residues: 1-121 <CAT>
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R;Caton, A.
A;Molecule type: DNA
A;Residues: 1-123 <CAT>
A;Experimental source: strain Balb/c
A;Note: this sequence was determined
                                                                                    A,Title: Structural and functional implications of a restricted A,Reference number: A91043; MUID:86300658; PMID:2427335 A,Accession: G27888
                                                                                                                                                                                      Ig heavy chain V region (H28-A2) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C;Accession: G27888
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A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-119 < CAT>
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C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C:Accession: B27889
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A;Molecule type: mRNA,
A;Molecule type: mRNA,
A;Residues: 1-120 <BOE>
A;Cross-references: EMBL:X82593; NID:g854312; PIDN:CAA57929.1; PID:g854313
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;14-97/Domain; immunoglobulin homology <IMM>
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Pred. No. 3.5e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 515.5;
Pred. No. 5.7
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             from
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             the
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        germline gene
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RESULT 13

B31190
Ig heavy chain V region (17/9) - mouse
C; Species: Mus musculus (house mouse)
C; Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-May-1997
C; Accession: B31790
R; Schulze-Gahmen, U; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson
J. Biol. Chem. 263, 17100-17105, 1988
A; Title: Preliminary crystallographic data, primary sequence, and binding data f
A; Reference number: A92686; MUID:89034213; PMID:3182835
A; Accession: B31790
                                                                                                          R;Stura, B.A.; Stanfield, R.L.; Fieser, T.M.; Balderas, R.S.; Smith, L.R.; Lerne J. Biol. Chem. 264, 15721-15725, 1989
A;Title: Preliminary crystallographic data and primary sequence for anti-peptide A;Reference number: A34353; MUID:89359424; PMID:2504725
A;Accession: B34353
                                                                                                                                                                                                                                                                                              RESULT 14
B34353
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A; Residues: 1-254 <SCH>
A; Residues: 1-254 <SCH>
C; Superfamily; immunoglobulin C region; immuno
C; Keywords: heterotetramer; immunoglobulin
P; 15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                              anti-peptide Fab' B1312 heavy chain - m
C;Species: Mus musculius (house mouse)
C;Date: 22-Jun-1990 #sequence_revision
C;Accession: B34353
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                A;Cross-references: GB:M29252; NID:g195657; PIDN:AAA38388.1; C;Superfamily: immunoglobulin V region; immunoglobulin homolo
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                                                        A;Residues: 1-119 <STU>
                                                                       A; Molecule type: mRNA
                                                                                              A;Status: preliminary
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immunoglobulin homology <IMM>
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Pred. No. 1.1e-37;
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Pred. No. 4.2
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PHOOSE
PHOOSE
If heavy chain V region (anti-cyclosporin G) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 16-Aug-1996
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 16-Aug-1996
C;Caccession: PHOO98
R;Schmtter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesniaux, V.P.J.; V
Mol. Immunol. 27, 1029-1038, 1990
A;Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.
A;Reference number: PHOO87; MUJD:91042649; PMID:2122240
A;Accession: PHOO98
A;Molecule type: mRNA
A;Residues: 1-119 <SCH3
A;Note: the authors translated the codon GTG for residue 104 as Gly
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin
F;15-98/Domain: immunoglobulin homology <Almons
F;31-35/Region: complementarity-determining 2
F;99-106/Region: complementarity-determining 3
F;99-106/Region: complementarity-determining 3
Search completed: November 7, 2003, 07:36:19
Job time: 15.7702 secs
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Perfect score:
Sequence:
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Maximum DB
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Maximum Match 100%
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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441.5
430.5
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2003 Compugen Ltd.
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HY59_MOUSE
HY36_HUMAN
HY59_MOUSE
HY37_HUMAN
HY38_HUMAN

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p18530 mus musculu
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61 1	atc) cal	SMART; SMO0406; 1Gv; PROSITE; PS50835; IG: Immunoglobulin V reg DOMAIN 1 > NON TER 98 SEQUENCE 98 AA; 1	HSSP; PO10702; AVROSO- HSSP; PO1772; ZFB4. InterPro; IPR007110; InterPro; IPR003006; InterPro; IPR003596; Pfam: PF00047; ic: 1	J. EXP. Med. 169:2007-2019(19)	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  STRAIN=BALB/CJ;  MEDLINE=89279149; PubMed=2499654;  MEDLINE=89279149; PubMed=89279149;  MEDLINE=89279149; PubMed=89279149;  MEDLINE=89279149; PubMed=89279149;  MEDLINE=89279149; PubMed=89279149;  MEDLINE=89279149; PubMed=89279149;  MEDLINE=89279149;  heavy ( muscularyota malia; I_TaxII	01-NOV-1990 01-NOV-1990	MOUSE HV57 MOUSE		384.5 382.5	385 385	387.5		
QLVBSGGGI            QLVBSGGGI  QLVBSGGFT18           SVKGRFT18	rity mserv	00406;	TPR003006; IPR003596; IPR003596;	Exp. Med. 169:2007-2019 MISCELLANEOUS: THIS SEC SIMILARITY: Contains 1	FROM N.A. LB/CJ; 19279149; Pu 1927949; Pu	chain V reg lus (Mouse) ; Metazoa; Eutheria; D=10090;	(Re	STANDARD;		59.8 59.8 59.7	9.00		
JVKPGGSI          XKPGGSI  XKPGGSI 	74.0%; 92.9%; tive	Gy; 1. IG_LIKE; 1 region. >98 98 11007 MW;	ig-like	HIS ain	bMed=24	Chordat Rodenti	. 16, Created) . 16, Last sec	)ARD;		122 1 119 1 120 1	113 123 1		120 1 123 1 113 1
KISCAASG		∺ .	: * 6	019(1989). SEQUENCE BE S 1 immunogl	199654; Lebecque action in	a; Crani	ed)	PRT;	ALIG	HV23 MOUSE HV31 HUMAN HV3U HUMAN	HV28 MOUSE	HV3M_HUMAN	HV18 MOUSE
MSWVRQTP          MYWVRQTP YYCTR 98 	Leng	G-LIKE. B8644F7F92FBF95B CRC64;		1989). DENCE BELONGS TO THE VH7183	S.G., Gearhart immunoglobulin	brata; luridae;	ed) sequence update) sequence update)	98 AA.	ALIGNMENTS				
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RESULT 2
HY55 MOUSE STANDARD; PRT; 117 AA.
AC P18526; 90 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-UV-1990 (Rel. 38, Last annotation update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 345 precursor.

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RESULT
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Best Local (
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P01783;
P01783;
P01783;
P117UL-1986 (Rel. 01, Last sequence update)
P1-7UL-1986 (Rel. 42, Last annotation updat
P15-SEP-2003 (Rel. 42, Last annotation updat
P15 Heavy chain V region MOPC 21 precursor (
P15 Mus musculus (Mouse)
P15 P16 P1783 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P1784 P17
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SEQUENCE FROM N.A.
MEDLINE=81234548; PubMed=6788376;
MEDLINE=81234548; PubMed=6788376;
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                          SEQUENCE OF 17-136.
MED; TMS=77100368) FubMed=401950;
Adetugbo K., Milstein C., Secher D.S.
"Molecular analysis of spontaneous so
Nature 265:299-304(1977).
                                                                                                                                                                                                                   "Heavy chain variable region antibodies: somatic mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Sign
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SMART; SM00406; IGv;
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HSSP; P01810; 2FBJ.
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Levy N.S., Malipiero U.V., Lebecg
"Early onset of somatic mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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Rodentia;
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evident in a
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
BY SIMILARITY.
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immunoglobulin
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                                                                                                                                                                                                                                                                                              Imanishi-Kari T., Rajewsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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                                                                              "Barly onset of somatic mutation the primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
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01-NOV-1990 (Rel. 16, Last seq
15-JUL-1999 (Rel. 38, Last ann
1g heavy chain V region 5-84 p
Mus musculus (Mouse)
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                   PIR; JT0505; HVMS84.
HSSP; P01810; 2FBJ.
InterPro; IPR007110;
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P18525;
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SMART; SM00406; IGV; 1.
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Levy N.S., Malipiero U.V., Lebecq
                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
    InterPro; IPR003006;
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HSSP; P01810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region 5-76 precursor.
Nus musculus (Mouse)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                 71.7%;
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88.8%;
                                                                    XW.
                                                                                                IG HEAVY CHAIN V REGION 5-76. FRANSWORK-1.
COMPLEMSTYARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMSTYARITY-DETERMINING-2.
FRAMEWORK-3.
BY SIMILARITY.
 Score 461; Di
Pred. No. 4.3:
3; Mismatches
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Pred. No.
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAMEWORK-3.
BY SIMILARIT
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                                                                  93A04782B78B8FA0
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                 DB 1;
.3e-39;
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                             Length 117;
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                                                                  CRC64;
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   Indels
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VH ge
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                     genes
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RESULT 7
HV3K_HUMAN
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                                                                           HV3K HUMAN STANDARD; PRT; 126 AA. p01772;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region KOL.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebr.
Mammalia; Butheria; Primates; Catarrhini; Homin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990 (Rel. 16, Created
01-NOV-1990 (Rel. 16, Last se
15-SEP-2003 (Rel. 42, Last ar
Id heavy chain V region 914.
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SEQUENCE
SEQUENCE, AND DISULFIDE BONDS.
MEDLINE=83289131; PubMed=6884994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the primary immune response.";

0. Exp. Med. 169:2007-2019(1989).

--- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183

--- SIMILARITY: Contains 1 immunoglobulin-like domain.

PRR; JT0504; HVMS91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=89279149; PubMed=2499654;
Levy N.S., Malipiero U.V., Lebecq
"Early onset of somatic mutation
                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS0835; IG LIKE; 1.
Immunoglobulin V region.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V reg
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P18527;
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                                                                                                                                                                                                                                                                                                                                                                                                    PDSVKGRFTISRDNARNILYLQMSSLRSEDTAMYYCAR
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16, Last sequence update)
42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10661 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.2%;
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station in
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6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 457.5;
Pred. No. 7.8
                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C23CB33FF55DA893 CRC64;
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VH genes
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                                                                                                                              Query Match
Best Local S
Matches 84
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DOMAIN 1
DOMAIN 1
MOD RES 1
DISULFID 22
DISULFID 105
STRAND 11
TURN 14
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TURN
STRAND
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HELIX
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HELIX
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SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
                                                                                                                              SEQÜENCE
                                                                                                                                                                                                                             TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.; "Three-dimensional structure determination of antibodies. Prin structure of crystallized monoclonal immunoglobulin IgG1 KOL, Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Contains 1 immunoglobulin-like domain
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              116
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2IG2; 12-JUL-89.
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121
                               6
                                             61
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                                                                                              84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FB4; 12-JUL-89.
                                                                                                      Similarity
SSALAd
                                            PDSVRGRFTISRDNAKWTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSF-----DYWGQGT 115
                                                             QVQLVESGGGVVQPGRSLRLSCSSSGFI
                                                                      TLTVSS
                               ADSVKGRFTISRDNSKNTLFLQMDSLRPEDTGVYFCARDGGHGFCSSASCFGPDYWGQGT
                                                                                                                                     Conservative
                                                                                                                              .26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141:369-391(1980).
126
               121
                                                                                                                                       110
                                                                                                     68.7%;
66.7%;
                                                                                                                              13718 MW;
                                                                                              16;
                                                                                             Pred. No. 4.1e-37;
5; Mismatches 21
                                                                                                      Score 441.5;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                     IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID
                                                                                                                              E4D71B52B16F8776 CRC64;
                                                             FSSYAMYWVRQAPGKGLEWVAIIWDDGSDQHY
                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAS
                                                                                             21;
                                                                                              Indels
                                                                                                           Length
                                                                                                              126;
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RESULT 8
HV59 MOUSE
ID HV59 M
AC P18530
DT 01-NOV
DT 01-NOV
DT 01-NOV
DT 01-NOV
DT 01-NOV
DT 01-NOV
DT 01-NOV
DT 01-NOV
DT 01-NOV
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DT 15-JUL
DE STRAIN
RX NCBLI
RN 11-EXI
RR 11-EXI
DR 11-EXI
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Best Local :
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NON_TER
SEQUENCE
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P01768;
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DOMAIN
DOMAIN
MEDIJINE=81013859; PubMed=6774332;
Lebman D.W., Putnam F.W.;
Lebman D.W., Putnam F.W.;
"Amino acid sequence of the variable region
location of a possible JH segment.";
Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243()
                                                                                                                           Bukaryota; Metazoa;
Mammalia; Butheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                    NAMOH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                              SEQUENCE
                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up.
15-SEP-2003 (Rel. 42, Last annotation if heavy chain V-III region CAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; JT0507; HVMS39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Exp. Med.
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Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110;
InterPro; IPR003006;
InterPro; IPR003596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01810; 2FBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Exp. Med. 169:2007-2019(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89279149; PubMed=2499654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BALB/CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain V region Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Levy N.S., Malipiero U.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mmunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                          PDSVKGRFTISRDNAKNNLYLQMNSLTSEDTALYYCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                               PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS50835;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117
117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 16, Last sequence update) (Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                   STANDARD;
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49
54
68
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115
                                                                                                                                                Chordata;
Primates;
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Ig_MHC.
Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12972 MW;
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84.7%;
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tation in
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5; Mismatches
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG HEAVY CHAIN V REGION 7-39. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
     77:3239-3243 (1980)
                                                                                                                                                Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                 PRT;
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No. 1
                                                                                                                                                                                                                                           update)
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immunoglobulin
                                                                                                                                                                                                                                                                                                 122
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                                                                                                                                                                                                                        update)
                                                                                                                                                  Vertebrata; Euteleostomi;
i; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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VH genes
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                                          chain:
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RESULT 10
HV53_MM
HV53_MV
DT 11-NOV
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OS Mus mu
OC Eukary
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OX NCBI_T
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RP SEQUEN
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Best Local (
                                                                                                                      the primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
-! MISCELLANBOUS: THIS SEQUENCE B
PIR; JT0503; HVMSRF.
HSSP; PO1810; 2FEJ.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-MHC.
                                                                           Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LI
Immunoglobulin V region
             SIGNAL
CHAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                MEDLINE=89279149; PubMed=2499654;
Levy N.S., Malipiero U.V., Lebecque
"Early onset of somatic mutation in
                                                                                                                                                                                                                                                                                                                                                  HV53 MOUSE STANDARD; PRT; 117 AA. P18524; O1-NOV-1990 (Rel. 16, Created) O1-NOV-1990 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last amnotation update) Ig heavy chain V region RF precursor.

Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOD_RES
                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS
GO; GO:0006955; P:immune_response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF PATIENT WITH MACROGLOBULINEMIA.
-i- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR: A02051; M3HUAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
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122 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
    65500
9500
9500
9500
                                                                             region; Hybridoma;
                                                                                       GV; 1.
IG_LIKE;
  117
49
68
85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13668 MW; A42D0F17D252F1C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
IG HEAVY CHAIN V REGION RF. FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 430.5;
Pred. No. 4.
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HSSP; P01772; 2784.
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GO; GO:0005823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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12866 MW;
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Pred. No. 5
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BY SIMILARITY.
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RESULT
HV39 M
HD AC 99
DT 2
DT 2
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RN RR
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Best Local S
Matches 81
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HSSP, PO1810; 2FBJ.
InterPro; IPR0077110; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-v.
Pfam; PF00040; Ig: 1.
SMART; SM00406; IGv; 1.
                                                                                                             P01809;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 heavy chain V region X24.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50835; IĞ LIKE; 1.
Immunoglobulin V region.
DOMAIN
1 112
NON TER 119 119
SEQÜENCE 119 AA; 13169 MW;
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V region T601.
Mus musculus (Mouse).
SEQUENCE.

MEDLINB=79223895; PubMed=111245;

Rao D.N., Rudikoff S., Krutzsch H., F
"Structural evidence for independent
immunoglobulin heavy chains from anti
                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                   TSOOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complementarity-determining regions.";
Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979)
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=79223895; PubMed=111245; Rao D.N., Rudikoff S., Krutzsch H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                     HV39_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
"Structural evidence for independent joining region gene in immunoglobulin heavy chains from anti-galactan myeloma proteins its potential role in generating diversity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THAT BINDS GALACTAN.

- !- SIMILARITY: Contains 1 immunoglobulin-like
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                                                                                 _TaxID=10090;
                                                                                                                                                                                                                                                                       118
                                                                                                                                                                                                                                                                                               121 S
                                                                                                                                                                                                                                                                                                                          61 TPSLKDKFIISRDNAKVTLYLOMSKVRSEDTALYYCARLGYYGY---FDVWGAGTTVTVS
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                                                                                           Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 415.5; DB 1
Pred. No. 1.5e-34;
3; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IG-LIKE
                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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dent joining region gene in anti-galactan myeloma proteins
               Potter M.;
t joining r
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Best Local S
Matches 82
PIR; A02064; M3HUGL.

HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR0077110; Ig-1ike.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003956; Ig_v.
Pfam; PF000474; Ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                 Hilschmann N.;
Submitted (JUN-1975) to
Submitted LANEOUS: THIS
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SEQUENCE
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SMART; SM00406; IGv; 1.
SPROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
DOMAIN
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Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979)
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM
                                                                                                                                                                                                                                                                                                                                                                                                                             Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N., "The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mtype), subgroup H III. Architecture of the complete IgM-molecule.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Mammalia; Butheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V-III region GAL.
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-!- SIMILARITY: Contains 1 immunoglobulin-like domain
                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                              REVISION TO 28-33.
                                                                                                                                                                                                                                                                                                                                                                                                                Hoppe-Seyler's
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Watanabe S., Barni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                  MACROGLOBULIN.
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Pred. No. 2.1e-34;
2; Mismatches 23
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RESULT 15
HV35 MOUSE
FO1804;
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Bernard O., Gough N.M.;

Bernard O., Gough N.M.;

"Nucleotide sequence of immunoglobulin heavy chain joining segments between translocated VH and mu constant regions genes.";

Proc. Natl. Acad. Sci. U.S.A. 77:3630-3634(1980).

-!- MISCELLANBOUS; THE SEQUENCE OF THE FIRST 197 RESIDUES OF THE C REGION WAS ALSO DETERMINED & DIFFERS IN ONLY 3 POSITIONS FROM THE CORRESPONDING PORTION OF THE MOUSE MOPC 104E MU CHAIN.

-!- SIMILARITY; Contains 1 immunoglobulin-like domain.
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KGRFTISRDDSKSSVYLOMNIRAEDTGIYYCTRPGVP-----DYWGQGTTLTVSS 111
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116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;
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Search completed: November 7, 2003, 07:28:08
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Copyright (c) 1993 - 2003 Compugen Ltd.
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## ALIGNMENTS

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OC Euka
OC Mamm
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Q99KA4;
O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 52.6 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 4.
PROSITE; PS00406; IGV; 1.
PROSITE; PS00835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
HYPOTHAETCAL PROTEIN.
HYPOTHAETCAL PROTEIN.
SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC004786; AAH04786.1; -.
HSSP; P01810; 2FBJ.
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                                                              PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRD-GGHGYG--SSFDYWGQGTTL 117
                                                                                                                                                                                                                            EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
PDNVKGRFTISRDNAKNNLYLOMSHLKSEDTAMYYCARDMGGSPYGGYSRFDYWGQGTTI 139
                                                                                                                                                     EVQLVESGGGLVKPGGSLKLSCAASGETESSYAMSWVRQTPEKRLEWVATISDGGSYTYY
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                           87.6%; Score 563.5; DB 11; Length 87.9%; Pred. No. 1e-47; tive 4; Mismatches 8; Indels
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Matches 104
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Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
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SEQUENCE FROM N.A.

Jennings I.G., Horaitis O., Cotton Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton In Mammalian Cells.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF307937, AAL09421.;

InterPro; IPR007010; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_W.

InterPro; IPR003596; Ig_W.
SEQUENCE FROM N.A.

SET TRUST FROM N.A.

SUBTRICT OF THE EMBL/GenBank/DDBJ

SUBTRICT OF THE EMBL/GenBank/DDBJ

EMBL, BC010324, DAH10324.1; -.

InterPro; IPR007110; Ig-1ike.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_V.
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Q920E7;
Q920E7;
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Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTDEKRLEWVATISSGGSYTYY
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119 AA;
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
cking anti-idiotope heavy chain variable
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Pred. No. 4e-46;
6; Mismatches
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Sciurognathi; Muridae;
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Sciurognathi; Muridae;
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; Murinae; Mus
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; Murinae; Mus.
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Best Local S
Matches 91
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Best Local S
Matches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ day
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ day
EMBL; BC013656; AAM13656.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
PEam; PP00047; ig; 4.
PRAM; SM0446; IGv; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS050835; IG_IXKE; 4.
PROSITE; PS050835; IG_IXKE; 4.
PROSITE; PS050835; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4
PROSITE; PS00290; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 486 AA; 52682 MW
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Q91WP5;
Q91WP5;
Q91WP5;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 29, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 51.6 kDa protein.
Mus musculus (Mouse).
Murana: Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Colon;
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77.4%;
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Pred. No. 3.2e
10; Mismatches
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Pred. No. 7.8e-
9; Mismatches
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7.8e-39;
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1.2e-40;
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Best Local S
Matches 91
      Query Match
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PROSITE; PS50
PROSITE; PS00
Hypothetical
SEQUENCE 47
                                                                                                                                                                                                                                Strausberg R.;
Submitted (UTL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010798; AAH10798.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003086; Ig_MC.
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Q91XE1;
Q91XE1;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Q2-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Q2-MAR-2003 (TrEMBLrel. 19, Created)
Q2-MAR-2003 (TrEMBLrel. 19, Created)
Q3-MAR-2003 (TrEMBLrel. 19, Created)
Q3-MAR-2003 (TrEMBLrel. 19, Created)
Q3-MAR-2003 (TrEMBLrel. 19, Created)
Q3-MAR-2003 (TrEMBLrel. 19, Created)
Q1-MAR-2003 (TrEMBLrel. 19, Last sequence update
Q1-MAR-2003 (TrEMBLrel. 19, Last sequence update
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update
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Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update
Q1-MAR-2003 
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PROSITE;
NON_TER
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01-DEC-2001 (TremBLrel.
01-MAR-2003 (TremBLrel.
Hypothetical 51.9 kDa pr
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Submitted (JUL-2001) to the
EMBL; BC010327; AAH10327.1;
MGD; MGI:2144967; AU044919.
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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SMART; SM00406; IGv; 1.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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; SM00406; IGv; 1.
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PS00290; IG_MHC; 2.
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PS50835; IG_LIKE; 4
PS00290; IG_MHC; 1
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                                                                     51936 MW;
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      Score 464;
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      DB 11;
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Length 480;
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Matches
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024289; AAH24289.1; -.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR003006; Ig_MHC.
R InterPro; IPR003596; Ig_v.
R InterPro; IPR003596; Ig_v.
R Pfam; FP00047; ig; 4.
R Pfam; FP00047; ig; 4.
R SMART; SM00406; IGv; 1.
R SMART; SM00406; IGv; 1.
R PROSITE; PS0035; IG_LIKE; 4.
R PROSITE; PS00290; IG_MHC; 2.
W Hypothetical protein.
SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
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01-JUN-2002 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
Hypothetical protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chord
Mammalia; Butheria; Prima
                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 23, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
Hypothetical protein FLJ14473.
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Crania
Mammalia; Eutheria; Primates; Catarr
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NCBI_TaxID=9606;
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Primates;
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Last sequence update)
Last annotation update)
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Pred. No. 1.:
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3; Mismatches
                     Craniata; V
Catarrhini;
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tches 13;
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                     Vertebrata;
i; Hominidae;
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                       Buteleostomi;
Homo.
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Best Local Similarity
Matches 89; Conserv
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EMBL; AK027379; BAB55072.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGy 1.
PROSITE; PS00835; IG_LIKE; 4.
PROSITE; PS00836; IG_MHC; 1.
                                                                    InterPro; IPR007110; Ig-like.
InterPro; IPR00306; Ig_MC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PR0SITE; PS50835; IG_LIKE; 1.
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SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last amnotation update)
Myosin-reactive immunoglobulin heavy chain variable
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Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
                                                                                                                                                                                                                                  fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035021; AAD56257.1; -.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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"NEDO human cDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A.
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        AA,
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Primates;
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        12434 MW;
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%; Pred. No. 7.1e-37;
13; Mismatches 17;
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Q96BB9
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COS Homo
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OX NCBI
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RP SEQUE
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Best Local Similarity
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Strausberg R.;
Submitted (OCT-2001) to the EMB
EMBL; BC015760; AAH15760.1; -.
InterPro; IPR007710; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003996; Ig_v.
                                                                               01-MAR-2002 (TREMBLrel. 20, Cre
01-MAR-2002 (TREMBLrel. 23, Las
01-MAR-2003 (TREMBLrel. 23, Las
Hypothetical protein.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, C
Mammalia, Butheria, Primates, C
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SMART; SM00406; IGv; 1.

PROSITE; PS50035; IG_LIKE; 5.

PROSITE; PS00290; IG_MHC; 3.

Hypothetical protein.

SEQUENCE 597 AA; 65039 MW;
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TISSUE=B-cell;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
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                       SEQUENCE FROM N.A
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  TISSUE=Tonsil
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10; Mismatches
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Pred. No. 1.6e-36;
8; Mismatches 16
                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF035024; AA
HSSP; P01772; 2FB4
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Mammalia; Eutheria; Primates;
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PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fetus.";
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InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 5.
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86; Conserv
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PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS
                                                                    ŔVQĽVEŚĠĠĠVVQÞĠĠŚĽŖĽŚĊĂĀŚĠŦŤŦŚŚYGMIMVRQĀÞGKGĽEWVĀFŢŖYDĠŚNKŸŶ
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                                                                                                                                                                  Conservative
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Ig_MHC.
Ig_v.
                                                                                                                                                                                                                                                          12437 MW;
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70.2%;
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71.1%; Pred. No. 3.6e-36;
tive 14; Mismatches 20
                                                                                                                                                                13;
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Pred. No. 2.1e-36;
3; Mismatches 15;
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VH3 protein
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Q9Y509;
01-NOV-1999
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.,
                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TaxID=9606;
                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
MYOSIn-reactive immunoglobulin heavy chain variable
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                     (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A CD10-positive subset of malignant cells is identified in multiple myeloma using PCR with patient-specific immunoglobulin gene primers. Leukemia 9:1948-1953(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Pred. No. 5e-
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  Kalis N.N.,
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                                                                                                                Hominidae;
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  Berney S.M.,
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                                                                                                                                       Euteleostomi;
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Best Local S
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Q9R1A4;
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NON TER
SEQUENCE
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Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

Wab 7, its light and heavy chains) and construction of a single chain antibody (scFV).";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF15272; AAD40243.1; -.

HSSP; P01842; 7FAB.

MGD; MGI:96446; Igh-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse), Mus musculus (Mouse), Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Gammal heavy chain of Mab7 (Fragment).
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 4.
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VGD; MGI96446; Igh-4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Myosin-reactive autoantibodies in rheumatic carditis and normal
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63 DSVRGRETISRDNAKNTLYLOMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVSS 121
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87; Conservat
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                                                                                                                                                                    2 VQLVESGGGLVXPGGSLKLSCAASGFTFSTYIMSWVRQTPEKRLEWVATISSGGSYTYYP 61
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                                                                                                                         VQLQESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVASFSSGG-IIYYT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                         437
437 AA;
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                                                                                                                                                                                                                                                                                     67.3%;
ilarity 72.5%;
Conservative
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1; 12843 MW; D0633949F2AC149D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                437
                                                                                                                                                                                                                                                                                                                                                                                                                                                         48142 MW; 5C3A7BB3EE7D697C CRC64;
                                                                                                                                                                                                                                                                                Score 432.5; DB 11; Length 437; Pred. No. 9.4e-35; 8; Mismatches 18; Indels 7;
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Db 60 DSVKGRFTIYKDKDRNILSLQMSSLRSEDTAMYYCAR-----GDYSAYMGPGTLVTVSA 113

Search completed: November 7, 2003, 07:34:35 Job time: 41.0025 secs

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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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     AAB20434
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                                                                                                                                                                                                                                            SUMMARIES
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Mouse monoclonal a
Anti-Streptococcus
Chimeric construct
Chimeric construct
Mouse mAb 26-2F he
Humanised mouse TR
Murine antibody 14
Mouse mAb 26-2F he
                                                                                                                                                                                    Description
                                                                                                                               Anti-FIX/FIXa anti
Mouse monoclonal a
 Key
Protein
22-MAR-2001.
                                                                                                                                                                                                                                                                                                                                          Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.
                                    WO200119992-A2
                                                                                        Region
                                                                                                                                                               Peptide
                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                          Chimeric - Mus musculus.
Chimeric - Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-FIX/FIXa antibody 193/K2 scFv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB20434;
                                                                                                                             Protein
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544.5
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/label= CDR3
122..135
/label= Linker
                                                                                                                                                                                                                 1..121
/label= VH
                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                       230..238
/label= CDR3
                                                                                                                             136..249
                                                                                                         /label= VL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB95208
ABJ36667
AAU72813
AAB48934
AAB97193
AAB48937
AAY43867
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AAB20442
AAB20438
AAB20433
AAB20433
AAB20433
AAB20435
AAC18391
AAW166099
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AAW39944
AAW29994
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Peptide seq ID No:
Amino acid sequenc
Mouse anti-PTHrP mouse
Human PTHrP mouse
Human PTHrP mouse
Human PTHrP mouse
Human PTHrP mouse
Mouse joint diseas
Angiogenesis inhib
Chimeric antibody
Mouse humanised an
Mouse antibody H c
Amino acid sequenc
Mouse joint diseas
Angiogenesis inhib
Humanised mouse TR
Anti-Trka single c
Murine anti-PI-3, A
Anti-Trka single c
Murine anti-PI-3, A
Anti-Trka murine m
Heavy chain (VH) g
Mouse antibody MB3

anti-CD22 monoclon Mouse anti-verotox Heavy chain variab Chimeric H chain S Mouse humanised an

Anti-FIX/FIXa anti Murine CBE11 heavy

TRA-8 heavy chain.
Anti-FIX/FIXa anti
Anti-FIX/FIXa anti
Anti-FIX/FIXa anti
Anti-FIX/FIXa anti
Anti-FIX/FIXa anti
Monoclonal antibod
Mouse antibody 2A4

Database :

Scoring table: Sequence: Perfect score:

643

OM protein -

Result No.

Score

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AAU76122
ID AAU7
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XX VH;
XX VGul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 121; Conser
                                                                        Wouse; monoclonal antibody; heavy chain variable region; VH; angiogenin; 26-2F; angiogenesis; tumour; cancer; retinopatl ocular neovascular disease; vitamin A deficiency; syphilis; Kaposi's sarcoma; rheumatoid arthritis; macular degeneration; Sickle cell anaemia; Paget's disease; mycobacterial infection; osteoarthritis; graft versus host disease; autoimmune disease; type I diabetes; multiple sclerosis; systemic lupus erythemato.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU76122 standard; Protein; 140 AA
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                                      myasthenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse monoclonal antibody 26-2F heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAY-2002
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100.0%; Pred. No. 1.7e-52;
Live 0; Mismatches 0;
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CC affinity to the angiogenin or its fragment in Combination with human CC derived polypeptide regions (e.g. mouse monoclonal antibody 26-2F). CC Also included are an expression vector comprising a nucleic acid cenoding the antibody and a host cell transformed with the vector. CC enciding the antibody and a host cell transformed with the vector. CC the antibody or its fragment is useful for inhibiting a tumour in the antibody and the ability of reducing or eliminating a tumour cc discasses mediated by angiogenesis, reducing or eliminating a tumour cc with abnormal or unwanted angiogenesis, including cancer, and other cdiscasses mediated by angiogenesis, including contar neovascular disease. CC diseases associated with corneal neovascularisation including epidemic cc terpication, neovascular glaucoma and retrolental fibroplasia, and other cdiseases associated with corneal neovascularisation including epidemic cc terpic keratitis, vitamin A deficiency, contact lens overwear, cc atopic keratitis, vitamin A deficiency, contact lens overwear, cc atopic keratitis, superior limbic keratitis, bacterial ulcers, for processon infections, kaposi s sarcoma, Mooren ulcer, rheumatoid carhititis, polyarteritis, trauma, Wegener's sarcoidosis, Soleritis, contact ed with retinal/choroidal neovascularisation include macular cc associated with retinal/choroidal neovascularisation include macular cc mycobacterial infections, Bechets disease, trauma, osteoarthritis, contact elemente disease, graft versus host disease, multiple crejection, autoimmune diseases such as type I disbetes, multiple creptional artichal gravis. The heavy chain variable region of mouse
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note= "This region is specifically claimed
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Best Local
                   The present sequence is the protein sequence of the heavy chain variable region (VH) of the murine monoclonal antibody SWLA3 (IgG), which binds specifically to the surface antigens of cariogenic type c streptococcus mutans (ATCC 25175). The monoclonal antibody is produced by SWLA3 (ATCC HB 12558) hybridoma cells. In an example from the invention, chimeric monoclonal antibody TEFE was produced comprising SWLA3 variable regions and human antibody constant regions. Such chimeric monoclonal antibodies can be used to prevent or treat dental caries in humans. The antibodies engage the effector apparatus of the human immune system when they bind cariogenic organisms, resulting in their destruction. The chimeric antibodies may be produced in edible plants, in transgenic animals,
                                                                                                                                                                                                                                                                                                                                                                                                                Treatment and prevention of dental caries in mammals, in particular humans by orally administering genetically engineered or purified antibodies that bind to surface antigens of cariogenic organisms -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus mutans; monoclonal antibody; MAb; mouse; chimeric antibody; antibody; anticaries; transgenic plant; transgenic animal; caries; immunotherapy; therapy.
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                                                                                                                                                                                                                                                                                                                                                                 Claim 14; Fig 3B; 30pp; English.
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                                                                                                                                                                                                                                                                        A composition comprising a targeting moiety and an anti-microbial peptide moiety, useful for treating microbial infections, e.g. on
                                                                                                                                                                                                                               mucosal surfaces, caused by protozoa, or parasites -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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N-PSDB; ABZ58398.
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14-FEB-2002; 2002US-0077624
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                                                                                                                                                                                                                                                                                                                                                                                                                      Morrison SL,
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Pred. No. 3.9e-44;
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The present sequence is that of a chimeric construct composed of the antimicrobial peptide dhvar1 (see also ABP72291) joined via a peptide linker to the heavy chain variable region of SWLA3, a monoclonal antibody made against the cariogenic organism, Streptococcus mutans. The chimeric construct shows antimicrobial activity toward S. mutans strains ATCC 25175, LMT and OMZ175, but not against a range of other oral bacterial strains. It is an

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RESULT 5
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                                                                    A composition comprising a targeting moiety and an anti-microbial peptide moiety, useful for treating microbial infections, e.g. on mucosal surfaces, caused by bacteria, rickettsia, fungi, yeasts,
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                                                                                                                                                                             N-PSDB; ABZ58397.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
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Example 1; Fig 3; 53pp; English
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14-FEB-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTFEKRLEWVATISSGGSYTYY
                                                                                                                                                                                                                                                                                              WASHINGTON DENTAL SERVICE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWLA3; antibody; antimicrobial; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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2002US-0077624.
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41..165
/label= SWLA3_V
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Pred. No. 4.2e-44;
1; Mismatches 4;
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Best Local s
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU76132;
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                            05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse mab 26-2F heavy chain variable region mutant M100Y.
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                                                                                     05-APR-1999;
                                                                                                                                                                                                          US2002010320-A1.
                                                                                                                                                                                                                                                                                                   Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 angiogenin; angiogenesis; tumour; cancer; retinopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neovascular disease; vitamin A deficiency; syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                     99US-0286240
                                                                                                                                                                                                                                                                                                                                                         /label= Signal_peptide
20..140
                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                /note= "Wild-type Met substituted by Tyr"
                                                                                                                                                                                                                                                                                                                         /label= Mature_VH
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Pred. No. 4.5e.
11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC affinity to the angiogenin or its fragment in combination with human derived polypeptide regions (e.g. mouse monoclonal antibody 26-2F). CC Also included are an expression vector comprising a nucleic acid CC encoding the antibody and a host cell transformed with the vector. CC The antibody or its fragment is useful for inhibiting the angiogenic activity of angiogenin. The antibody is useful for treating a tumour in thumans, by inhibiting, prohibiting, reducing or eliminating a tumour CC growth, or inhibiting the ability of circulating tumour cell to form a creating a tumour growth, or inhibiting the ability of circulating tumour cell to form a creating a tumour ccl with abnormal or unwanted angiogenesis, including cancer, and other creating attraction and control of seases mediated by angiogenesis, including cancer, and other creations associated with corneal prefit creations, and other creations associated with corneal neovascularisation including epidemic keraticis, upcrior limbic keratitis, syphilis, mycobacteria creations, lipid degeneration, chemical burns, bacterial ulcers, fargosi's sarcoma, Mooren ulcer, rheumatoid creations, contact lens coverweat, cc fungal ulcers, herpes simplex infections, herpes zoster infections, fargosi's sarcoma, Mooren ulcer, rheumatoid creations, contact with retinal/choroidal neovascularisation include macular degeneration, sickle cell anaemia, sarcoid, Paget's disease, Scleritis, cc associated with retinal/choroidal neovascularisation include macular rejection, autoimmune diseases such as type I diabetes, multiple collections, becheet disease, transplant creationy systemic lungua erythematosus, and myasthenia gravis. The present sequence represents the MOOY mutant of the mouse monoclonal constituted by the indexer using the sequence appearing as ANIT6122 and the creation in the specification but was the creation of the mouse monoclonal created by the indexer using the sequence appearing as ANIT6122 and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
    AAU72814;
                                          AAU72814 standard; Protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an antibody immunologically reactive to angiogenin or a fragment of angiogenin comprising light and heavy chanonhuman-derived complementarity determining regions having a binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page -; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antibody immunologically reactive to angiogenin useful for inhibiting angiogenesis and for treating conditions associated abnormal angiogenesis e.g. cancer, ocular neovascular disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rheumatoid arthritis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by the indexer using the sequence appearing as AAU76122 and tion in the claims.
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                  S 140
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                                                                                                                                                                                                                                                              PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS
                                                                                                                                                                                                                                                                                                                     EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPBKRLEWVATISSGGGNTYY
                                                                                                                                                                                                                                   PDSVKGRFTISRDIAKNTLYYOMSSLRSEDTALYYCTRLGDYGYAYTMDYWGQGTSVTVS
                                                                                                                                                                                                                                                                                                                                                               EVOLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPSKRLEWVATISSGGSYTYY
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Pred. No. 8.9e-44;
8; Mismatches 10
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                                                                                                                                                                                                                                             CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAII) receptor CC DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing CC activity to a cell expressing DR5 in vivo. It is also useful for CC preparing a therapeutic for selective apoptosis of abnormal or CC preparing a therapeutic for inhibiting cell proliferation in a cell, CC preferably a human breast, ovary, colon, haematopoletic, prostate, CC lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may CC also be administered e.g. paclitaxel, taxol or cycloheximide. The CC antibody is used to treat an autoimmune disease, systemic lupus CC erythematosus, Hashimoto's disease, rheumatod arthritis, CC graft-versus-host disease, Sjogren's syndrome, Chron's disease, syndrome, CC pernicious anaemia, Addison disease, selexoderma, Goodpasture's syndrome, CC glomerular nephritis anaemia, sterrility, myasthenia gravis, multiple CC selerosis, Basedow's disease, insulin-dependent disbetes mellitus, CC glomerular nephritis, hypoplastic anaemia, rejection after organ CC covary, lymphatic or breast tissue. This sequence shows one of the invention.
                                                                                                                                                                       Query Match
Best Local S
Matches 106
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                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 26; Page 212-213; 229pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel antibody specific for tumour apoptosis-inducing ligand, useful f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-049338/06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes a novel antibody which recognizes a tumour
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121 $ 121
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                                                       PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS
                                                                                                   EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTPEKRLEWVATISSGGSYTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ichikawa K,
                                  PDSVKGRETISRDNAKNTLYLOMSSLRSEDTAMYYCARRGDSMI--TTDYWGQGTTLTVS
                                                                                                                                    EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
                                                                                                                                                                                                                                           119
                                                                                                                                                                         Conservative
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                                                                                                                                                                                         84.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kimberly
                                                                                                                                                                   Score 545; DB
Pred. No. 1.1e
4; Mismatches
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                                                                                                                                                                                       545; DB 23;
No. 1.1e-43;
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                                                                                                                                                                   identifying characteristics of, or that is a monoclonal antibody 14F3. An antibody of the invention has osteopathic, antipsoriatic, antidiabetic, antiarthritic, antiinflammatory, cytostatic, antipsoriatic, antidiabetic, and neuroprotective activity. The polynucleotides encoding the antibodies of the invention may have a use in gene therapy. The antibodies and polypeptides are useful for treating or preventing osteopathic diseases, such as rheumatoid arrhritis, osteoporosis, metastatic and primary bone cancer, wear debris induced osteolysis or osteoarthritis, and immune diseases such as psoriasis, insulin-dependent diabetes, inflammatory bowel disease or multiple sclerosis. The present sequence represents the heavy chain variable region of the murine monoclonal antibody 14F3 of the invention. The sequence contains three complementary determining regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bone cancer; osteolysis; osteoarthritis; immune disease; psoriasis; insulin-dependent diabetes; inflammatory bowel disease; multiple sclerosis; heavy chain variable region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New monoclonal antibody having the characteristics of a monoclonal antibody 14F3, useful for treating or preventing osteopathic diseases, e.g. rheumatoid arthritis, or osteoporosis, and immune diseases e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sweet
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                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel monoclonal antibody having the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 8; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
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)B; ABV99887.
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SMITHKLINE BEECHAM PLC.
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaposi's sarcoma; rheumatoid arthritis; macular degeneration; sickle cell anaemia; Paget's disease; mycobacterial infection; osteoarthritis; graft versus host disease; autoimmune disease; type I dishares.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse; angiogenin; angiogenesis; tumour; cancer; retinopathy; ocular neovascular disease; vitamin A deficiency; syphilis;
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                                                                                                                                                                                                                                                    New antibody immunologically reactive to angiogenin useful for inhibiting angiogenesis and for treating conditions associated abnormal angiogenesis e.g. cancer, ocular neovascular disease, rheumatoid arthritis
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20..140
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The invention relates to an antibody immunologically reactive to angiogenin or a fragment of angiogenin comprising light and heavy chain nonhuman-derived complementarity determining regions having a binding affinity to the angiogenin or its fragment in combination with human derived polypeptide regions (e.g. mouse monoclonal antibody 26-27). Also included are an expression vector comprising a nucleic acid

encoding

the antibody

and a host cell transformed

with the vector.

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AAU72801
ID AAU7
XX AAU
AC AAU
DT 26-
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CC clerosis, systemic lupus erythematosus, and myasthenia gravis. The created by the indexer using the sequence appearing as AAD76122 and the CC information in the claims.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                          allergy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; cancer; antibody; chromosome 8p2:
                                                     08-NOV-2001
                                                                                                                                         WO200183560-A1
                                                                                                                                                                                                                                      Mus musculus
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Sequence

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CC necrosis factor (TNP)-related apoptosis inducing ligand (TRAII) receptor CC DR5 (located on chromosome Bp21-22). The antibody has apoptosis-inducing CC activity to a cell expressing DR5 in vivo. It is also useful for CC preparing a therapeutic for selective apoptosis of abnormal or CC dysregulated cells, and for inhibiting cell proliferation in a cell, preferably a human breast, ovary, colon, haematopoietic, prostate, colon, haematopoietic, prostate, colon, haematopoietic, prostate, colon, haematopoietic, prostate, colon, haematopoietic, prostate, colon, haematopoietic, prostate, colon, haematopoietic, prostate, colon, haematopoietic, prostate, colon, haematopoietic, prostate, colon, haematopoietic, prostate, colon, haematopoietic, prostate, colon, haematopoietic, prostate, colon, haematopoietic, prostate, colon, haematopoietic, prostate, colon, haematopoietic, prostate, colon, haematopoietic, prostate, colon, haematopoietic, prostate, colon, haematopoietic, prostate, colon, haematopoietic, prostate, colon, haematopoietic, prostate, colon, haematopoietic, cardiomyopathy, coloneximal haematopoietic, prostate, liver, coloneximal haematopoietic, prostate, liver, covary, lymphatic or breast tissue. Peptides used to design primers for colating heavy and light chain cona of the mouse Trail (AAU72801) and colon, the mouse trail (AAU72801), TRA-8 are shown in AAU72799 and AAU72800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel antibody specific for tumour necrosis factor-related apoptosis-inducing ligand, useful for inhibiting cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes a novel antibody which recognizes a tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 26; Page 198-199; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAS97062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-049338/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-MAY-2000; 2000US-201344P
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RBSULT 11
AAB20436
ID AAB20
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AC AAB20
XX
DT 21-JU
XX
DE Anti-
XX
KW Factc
KW Factc
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Chimeric - Mus musculus
                    Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.
                                                                                                        21-JUN-2001
                                                                           Anti-FIX/FIXa antibody 198/A1 scrv
                                                                                                                                                       AAB20436 standard; Protein; 249
                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                   121
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                                                                                                                                                                                                                                                                                                                                              1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                   $ 121
                                                                                                                                                                                                                                                                                                     PDSVRGRETISRDNAKNTLYLOMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS
                                                                                                                                                                                                                                                                                                                              EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSHVRQTPBKRLEHVATISSGGSYTYY
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                84.8%;
                                                                                                                                                                                                                                                                                                                                                                                    4.
                                                                                                                                                                                                                                                                                                                                                                                               Score 545; DB 23; pred. No. 5.3e-43;
                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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Chimeric

Synthetic

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                                                                                                                                            Query Match
Best Local Simi
Matches 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                  inhibitor patients. The antibodies and derivatives are used in a claimed pharmaceutical composition for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scheiflinger F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-SEP-1999;
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                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 10; Fig 17; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BAXT )
                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-290358/30.
 121
                       120
                                               63
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                       SS
                                                                                                               PDSVKGRFTISRDNAKNTLYLOMSSLKSEDTAMYHCTREGGGYYVNWYFDVWGAGTTLTV
                                                             PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGS-SFDYMGQGTTLTV
                                                                                               EVQLQESGGGLVKPGGSLKLSCAASGFIFSSXTMSWVRQTPEKRLEWVATISSGGSSTYY
                                                                                                                                                                                               249
                       121
                                                                                                                                                Conservative
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                                                                                                                                                                                               AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     labe.
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                                                                                                                                                           84.7%;
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Pred.
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                                                                                                                                               Mismatches
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                                                                                                                                                           No. 2.9
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                                                                                                                                                            .9e-43;
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                                                                                                                                                Indels
                                                                                                                                                                     Length
                                                                                                                                                                        249;
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                                                                                                                                             Gaps
                                                                      119
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RESULT 12
AAB20442
IID AAB20
XX AAB20
AC AAB20
AC AAB20
XX DIT 21-JU
XX Pactc
XW Factc
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Chimeric
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Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-FIX/FIXa antibody 198/B1-myc-tag fusion
                                                                                                                                                                                                                         coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-2000; 2000WO-EP08936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200119992-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
Factor VIII cofactor; blood coagulation disorder; haemophilia A
                                                                                                                                                                              Example 18;
                                                                                                                                                                                                                         New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
                                                                                                                                                                                                                                                                                                                                                                              Scheiflinger F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                             (BAXT ) BAXTER
                                                                                                                                                                                                                                                                                                              2001-290358/30.
DB; AAF30732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus.
                                                                                                                                                                          Fig 34; 138pp;
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23..294
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287..288
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                                                                                                                                                                                                                                                                                                                                                                                Kerschbaumer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= His_tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "encoded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           abel=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   abel- VL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .abel= Linker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spacer
                                                                                                                                                                            English.
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                                                                                                                                                                                                                                                                                                                                                                                   Falkner
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                                                                                                                                                                                                                                                                                                                                                                                   Dorner
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The present sequence is that of a fusion protein comprising: a PelB leader; a single chain Fv (6cFv) derivative of antibody 198/B1 comprising the heavy (VH) and light (VL) chain variable regions of 198/B1 joined by an artificial, flexible linker peptide; a spacer; a Myc-tag peptide; a spacer; and a C-terminal 6His affinity tail.
198/B1 is an example of anti-human Factor IX (FIXA) antibodies and IX (FIXA) antibodies of the invention. Anti-FIX/FIXA antibodies and

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RESULT 13
AAB20438
ID AAB20
XX AAB20
AC AAB20
XX AR1:-
XX Pacto
XW Pacto
XW Pacto
XW Pacto
XW Pacto
XW Chime
OS Chime
CS Chime
CS Chime
FT Pepti
FT Prote
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              their derivatives, including scFv fragments, have FVIIIa cofactor activity or FNX activating activity. Administration leads to an increase in the procoagulant activity of FIXA, even in the presence of FVIIIa inhibitors. This allows for rapid blood coagulation even in the absence of FVIII or FVIIIa, and in the case of FVIII inhibitor patients. The antibodies and derivatives are used in a claimed pharmaceutical composition for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic diathesis. The scFv-myc-tag fusion was expressed in B. coli. It exhibited FVIII-like activity.
                                                                                                                                                                                                                                                                                                                                                                     Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                            Factor IX, FIX; Factor IXa; FIXa; miniantibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse; bivalent antibody; plasmid pZip-198AB2#102.
              Protein
                                                                     Misc-difference
                                                                                                Misc-difference
                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                         Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-FIX/FIXa antibody 198/B1 bivalent miniantibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB20438 standard; Protein; 325 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDSVKGRETISRDNAKNTLYLQMSSLRSEDTAMYYCTREGG-GFTVNWYFDVWGAGTSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDSVRGRFTISRDNAKNTLYLOMSSLKSEDTAMYYCTRDGGHGYGSS--FDYWGQGTTLT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVKLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY 82
                                                                                                                                                                                                                                                                                                                                                        Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                          /label= Spacer
                                                                                                                                                        145..159
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
/label= Hinge
                                                                                   /note= "encoded
                                                                                                                                          /label= Linker
                                                                                                                                                                                                                                                                                 /label= Signal_peptide
/note= "PelB leader"
                                                                                                               'label= VL
                                                                                                                                                                    'note= "encoded
                                                                                                                                                                                                'label= VH
                                                                                                                                                                                                                                                    'label= Mature_protein
                                                        note= "encoded
                                                                                                                                                                                                                          label= scrv
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                                                                                                                            .271
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Pred. No. 3.5e-43;
9; Mismatches 5
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                                                        TCN.
                                                                                                                                                                      GGN.
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                                                                                                                                                                                                                                                                                                                                         The present sequence is that of a bivalent miniantibody comprising CC a PelB leader peptide, the single chain Fv (scFv) fragment of antibody 198/B1 (subclone AB2), an amphipathic helical structure CC and a C-terminal GHIs tag. The protein was expressed in Escherichia coli from plasmid pZip198AB2#102 (see AAF30728). Antibody 198/B1 is an example of anti-human Factor IX (FIX)/activated Factor IX (FIX) antibodies of the invention. CC Anti-FIX/FIXa activating activity. Administration leads to an increase in the procoagulant activity of FIXa, even in the presence CC of FVIIIa inhibitors. This allows for rapid blood coagulation even CC in the absence of FVIII or FVIIIa, and in the case of FVIII or FVIII or FVIIIa inhibitors. The antibodies and derivatives are used in a CC inhibitor patients. The antibodies and derivatives are used in a CC claimed pharmaceutical composition for treating patients with blood coagulation disorders, especially haemophilia A and haemoxrhagic continty. The bivalent miniantibody exhibited FVIII-like
                                                                                                                                                                                                                                                                                                       Query Match
AAB20437 standard; Protein; 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 16; Fig 28; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scheiflinger F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-2000; 2000WO-EP08936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200119992-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BAXT ) BAXTER
                                                                                                                                                                                                                                                                                        Local
                                                                             142
                                                                                                           119 VSS 121
                                                                                                                                                                                                                                                                       106;
                                                                                                                                           83
                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                             PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSS--FDYWGQGTTLT
                                                                                                                                           PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGG-GFTVNWYFDVWGAGTSVT
                                                                                                                                                                                                                                      EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
                                                                                                                                                                                                                                                                                                                                      325
                                                                                                                                                                                                                                                                    84.7%;
ilarity 86.2%;
Conservative
                                                                             144
                                                                                                                                                                                                                                                                                                                                    AA;
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/label= Helix
320..325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kerschbaumer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= His_tag
                                                                                                                                                                                                                                                                    ; Score 544.5; ]; Pred. No. 3.9e
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Falkner F,
                                                                                                                                                                                                                                                                 ; 2-
3.9e-43;
5;
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                                                                                                                                                                                                                                                                                                    Length
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Anti-FIX/FIXa antibody 198/B1-alkaline phosphatase fusion

21-JUN-2001 AAB20437;

(first entry)

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The present sequence is that of a fusion protein comprising: a PelB cleader; a single chain Fv (scFv) derivative of antibody 198/B1 comprising the heavy (VH) and light (VL) chain variable regions of 198/B1 joined by an artificial, flexible linker peptide; a spacer; Escherichia coli alkaline phosphatase; and a C-terminal 6His affinity tail. 198/B1 is an example of anti-human Factor IX (FIX)/activated Factor IX (FIX) antibodies of the invention. Anti-FIX/FIXa antibodies and their derivatives, including scFv fragments, have FVIIIa cofactor activity or FIXa activating activity. Administration leads to an increase in the procoagulant activity of FIXa, even in the presence of FVIIIa inhibitors. This allows for rapid blood coagulation even in the absence of FVIII or FVIIIa, and in the case of FVIII hibitor patients. The antibodies and derivatives are used in a claimed pharmaceutical composition for treating patients with blood coagulation disorders, especially haemophilia A and haemornhagic diathesis. The scFv-alkaline phosphatase was expressed in E. coli. It exhibited continued the scFv-alkaline phosphatase was expressed in E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
                                                                                                                                                                                                                                                                                                                               New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Scheiflinger F,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200119992-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                    Example 16; Fig 26; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BAXT ) BAXTER
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DB; AAB30727.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphatase.
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Synthetic.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99AT-0001576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Mature_protein
23..271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276..725
                                                                                                                                                                                                                                                                                                                                                                                                                                      Kerschbaumer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= His_tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= Alkaline_phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145..159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= Signal_peptide
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label= VL
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Sequence

732

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61

61

EVQGVESGGGLVKPGGSLKLSCAASGFTFSDYYMYWVRQTPEKRLEWVATISDGGSYTYY 

118 120

60 60

PDSVKGRETISRDNAKNNLYLQMSSLKSEDTAMYYCARDKAYYGNYGDAMDYWGQGTSVT PDSVRGRETISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGH--GYGSSEDYWGQGTTLT Query Match Best Local S Matches 104

Similarity

84.3%; ilarity 84.6%; Conservative

Score 542; DB 21; Pred. No. 2.3e-43; 5; Mismatches 12

12:

Indels

<u>ب</u>

Gaps

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21;

Length 123;

104;

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119

VSS 121

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Best Local S
Matches 106
                   of the variable domain of an antibody for detection, immunotherapy or for scintigraphs. The peptides of the invention are used in a method to detect analytes in a sample by eliminating interference in the sample. AAY51254-Y51267 represent peptides derived from the framework regions of the variable domain of an antibody which are used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                      Framework region; monoclonal antibody; variable domain; detection; immunotherapy; MAK 33.
                                                                                                                                                                                                                                                                                                                                                                      Monoclonal
                                                                                                                                                                                                                                                                                                                                                                                             14-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY51266 standard;
                                                                            This invention describes novel peptides derived from a framework re
                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                  AAY51266;
Sequence
                                                                                                                                                        WPI; 2000-107255/10
                                                                                                                                                                             Nussbaum S,
                                                                                                                                                                                                                        26-JUN-1998;
                                                                                                                                                                                                                                               26-JUN-1998;
                                                                                                                                                                                                                                                                    30-DEC-1999.
                                                                                                                                                                                                                                                                                         DE19828466-A1.
                                                                                                             Disclosure; Page 18; 20pp; German.
                                                                                                                                                                                                  (HOFF ) ROCHE DIAGNOSTICS GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDSVRGRETISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSS--FDYWGQGTTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVKLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKKLEWVATISSGGSSTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVQLVBSGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSS 144
                                                                                                                                                                                                                                                                                                                                                                      antibody MAK 33 heavy chain variable region peptide.
                                                                                                                                  peptides derived from antibodies for use in immunoassays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
123 AA;
                                                                                                                                                                             Moessner E,
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                        98DE-1028466
                                                                                                                                                                                                                                                98DE-1028466
                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide;
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                                                                                                                                                                               Lenz H,
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Pred. No. 9.8e-43;
9; Mismatches 5
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                                                                                         framework region
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121 VSS 123

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Search completed: November 7, 2003, 07:27:02 Job time: 53.1802 Becs

Page 11

OM protein -

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pand is derived by analysis of the total score distribution.
                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*

1: /cgn2=6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2-6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /cgn2-6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2-6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

5: /cgn2-6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

6: /cgn2-6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

6: /cgn2-6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2-6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2-6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

10: /cgn2-6/ptodata/2/pubpaa/US09E PUBCOMB.pep:*

11: /cgn2-6/ptodata/2/pubpaa/US09E PUBCOMB.pep:*

12: /cgn2-6/ptodata/2/pubpaa/US09E PUBCOMB.pep:*

13: /cgn2-6/ptodata/2/pubpaa/US09E PUBCOMB.pep:*

14: /cgn2-6/ptodata/2/pubpaa/US09E PUBCOMB.pep:*

15: /cgn2-6/ptodata/2/pubpaa/US10E PUBCOMB.pep:*

16: /cgn2-6/ptodata/2/pubpaa/US10E PUBCOMB.pep:*

16: /cgn2-6/ptodata/2/pubpaa/US10E PUBCOMB.pep:*

17: /cgn2-6/ptodata/2/pubpaa/US10E PUBCOMB.pep:*

16: /cgn2-6/ptodata/2/pubpaa/US10E PUBCOMB.pep:*

17: /cgn2-6/ptodata/2/pubpaa/US10E PUBCOMB.pep:*

18: /cgn2-6/ptodata/2/pubpaa/US10E PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                          %
Query
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195.799 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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        US-09-286-240-4
US-09-881-823-12
US-10-977-624-7
2 US-10-275-180A-61
2 US-10-275-180A-62
2 US-10-286-132A-61
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2 US-10-286-132A-23
3 US-10-286-132A-23
3 US-10-275-180A-23
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3 US-09-144-886-63
5 US-09-144-886-63
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Sequence 12, Appli
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Sequence 63, Appl
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g printed,
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Patent No. US20020010320A1

GENERAL INFORMATION:
APPLICANT: Fett, James W

TITLE OF INVENTION: Chimeric and Humanized Antibodies to Angiogenin
FILE REFERENCE: 10498/74073

CURRENT APPLICATION NUMBER: US/09/286,240

CURRENT FILING DATE: 1999-04-05

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 140

TYPE: PRT

ORGANISM: Mus musculus

US-09-286-240-4
                           RESULT 2
US-09-881-823-12
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US-09-286-240-4
     Sequence 12,
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Similarity 86.0%;
.04; Conservative
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  Application US/09881823
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2 US-10-281-479A-60
2 US-10-286-132A-60
0 US-09-144-886-60
1 US-09-518-737-2
1 US-10-206-733-3
2 US-10-206-73-4
2 US-10-300-215-90
3 US-10-300-215-90
3 US-10-300-215-133
0 US-09-144-886-64
5 US-10-305-268-2
0 US-09-144-886-64
5 US-10-286-132A-56
2 US-10-286-132A-56
2 US-10-286-132A-59
0 US-09-917-410-4
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0 US-10-286-132A-59
0 US-10-286-132A-59
0 US-10-286-132A-59
0 US-10-286-132A-59
0 US-10-286-132A-59
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0 US-10-286-132A-31
2 US-10-286-132A-31
2 US-10-286-132A-31
2 US-10-286-132A-31
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Pred. No. 8.6e-44;
8; Mismatches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 140;
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Result No.

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                                                               ; OTHER INFORMATION: Synthesized using squential PCR techniques
US-10-077-624-7
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                                                                                                                                                                                  APPLICANT: Q1. Fengxia
TITLE OF INVENTION: ANTI-MICROBIAL TARGETING CHIMERIC PHARMACEUTICAL
FILE REFERENCE: 2101363-991200
CURRENT APPLICATION NUMBER: US/10/077,624
CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 09/910,358
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 09/378,577
PRIOR APPLICATION NUMBER: US 09/378,577
SPOID NOT SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA APPLICANT: WASHINGTON DENTAL SERVICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/10077624 Publication No. US20030143234A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SHI, WENYUAN
APPLICANT: ANDERSON, MAY
APPLICANT: MORRISON, SHI
APPLICANT: TRINH, RYAN
APPLICANT: WIMS, LETITII
APPLICANT: CHEN, LI
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/881,823
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 07/378,577
PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Method for the Treatment FILE REFERENCE: 22851-032
                                                                                                         FEATURE:
                                                                                                                         LENGTH: 155
TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 144
TYPE: PRT
ORGANISM: Murine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anderson, Maxwell
Morrison, Sherie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shi, Wenyuan
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CHEN, LI
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MORRISON, SHERIE
TRINH, RYAN
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Chen, Li
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84.7%;
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84.7%; Pred. No. 1.1e-43;
Score 551;
Pred. No. :
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1.2e-43;
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APPLICANT: Qi, Fengxia
TITLE OF INVENTION: ANTI-MICROBIAL TARGETING CHIMERIC PHARMACEUTICAL
FILE REFERENCE: 201363-991200
CURRENT APPLICATION NUMBER: US/10/077,624
CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 09/910,358
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 09/378,577
PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 31
SOFTMARE: PATENTIN OF SEQ ID NOS: 31
IRNOTATE: 1997-08-20
IRNOTATE: 1997-08-20
IRNOTATE: 1997-08-20
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                                                                                                                                                                      RESULT 5
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US-10-077-624-4
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                                                                                  Sequence 61, Application US/10281479A Publication No. US20030133932A1 GREERAL INFORMATION:
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Best Local :
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                           APPLICANT: The UAB Research Foundation APPLICANT: Zhou, Tong APPLICANT: Ichikawa, Kimihisa
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APPLICANT:
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TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
                                                                                                                                                                                                                               160
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Zhou, Tong
Ichikawa, Kimihisa
Kimberly, Robert P.
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Morrison, Sherie
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; OTHER INFORMATION:
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US-10-275-180A-61
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US-10-281-479A-61
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PRIOR FILING DATE: 2002-06-24
PRIOR PELICATION NUMBER: 60/346,402
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR APPLICATION NUMBER: 60/201,344
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-05-02
NUMBER OF EQUID NOS: 102
NUMBER OF EQUID NOS: 102
                                                                                                                                                                                                                                                                               APPLICANT: Ichikawa, Kimihisa
APPLICANT: Komberly, Robert P.
APPLICANT: Komberly, William J.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOS
TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF
FILE REFERENCE: 21085.0029U5
CURRENT APPLICATION NUMBER: US/10/275,180A
CURRENT FILING DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 102
SOFTWARDER OF SEQ ID NOS: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 61, Application US/10275180A Publication No. US20030190687A1 GENERAL INFORMATION:
Query Match
Best Local Similarity
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SEQ ID NO 61
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Best Local Similarity
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APPLICANT: Oshumi, Jun
APPLICANT: Oshumi, Jun
APPLICANT: LOBUGLIO, Albert S.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTF
TITLE OF INVENTION: AGENTS
                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: The UAB Research Foundation
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                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                               TYPE: PRT
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ORGANISM: artificial sequence
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                                                                                          Description of Artificial Sequence:/No. US20030190687Ale = Synthetic Construct
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Pred. No. 3.2e-43;
Score 545; DB 12;
Pred. No. 3.2e-43;
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                    Length 119;
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RESULT 8
US-10-281-479A-23
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                                                                            Sequence 23, Application US/10281479A Publication No. US20030133932A1 GENERAL INFORMATION:
APPLICANT: The UAB Research Foundation
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Best Local :
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Publication No. US20030198637A1
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CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US 60/346,402
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR PILING DATE: 2001-05-02
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-05-02
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APPLICANT: Kimberly, Robert P.
APPLICANT: Kopman, William J.
APPLICANT: Kopman, William J.
APPLICANT: LoBuglio, Albert S.
APPLICANT: Buchsbaum, Donald J.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: AND AVTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF FILE REFERENCE: 21085.0029U7
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      APPLICANT:
                                            APPLICANT:
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ORGANISM: artificial sequence
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Ichikawa, Kimihisa
Kimberly, Robert P.
Koopman, William J.
                                                             Zhou, Tong
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Pred. No. 3.2e-43;
4; Mismatches 9
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CURRENT APPLICATION NUMBER: US/10/281,479A
CURRENT FILLING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: 60/391,478
PRIOR FILLING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 60/346,402
PRIOR APPLICATION NUMBER: 60/346,402
PRIOR FILING DATE: 2001-11-01
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,344
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-05-02
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Sequence 23, Application US/10286132A
Publication No. US20030198637A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         FILE REFERENCE: 21085.0029U7
CURRENT APPLICATION NUMBER: US/10/286,132A
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US 60/346,402
PRIOR PRILING DATE: 2001-11-01
PRIOR PRPLICATION NUMBER: PCT/US01/14151
PRIOR PILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/201,344
PRIOR PILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: US 60/201,344
PRIOR PILING DATE: 2000-05-02
NUMBER: OF SEQ ID NOS: 102
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Best Local Similarity 87.6
Matches 106; Conservative
                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.0 SEO ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kimberly, Robert P.
APPLICANT: Kimberly, Robert P.
APPLICANT: Koppman, William J.
APPLICANT: LoBuglio, Albert S.
APPLICANT: LoBuglio, Popular J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LOBUGLIO, Albert S.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THEN TITLE OF INVENTION: AGENTS FILE REFERENCE; 21085.0029U6
                                                                                                                                      LENGTY: 462
TYPE: PRT
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TYPE: PRT
OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637Ale = Synthe
                                                                                ORGANISM: artificial sequence
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Pred. No. 1
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RESULT 11
US-09-144-886-63
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APPLICANT: Ichikawa, Kimihisa
APPLICANT: Ichikawa, Kimihisa
APPLICANT: Kimberly, Robert P.
APPLICANT: Koopman, William J.
APPLICANT: Koopman, William J.
APPLICANT: Koopman, William J.
APPLICANT: Koopman, William J.
APPLICANT: Koopman, William J.
APPLICANT: Koopman, William J.
APPLICANT: APPLICANTON: INDUCING LIGAND RECEPTOR AND USES THEREOF
FILE REFERENCE: 21085,0029US
CURRENT APPLICATION NUMBER: US/10/275,180A
CURRENT FILING DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
                                                                                                                     Sequence 63, Application US/09144886 Patent No. US20020155114A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                 APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.117USO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: The UAB Research Foundation APPLICANT: Zhou, Tong APPLICANT: Ichikawa, Kimihisa APPLICANT: Kimberly, Robert P. APPLICANT: Koopman, William J.
CURRENT APPLICATION NUMBER: US/09/144,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 464
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e = OTHER INFORMATION: Synthetic Construct
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Pred. No. 1.4e-42;
4; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
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Pred. No. 1.4e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 464;
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RESULT 13
US-09-423-800-46
; Sequence 46, Application US/09423800
; Fatent No. US20020165363A1
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; OTHER INFORMATION: C39 region VH epitope 2
US-09-144-886-62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 62
LENGTH: 118
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 62, Application US/09144886 Patent No. US20020155114A1 GENERAL INFORMATION;
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LENGTH: 118
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 84.3
Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.117USO
CURRENT FAPPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone OTHER INFORMATION: C25 region VH epitope 2
                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                   118 S 118
                                                                                                                                                         121 $ 121
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                                                                                                                                                                                                                                                                                                           1 EVOLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKKLEWVATISSGGSYTYY
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                                                                                                                                                                                                                                                                       QVQLQESGGGSVKPGGSLKLSCAASGFTFSDYYMSWVRQTPEKRLEWVATISDGGSYTYY 60
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83.5%;
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Pred. No. 1.6e-41;
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Pred. No. 4.6e-42;
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FILE REPERENCE: 04853-0036
CUDRENT APPLICATION NUMBER: US/09/423,800
CUDRENT FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: PCT/JEP8/02116
PRIOR APPLICATION NUMBER: PCT/JEP8/02116
PRIOR APPLICATION NUMBER: JP 125505/1997
PRIOR FILING DATE: 1997-05-15
PRIOR APPLICATION NUMBER: JP 194445/1997
PRIOR APPLICATION NUMBER: JP 194445/1997
PRIOR APPLICATION NUMBER: JP 194445/1997
PRIOR FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 46
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; Sequence 46, Application US/10337981
; Publication No. US20030138424A1
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                                                                                                                                                                                                                                                   APPLICANT: TSUMENARI, TOSHIAKI
APPLICANT: ISHI, KIMIE
FILE OF INVENTION: CACHEXIA REMEDY
FILE REFERENCE: 04853-0036
CURRENT APPLICATION NUMBER: US/10/337,981
CURRENT FILING DATE: 2003-01-08
FRIOR APPLICATION NUMBER: US/10/398/02116
PRIOR RILING DATE: 1998-05-13
FRIOR RILING DATE: 1998-05-13
FRIOR APPLICATION NUMBER: UF 125505/1997
FRIOR APPLICATION NUMBER: UF 194445/1997
FRIOR FILING DATE: 1997-05-18
PRIOR APPLICATION NUMBER: UF 194445/1997
FRIOR FILING DATE: 1997-07-18
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                                                                                                                                                                          NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver.
SEQ ID NO 46
LENGTH: 118
                                                          Query Match
Best Local Similarity
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APPLICANT: TSUN
                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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TITLE OF INVENTION:
FILE REFERENCE: 048
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TYPE: PRT
ORGANISM: Homo sapiens
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1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY 60
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                                         Conservative
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                                                          81.4%;
83.5%;
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                                       7; Mismatches
                                                          Score 523.5;
Pred. No. 3.1
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Pred. No. 3.1e-41;
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                                                          3.1e-41;
                                                                            DB 12;
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EVQLVESGGDLVKPGGSLKLSCAASGFTFSSYGMSWIRQTPDKRLEWVATISSGGSYTYY

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RESULT 15
US-10-182-018-46

US-10-182-018-46

Sequence 46, Application US/10182018

Publication No. US20030049211A1

GENERAL INFORMATION:

APPLICANT: CUUGAI SEIYAKU KABUSHKI KAISHA

TITLE OF INVENTION: THERAPEUTIC AND PREVENTIVE AGENTS FOR DENTAL DISEASES

FILE REFERENCE: PH-1092-PCT

CURRENT APPLICATION NUMBER: US/10/182,018

CURRENT FILING DATE: 2002-07-24

PRIOR APPLICATION NUMBER: JP 2000-83034

PRIOR FILING DATE: 2000-01-25

NUMBER OF SEQ ID NOS: 75

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 46

LENGTH: 118

TYPE: PRI

ORGANISM: Mus musculus
Search completed: November 7, 2003, 08:16:53 Job time: 107.138 secs
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                                                                                                                                                                                                                                                                                     Query Match 81.4%; Score 523.5; DB 15; Length 118; Best Local Similarity 83.5%; Pred. No. 3.1e-41; Matches 101; Conservative 7; Mismatches 10; Indels 3;
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                                                                                                                                                                       61 PDSVRGRFTISRDNAKNTLYLOMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS 120
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Post-processing: Minimum Match 0% Maximum Match 100%
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seq length: 2000000000
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Gapop 10.0 ,
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643
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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  US-09-344-587-13
US-08-579-378A-16
US-08-435-516-3
US-08-435-516-3
US-08-435-516-3
US-08-435-516-3
US-08-653-402B-2
US-08-653-497A-13
US-08-553-497A-13
US-08-553-497A-13
US-08-553-497A-20
US-08-339-582-2
US-08-339-582-2
US-08-331-39-582-2
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US-08-653-402B-10
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US-07-956-399-4
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13, Appl

16, Appli

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Patent No. 6331402

GENERAL INFORMATION:
APPLICANT: Prast, Gerald
APPLICANT: Nossbaum, Sabine
APPLICANT: Nossbaum, Sabine
APPLICANT: Mossbaum, Sabine
APPLICANT: Mossbaum, Sabine
APPLICANT: Mossbaum, Sabine
TITLE OF INVENTION: REDUCTION OF INTERFERENCE OF IMMUNOASSAYS BY SUBSTANCES
TITLE OF INVENTION: REDUCTION OF INTERFERENCE OF ANTIBODIES
TITLE OF INVENTION: REDUCTION OF THE FRAMEWORK REGIONS OF ANTIBODIES
TITLE OF INVENTION: MAD 9228 4897/00/US-Im
CURRENT FILING DATE: 1992-06-25
EARLIER APPLICATION NUMBER: US/09/344,587

CURRENT FILING DATE: 1998-06-25

EARLIER APPLICATION NUMBER: DE 19828466.7

EARLIER APPLICATION NUMBER: DE 19828466.7

EARLIER APPLICATION NUMBER: DE 19828466.7

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EARLIER DE 19828466.7

EARLIER APPLICATION NUMBER: DE 19828466.7

EARLIER APPLICATION NUMBER: DE 19828466.7

EARLIER APPLICATION NUMBER: DE 19828466.7
                                                                                                                              RESULT 2
US-08-579-378A-16
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US-09-344-587-13
                  Sequence 16, Application US/08579378A
Patent No. 6210671
GENERAL INFORMATION:
APPLICANT: Co, Man Sung
TITLE OF INVENTION: Humanized Ant
TITLE OF INVENTION: L-Selectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  491.5
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                                                                                                                                                                                                                                                                                                                 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGH--GYGSSFDYMGQGTTLT
                                                                                                                                                                                                                                                                                                                                                                                          EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
                                                                                                                                                                                                                VSS 123
                                                                                                                                                                                                                                                                                      PDSVKGRFTISRDNAKNNLYLOMSSLKSEDTAMYYCARDKAYYGNYGDAMDYWGQGTSVT
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US-09-434-122-3
US-09-434-122-3
US-09-434-122-3
US-09-434-122-3
PCT-US94-14106-59
US-08-926-789-16
US-08-926-789-18
US-08-926-789-18
US-09-420-592A-5
US-09-420-592A-5
US-09-431-199-16
US-08-483-199-16
US-08-484-508-16
US-08-484-508-16
US-08-484-508-16
US-08-316-786-31
US-08-452-164A-57
US-08-452-164A-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 542; DB 4;
Pred. No. 4.5e-50;
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513.5
510.5
505.5
505.5
502.5
502.5
500.5
496

Score

Match

Query

Maximum

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Scoring table: Sequence: Title: Perfect score:

Sequence

6, Appli 23, Appli 23, Appli 29, Appli 16, Appli 18, Appli 18, Appli 18, Appli 16, Appli 16, Appli 16, Appli 16, Appli 16, Appli 16, Appli 16, Appli 16, Appli 16, Appli 16, Appli 17, Appli 18, Appli 19, Appli 19, Appli

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US-08-579-378A-16
                                                                                                                                                           Sequence 1, Application US/08875674A Patent No. 6572857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/160,074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95114696.8
APPLICATION NUMBER: EP 95114696.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 16:
                                                                  APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/160,074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CORRESPONDENCE ADDRESS:
                  NUMBER OF SEQUENCES:
                                     TITLE OF INVENTION:
                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Liebescheutz, Joe O. REGISTRATION NUMBER: 37,505 REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0:
FILING DATE: 27-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                     135 S 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103;
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One MarketPlaza, Steuart Tower, Suite 2000
                                                                                                                         MONTERO
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                                               P REZ RODR GUEZ,
SIERRA BL ZQUEZ,
TORMO BRAVO, B. R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                          LOMBARDERO
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                                  Anti-CD6 monoclonal antibodies and their uses
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                                                                                                                       CASIMIRO, J.
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                                                                                                      VALLADARES, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11823-002220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 531.5; DB 3
Pred. No. 6.4e-49;
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US-08-435-516-3
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OTHER INFORMATION: Sequence corresponding to the variable region
Patent No. 6572857

OTHER INFORMATION: of the heavy chain of the monoclonal antibody
OTHER INFORMATION: designated as sub-clone for tlA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                       GENERAL INFORMATION:
APPLICANT:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 17-July-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNDER: PCT/CU9
APPLICATION UNDER: PCT/CU9
FILING DATE: 18-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: HENRY A. MARZULLO, JR
REGISTRATION NUMBER: 20,910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIVIDUAL ISOLATE: io TISSUE TYPE: Murine hi IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: -N Terminal fragment.
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: P-12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 723-4300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Word Perfect 5.0 for Windows 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,674A
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  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk 3.5' (1.4 MB).
COMPUTER: Compatible PC IBM (80486, 8 M Ram).
OPERATING SYSTEM: Windows 95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: Amino acid.
STRANDEDNESS: Unkn
TOPOLOGY: Unknown.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                    118 SS 119
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                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                      61 PDSVRGRETISRDNAKNTLYLOMSSLKSEDTAMYYCT-RDGGHGYGSSFDYWGQGTTLTV 119
                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY 60
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                                                                                                                                                                                                                                                                 PDSVKGRFTISRDNVKNTLYLQMSSLRSEDTAMYYCARRDYDLDY--
                                                                                                                                                                                                                                                                                                                                               EVOLVESGGGLVKPGGSLKLSCAASGFKFSRYAMSWVRQTPEKRLEWVATISSGGSYIYY
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HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
                                                                             US/08435516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the heavy chain of the monoclonal antibody recognidesignated as sub-clone for tlA.
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Pred. No. 2.1e-48;
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                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08356272
Patent No. 5766946
GENERAL INFORMATION:
APPLICANT: Ciantriglia Dr., Mau
TITLE OF INVENTION: Monoclonal
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,272
FILING DATE: 15-DEC-1994
CLASSIFICATION: 435
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Best Local Similarity
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                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Monoclonal Antibodies to glycoprotein NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESS: Patent and Trademark Department, Sandoz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: MX TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 42.TION:
CLASSIFICATION: 42.TION:
ATTORNEY/AGENT INFORMATION:
NAME: ATTORNEY/BER: 35,430
MAME: MIMBER: 35,430
MX
                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 07936
OMPUTED TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA.
APPLICATION NUMBER: UK 92
FILING DATE: 04-NOV-1992;
CLASSIFICATION: 424
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NUMBER OF SEQUENCES: 2
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                          CITY: East Hanover
                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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GY: linear
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59 Route 10
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                                                                        Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UK 92 23377.4; PCT/US93/10384
V-1992; -02-NOV-1993
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Pred. No. 4.5e-47;
7; Mismatches 14
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PCT-US94-07659-2
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application PC/TUS9407659 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
            ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPES Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER:
COMPUTER: PLANTIN PC-DOS/MS-DOS
SOFTMARE: PATENTIN Release #1.0, VCURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 16-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Battle, Carl W.
REGISTRATION NUMBER: 30,731
REFERENCE/DOCKET NUMBER: 118
TELECOMMUNICATION INFORMATION:
TELESCOMMUNICATION INFORMATION:
TELESCOMMUNICATION INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                    TITLE OF INVENTION: Recombinan TITLE OF INVENTION: Antibodies TITLE OF INVENTION: Disorders: NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                          CITY: King of Prussia STATE: PA
                                                                                                                                                                                        ADDRESSEE: SmithKline Beecham Corporation - Corp
                                                                                                                                                                              STREET:
                                                                                                                              COUNTRY:
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CLASSIFICATION:
CLASSIFICATION:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                              709 Swedeland Road
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Jonak, Zdenka L.
                                                                                                                               USA
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Hurle, Mark
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                                                                                                                                                                                                                                                                                                                                                                                        Young, Peter
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G01N33/577
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83.7%;
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Antibodies for Treatment of II-1 Mediated Inflammatory
                                                                                                                                                                                                                                                            Disorders in Man
                                                                                                                                                                                                                                                                                                                                           Timothy
PCT/US94/07659
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Pred. No. 9.6e-47
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                             Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOCY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oequence 2, Application US/08653402B
Patent No. 5969107
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Best Local Similarity 82.0%;
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/653,402B
FILING DATE: 24-MAY-1996
CLASSIFICATION AJ5
CLASSIFICATION DATA:
APPLICATION NUMBER: EP 95107967.2
FILING DATE: 26-MAY-1995
ATTORNEY/AGENT INFORMATION:
ANAME: Leboyitz, Richard M.
REGERRENCE/DOCKET NUMBER: MERCK 1781
REFERRENCE/DOCKET NUMBER: MERCK 1781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: CARCEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: SUTTON, Jeffrey A. REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50171-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Anti-idiotypic antibodies which induce an TITLE OF INVENTION: immune response against epidermal growth factor receptor NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CARCELLER, Ana
APPLICANT: ROSELL, Elisabet
APPLICANT: GOMEZ, Alicia
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APPLICATION NUMBER: US 0:
FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Boulevard, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIULATS, Jaume
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                      MERCK 1781
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Pred. No. 5.3e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                       Version #1.30 (EPO)
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US-08-875-674A-3
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                                                                                                                                    MEDITER KEMARSHE FORM:

MEDITUM TYPE: Floppy disk 3.5' (1.4 MB).

COMPUTER: Compatible PC IBM (80486, 8 M Ram).

OPERATING SYSTEM: Windows 95.

SOFTWARE: Word Perfect 5.0 for Windows 95.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/875,674A

FILING DATE: 17-JUly-1997

CLASSIFICATION NUMBER: PCT/CU96/00004

FILING DATE: 18-NOV-1996

APPLICATION NUMBER: PCT/CU96/00004

FILING DATE: 18-NOV-1996

APPLICATION NUMBER: PCT/CU96/00004

FILING DATE: 18-NOV-1996

APPLICATION NUMBER: P-12

REGISTRATION NUMBER: 20,910

REFERENCE/DOCKET NUMBER: P-12

TELEPHONE: (914) 723-4300

TELEPHONE: (914) 723-4300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dequence 3, Application US/08875674A Patent No. 6572857
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Best Local &
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                                                                                     TELEFAX: (914)-723-4301
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: MONTERO
APPLICANT: LOMBARDE
APPLICANT: P REZ R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 703-243-633
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: ami
                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 GTSVTVSS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114
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                                                Amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10583
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                                                                  119 Amino acid residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         One Chase Road
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                   Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OMBARDERO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lackenbach Siegel Marzullo Aronson & Greenspan,
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Protein
                                   Unknown
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F: Anti-CD6 monoclonal antibodies and their uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RODR GUEZ, R.
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77.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
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Pred. No. 4.4e-46;
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Patent No. 6572857
OTHER INFORMATION:
OTHER INFORMATION:
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                               PILLING COLDER OF THE PRIOR PRICATION: 530

PRIOR APPLICATION NUMBER: WO PCT/EP95/00978

PRIOR APPLICATION NUMBER: EP 94104160.0
                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, VICURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tent No.
                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

COMPUTER: IEM PC compatible

COMPUTER: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
NUMBER OF SEQUENCES;
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TITLE OF INVENTION:
TITLE OF INVENTION:
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FRAGMENT TYPE: -N Terminal f
ORIGINAL SOURCE:
TISSUE TYPE: Animal cells.
CELL LINE: NSO " SP 2/0 "
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CLONE: Sub-clone for tlA
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               FILING DATE: 17-MAR-1994
 APPLICATION NUMBER:
                                                                                                                                                              APPLICATION NUMBER: US/01
FILING DATE: 17-NOV-1995
                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTIFICATION METHOD: By similarity with known sequence.
OTHER INFORMATION: Sequence corresponding to the humanized
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2200 CLARENDON BLVD. SUITE 1400
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ROSELL, ELISABET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANSELL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JAUME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR ANTIBODIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                variant of sub-clone ior t1A recognizing human CD6, particula to the variable region of its heavy chain.
EP 94118970.6
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Pred. No. 3.5e-46;
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                                                                                                                                                                                                                   Version #1.30
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PCT-US93-08435-10
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GENERAL INFORMATION:
ATILIANDA, MAZY E,
NAME: Bak, MAZY E,
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: SEC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-5218
TELEPAX: (215) 540-5218
TELEPAX: (215) 540-5018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity
   TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: the Army TITLE OF INVENTION: Novel Antibodies for Conferring Passive TITLE OF INVENTION: Immunity Against Infection by a Pathogen NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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REFERENCE/DOCKET NUMBER: ME
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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Box 457, 321 Norristown Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SmithKline Beecham, Corporation U. S. Government, Secretary of
                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                             SBC P50107
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Pred. No. 8.3e-46;
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US-08-339-582-2
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; TOPOLOGY: linear
; MOLECULE TYPE: prot
PCT-US93-08435-10
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                                                                                                                                                                                                                    TBLEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5558852
GENERAL INFORMATION:
                                                                                                                       Matches 101; Conservative
                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                          NAME: Sibley, Kenneth D
REGISTRATION NUMBER: 31.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE:
                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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61 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TGRFTISRDNAKNTLYLEMSSLRSEDTAMYYCASLIYYGYDGYAMDYWGQGTSVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28234
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: No. 5558852th Carolina
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                                                                           EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
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mino acid
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Zalutsky, Michael
Carrel, Stefan
                                                                                                                                                                                                                                                                                                                            919-420-2200
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O. Drawer 34009
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80.5%;
                                                                                                                                      78.2%;
83.5%;
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; Pred. No. 5e-46;
11; Mismatches
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                                                                                                                    Score 503; DB 1;
Pred. No. 5.8e-46;
6; Mismatches 10
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                                                                                                                                                      Length 121;
                                                                                                                     Indels
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US-08-579-378A-20
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                                                                                                                                                                                                   Query Match
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GENERAL INFORMATION:
APPLICANT: Co, Ma
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INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION: 1-1:
TITLE OF INVENTION: 1-2:
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-AUG-1995
PRIOR APPLICATION NUMBER: EP 95114696.8
FILING DATE: 19-SEP-1995
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING FARM
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/160,074
                                                                                                                                                                                                                                                   TOPOLOGY: 15 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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TELEPHONE: 415-326-2400
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Liebescheutz, Joe O. REGISTRATION NUMBER: 37,505 REFERENCE/DOCKET NUMBER: 11:
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                                                                                                                                                                                                                                                                                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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121 S 121
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                                                                                                                                 1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY
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: California
                                                                                                                                                                                    Similarity
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)GY: linear
                                                                PDSVRGRFTISRDNAKWTLYLOMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS
                                                                                                 EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVASISTGGS-TYY
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One MarketPlaza, Steuart Tower, Suite 2000
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                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                 protein
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                                                                                                                                                                                    78.1%;
80.2%;
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Pred. No. 7.5e-46;
                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                Length 135;
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          Sequence 2, Application US/08326362
Patent No. 5730981
GENERAL INFORMATION:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: 27-Dec-95
APPLICATION NUMBER: EP 95 112 895.8
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN D. HARBON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION UNMBER: PCT/US96/13152
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Martin, Ulrich, TITLE OF INVENTION: Anti-se NUMBER OF SEQUENCES: 4
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STRANDEDNESS: dou
                                                                                                                                                                                                                                                                                                                                                   Local
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CITY: New York
STATE: New York
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ADDRESSEE: Attn: Norman I
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                                                                                                                                                                                                                                                                                           1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSTYTMSWVRQTPEKRLEWVATISSGGSYTYY 60
                                                                                                                                                                                                                                                                                                                                97;
                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                         EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVASISTGGS-TYY 59
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35
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80.2%;
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Pred. No. 3.3e-45;
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RESULT 15
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                                                                                                                                Sequence 14, Application US/08379057
PATENT NO. 5876950
GENERAL INFORMATION:
APPLICANT: Sladak, Anthony W.
APPLICANT: Hollenbaugh, Diane L.
APPLICANT: Gilliland, Lisa K.
APPLICANT: Gilliland, Lisa K.
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Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/032,863
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: DE P 42 08 795...
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 02481-1276
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
APPLICANT: Gordon, Marcia L.
APPLICANT: Bajorath, Jurgen
APPLICANT: Aruffe, Alejandro A.
TITLE OF INVENTION: Monoclonal Antibodies Specific For
TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their
TITLE OF INVENTION: In Diagnosis and Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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APPLICANT: Dippold, Wolfgang
TITLE OF INVENTION: Monoclonal Anti-Ganglioside Antibody,
TITLE OF INVENTION: Its Preparation and Use as a Tumortherapeutic Agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: ami
TOPOLOGY:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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7; Mismatches
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CORRESPONDENCES: 57

CORRESPONDENCES DETECO-PYCER SQUIDD COMPANY

STREET: ADDRESSE: Bristol-PYCER SQUIDD COMPANY

STREET: ADDRESSE: Bristol-PYCER SQUIDD COMPANY

STREET: Seattle

STATE: Mabington

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Plopy disk

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## ALIGNMENTS

RESULT 1 PL0203

C;Accession: PL0203
R;Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodi A;Reference number: PL0198; MUID:90309768; PMID:2114528
A;Accession: PL0203

anti-DNA autoantibody BV17-31, kappa chain V region - mouse (fragment) C;Species; Mus musculus (house mouse) C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000

A;Cross-references: EMBL:L35138; NID:g522336; PIDN:AAA67525.1; PID:g522337 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-95/Domain: immunoglobulin homology <IMM> A; Molecule type: mRNA A; Residues: 1-219 < VAN> R; van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schoutted to the EMBL Data Library, August 1994
A; Description: Coordinate expression of antibody subunit genes yields high level Ig kappa chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence revision 21-Jul-1995 #text\_change 21-Jan-2000
C;Accession: S52028 A;Cross-references: GB:X53643; NID:g50196; PIDN:CAA37694.1; PID:g930142 C;Superfamily: immunoglobulin V region; immunoglobulin homology F;16-95/Domain: immunoglobulin homology cIMM> F;24-39/Region: complementarity-determining 1 F;55-61/Region: complementarity-determining 2 A; Status: preliminary A;Reference number: \$52028 A;Accession: \$52028 문 Ś 밁 Ş F;94-102/Region: complementarity-determining F;101-113/Region: D region A; Molecule type: mRNA A; Residues: 1-113 < SMI> Best Loca Matches Query Match N Local Similarity 107; బ 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113 2 VVMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLJIYKVSNRFS GVPDKFSGSGGGDFTLKISKVEAEDLGVYYCFQGSHVPFTFGSGTKLEIKR Conservative 95.4%; 4 Score 566; DB 2; Pred. No. 2.8e-45; Mismatches ۲. Length 113; Indels ò Gaps 61 61

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RESULT 4

839276

19 light chain precursor V-D-J region (6-19) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000

C;Accession: B39276

C;Accession: B39276

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Proc. Natl. Acad. Sci. U.S.A. 87, 10038-10042, 1990
A;Title: Cryoglobulinemia induced by a murine IgG3 rheumatoid factor: skin vasculitis ar A;Reference number: A39276; MUID:91088540; PMID:2263605
A;Accession: B39276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-219 <KWA>
A;Residues: 1-219 <KWA>
A;Cross-references: GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID:g1594226
C;Comment: This protein is specific for human plasma apolipoprotein A-I of
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-112/Domain: V region #status predicted <VRG>
F;113-219/Domain: C region #status predicted <CRG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: PC4203

R;Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.

Gene 173, 257-259, 1996
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C;Species: Mus musculus (bouse mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-131 < REI>
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A;Title: Cloning and characterization of cDNAs coding for heavy and light chains
A;Reference number: PC4202; MUID:97082978; PMID:8964510
A;Accession: PC4203
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                                                                                                                                                                                                                     ;Cross_references: GB:M55313; NID:g198095; FIDN:AAA63385.1; PID:g198096
                                                                                                                                                                 35-114/Domain:
                                                                                                                                                                                                      Superfamily: immunoglobulin V region;
                                                                                                         Query Match
Best Local :
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  21 VLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
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                                                                                                                                                               immunoglobulin homology < IMM>
                                                                                 Conservative
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93.7%;
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Pred. No. 1.3e-44;
3; Mismatches 2
                                                                           Score 556; DB 2;
Pred. No. 2.7e-44;
6; Mismatches 1
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Pred. No. 2.5e-44;
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A;Cross-references: EMBL:X59183; NID:g52314; PIDN:CAA41893.1; PID:g1334062
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                               C;Accession: S26335

R;Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A;Title: Antibodies that are specific for a A;Reference number: S26309; MUID:91341421; P

A;Accession: S26335
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A;Residues: 1-112 <TAU>
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
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Ig kappa chain V region (PAC1) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Uul-1989 #sequence_revision 20-Uul-1989 #text_change 21-Jan-2000
C:Accession: A31807
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A; Residues: 1-110 <STA>
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A:Title: A monoclonal antibody against the platelet fibrinogen receptor cont A:Reference number: A31807; MUID:89079661; PMID:2909518
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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F;16-95/Domain: immunoglobulin homology <IMM>
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                 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLB 110
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GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGGGTKLE
                                                                   VLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPXLLIYKVSNRFS
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                                                                                                                                                               Score 553; DB 2;
Pred. No. 4.3e-44;
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Pred. No. 3.5e-44;
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Ig kappa chain V region (R4A.12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change

21-Jan-2000

RESULT PT0359

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A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-114 <LEV>
A;Cross-references: GB:M30481; NID:g197157; PIDN:AAA38935.1; PID:g197158
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                       R;Levy, R.; Assulin, O.; Scherf, T.; Levitt, M.; Anglister, J. Biochemistry 28, 7168-7175, 1989
A;Title: Probing antibody diversity by 2D NMR: comparison of amino acid sequences, A;Reference number: A32967; MUID:90057406; PMID:2819059
A;Accession: A32967
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A; Residues: I-112 <CIMA
A; Cross-references: EMBL: X76021; NID:g416112; PIDN:CAA53608.1; PID:g1334264
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin
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R;Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
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S38719
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                                                                                                                                                                                                                                                                                Ig kappa chain V-II region TB33 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 21-Jan-2000
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F;16-95/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
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A;Residues: 1-118 <SHE>
A;Experimental source: strain BALB/c
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J. Exp. Med. 173, 287-296, 1991
A;Tille: A novel class of anti-DNA antibodies identified in BALB/c mice.
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A; Accession: $38719
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A; Accession: PT0359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 IVMTQTPLSLPVSLGDQASISCRSSQSIVYSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 91.1
02; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPLTFGAGTKLELK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.4%;
93.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 548; DB 2; Length 112; Pred. No. 1.3e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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2 VVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLRWYLQKPGQSPKVLIYKVSNRFS 2 IVLTQSPLSLFVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLL1XKVSNRFS

61

Matches Query Match

тосат

Similarity

91.6%; Score 543; DB 2; Length 112; 90.1%; Pred. No. 3.6e-43;

Conservative

8

Mismatches

Indels

0

Gaps

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Ig kappa chain V region (4-4-20) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 21-Jan-2000
C;Accession: B31485
R;Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
J. Biol. Chem. 264, 1565-1569, 1989
A;Title: Comparison of variable region primary structures within an anti-fluores A;Reference number: A31485; MUID:89109167; PMID:2492278
A;Reference number: A31485; MUID:89109167; PMID:2492278
A;Rocession: B31485
A;Scatus: preliminary
A;Molecule type: protein
A;Residues: 1-112 <BED>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Beddyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A;Tible: Active site structure and antigen binding properties of idiotypically
A;Reference number: A34903; MUID:90094387; PMID:2104617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain precursor V region (12-40 and 5-14) - mouse C;Species: Mus musculus (house mouse) C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jul-2000 C;Accession: B34904; H34903
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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F;16-95/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-131 <BED>
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B34904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPWTFGGGTKLEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 VVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFS
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A;Molecule type: protein
A;Residues: 20-52 <BE2>
                                                                                                                                                                                                                                                               R;Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W. J. Biol. Chem. 264, 1565-1569, 1989
A;Title: Comparison of variable region primary structures within A;Reference number: A31485; MUID:89109167; PMID:2492278
A;Accession: I31485
               片
                                                                                                                                                      C;Keywords: heter F;35-114/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                     J. Biol. Chem. 265, 133-138, 1770
A,Title: Active site structure and antigen binding properties of A,Reference number: A34903; MUID:90094387; PMID:2104617
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C34904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Bedzyk, W.D.; Herron, J.N.; Edmundson, J. Biol. Chem. 265, 133-138, 1990
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C;Accession: F27887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Structural and functional implications of a restricted A;Reference number: A91043; MUID:86300658; PMID:2427335 A;Accession: F27887
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A, Residues: 1-112 <CAT>
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C;Species: Mus musculus (house mouse)
C;Date: 15-Dec.1988 #sequence_revision 15-Dec-1988 #text_change
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                                                                                                                                                                     Superfamily: immunoglobulin V region; immunoglobulin Keywords: heterotetramer; immunoglobulin
                                                                                  Matches
                                                                                                                      Query Match
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MBO J. 5, 1577-1587, 1986
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21 VVMTQTPLSLPVSLGDQASPSCRSSQSLVHSNGNTYLHWYLQXPGQSPKLLIYKVSNRPS
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                        2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
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90.1%;
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                                                                            score 542; DB pred. No. 5.3e
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ص
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Pred. No. 4.5e-43;
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                                                                                                                                                                                                                                                                                                                                                                                   conceptual translation
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                                                                                               DB 2;
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                                                                                                            Length 131,
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A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: A27887
A;Accession: A27887
A;Accession: A27887
A;Residues: 1-112 <CAT-
A;Experimental source: strain Balb/c
A;Experimental source: strain Balb/c
A;Experimental source was determined from the germline gene C;Comment: This sequence was determined from a hybridoma protein that C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;16-95/Domain: immunoglobulin homology
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C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change
C;Accession: A27887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
A27887
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R;Vaesen, M.; Frosch, M.; Weisgerber, C.; Eckart, K.; Kratzin, H.; Bitter-Suerm Biol. Chem. Hoppe-Seyler 372, 451-453, 1991

A;Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 again A;Reference number: S16112; MUID:92000313; PMID:1910583
                                                                                                                                                                                                                                                                                                                                                                                                                           A,Title: Structural and functional implications of a restricted A,Reference number: A91043; MUID:86300658; PMID:2427335
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5, 1577-1587, 1986
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62
                   62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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Copyright (c) 1993 - 2003 Compugen Ltd.
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the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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MEDLINE=86041852; PubMed=2997711;
Klobeck H.G., Meindl A., Combriato
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COMPLEMENTARITY-DETERMINING-2.
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                         Catarrhini; Hominidae; Homo
                                                      Craniata; Vertebrata; Euteleostomi;
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J. Clin. Invest. 52:1276-1281(1973).

-i. MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.

-i. MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A
PATIENT WITH PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.

-i. MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
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InterPro; IPR003596; Ig_v.
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SEQUENCE (BENCE-JONES PROTEIN TEW
MEDLINE=74148480; PubMed=4596149;
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'TE; PS50835; IG LIKE; 1.
loglobulin V region; Bence-Jones protein; Amyloid.
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Pred. No. 4.5e-42;
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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COMPLEMENTARITY-DETERMINING-2.
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Acbersold R., Herbst H., Grutter T., Chang J.Y., Braymurine V kappa 25 and V kappa 27 amino-acid sequency origin; monoclonal antibodies 17829.1 and 22825.1 spgroup A-streptococcal polysaccharide.";
Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984)
                                                                                                                                                                                                                                                                                                                  PIR; A01912; KVMS17.
HSSP; P01607; 1REI.
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TISSUE=Hybridoma;
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COMPLEMENTARITY-DETERMINING-3
FRAMEWORK-4.
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KV2A_HUMAN
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Best Local S
Matches 82
                                                                          Matches
                                                                                            Query Match
Best Local 9
                                                                                                                                                                                         InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PR0SITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Bence-Jones pr DISULFID

24
95
BY SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KV2A HUMAN
P01614;
21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
NON TER
SEQUENCE
                                                                                                                                                                      DISULFID
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DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular basis of antibody formation.";
Naturwissenschaften 56:195-205(1965).
-i- MISCELLANBOUS: THE C REGION OF THIS CHAIN HAS
-i- MISCELLANBOUS: THIS IS A BENCE-JONES PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986 (Rel. 01, Last seque
15-JUL-1999 (Rel. 38, Last anno
15 kappa chain V-II region Cum.
                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                             PIR; B91639; K2HUCM.
HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hilschmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS TO 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoppe-Seyler's Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               type).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hilschmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=68242259; PubMed=5586923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=70063440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE.
                                                                                                                                                                                                                                                                                                                                             GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding activity; NAS
GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
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                                                                                                Similarity
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-IVMTQTPLSLPVTPGEPASISCRSSQSLLDSGDGNTYLNWYLQKAGQSPQLLIYTLSYRA 62
                  IVLTQSPLSLPVSLGDQASISCRSSQSIVHS-NGNTYLEWYLQKPGQSPKLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVPDRFSSSGSGTDFTLRISRVEAEDVGVYYCAHNLELPYTFGGGTKLEIKR 113
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                                                                            Conservative
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                                                                                                                                                      AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Physiol.
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                                                                                                                                                        12676 MW;
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73.2%;
                                                                                              73.1%;
74.3%;
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                                                                          15:
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annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.
                                                                        Score 433.5; DB 1;
Pred. No. 4.6e-40;
5; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 3.15
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 435;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                      59E9F90A379569EC
                                                                                                                                                                                           SIMILARITY.
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3.1e-40;
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                                                                                                                                                    CRC64;
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                                                                          Indels
                                                                                                             Length
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Best Local S
Matches 79
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NON_TER
SEQUENCE
                                                MOUSE

KY2F MOUSE

STANDARD;

PRT;

113 AA.

P01630;

21-JUL-1986 (Rel. 01, Created)

21-JUL-1986 (Rel. 01, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)

15-JUL-1999 (Rel. 17534.1.

Rus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
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--- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE
--- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
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DOMAIN
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SEQUENCE
                 NCBI_TaxID=10090;
                            Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A01887; K2HUML.
HSSP; P80362; 1WTL.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
Ig kappa chain V-II region MIL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P01616;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                             IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGVTYLEWYLQKPGQSPKLLIYKVSNRFS
                                                                                                                                                                       GVPNRFSGSGSGTBFTLKISRVZAZBVGVYYCMQALQTPLTFGGGTNVEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR
                                                                                                                                                                                            GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR
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PA;
                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                     23
53
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                                                                                                                                                                                                                                                                                                        12055 MW;
                                                                                                                                                                                                                                                                       72.4%;
70.5%;
                                                                                                                                                                                                                                                                                                                           n; Bence-Jones protein.

FRAMEWORK-1.

COMPLEMENTARITY-DETERMINING-1.

FRAMEWORK-2.

COMPLEMENTARITY-DETERMINING-2.

FRAMEWORK-3.

COMPLEMENTARITY-DETERMINING-3.

FRAMEWORK-4.

BY SIMILARITY.

; Score 429.5; DB 1
; Pred. No. 1.2e-39;
19; Mismatches 13
                                                                                                                                                                                                                   Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                DB 1;
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                                                                                                                                                                                                                                                                               Length
                                        Euteleostomi,
                            Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113
                                                                                                                                                                                                                                                              Gaps
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A Chang J.-Y., Herbst H., Abbersold R., Braun D.G.;

AT Inght sequence (V kappa 27) of the variable region of kappa-

RT light chains from a mouse hybridoma-derived anti-(streptococcal group

RT A polysaccharide) antibody containing an additional cysteine residue.

RT Application of the dimethylaming an additional cysteine technique

RT for the isolation of peptides.";

RT for the isolation of peptides.";

RE Biochem. J. 21:173-180(1983).

CC -!- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL

CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.

ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.

R INTERPOS 1 INTL.

DR INTERPOS 1 INTL.

R INTERPOS 1 INTL.

R INTERPOS 1 IPRO03506; Ig_MHC.

R InterPro; IPRO03506; Ig_MHC.

R InterPro; IPRO03596; Ig_MHC.

R Pfam: PF00047; iq: 1 Ig_V.
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21-JUL-1986 (
15-JUL-1999 (
Pfam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region; Monoclonal antibody.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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SMART; SM00406; IGv; 1.
PROSSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Mono
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in V-II region 2S1.3.
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-1.
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InterPro; IPR003006; Ig_MC.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-APR-1988 (Rel. 07, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 kappa chain V-IV region B17 precursor.
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MEDLINE=86041854; PubMed=2997713;
Marsh P., Mills F., Gould H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Detection of a unique human V kappa IV germline cDNA probe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                              GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding activity;
GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13:6531-6544(1985)
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72.1%;
                                                                                                                                                                     Signal.
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                                     IG KAPPA CHAIN V-IV REGION B17 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 416;
Pred. No. 3.
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BY SIMILARITY
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COMPLEMENTARITY-DETERMINING-3.
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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RESULT 12
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15-JUL-1999
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                                                                                                       Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; P850835; IG_LIKE; 1.
Immunoglobulin V region; Sign.
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G0; G0:0005576; C:extracellular; NAS.
G0; G0:0003523; P:antigen binding activ
G0; G0:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003906; Ig_MHC.
InterPro; IPR003906; Ig_WHC.
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P06313;
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the I the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
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Klobeck H.G., Borr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
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                                                                                                                                                                                                                                A01904; K4HUJI.
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(Rel. 06, Last sequence update)
(Rel. 38, Last annotation update)
ain V-IV region JI precursor.
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nkamm G.W., Combriato
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Primates;
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69.0%;
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FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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Pred. No. 4.4e-36;
                                                              IG KAPPA CHAIN V-IV REGION JI FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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                                                                                                                                                                                                activity;
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RESULT 14
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ID KV4A_HUMAN
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Matches 77
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
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HSSP; P80362; 1WTL.
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Mammalia; Eutheria; Rodentia;
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MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA
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COMPLEMENTARITY-DETERMINING-1.
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FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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  Eukaryota; Metazoa;
            Ig kappa chain V-III
Mus musculus (Mouse)
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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SMART; SM00406; IGv; 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding activity; NAS.
GO:0006955; P:immune response; NAS.
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1EEU; 03-FEB-01.
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5IVE; 28-MAR-01.
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Chordata; Craniata; Vertebrata;
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67.3%;
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
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Blochemistry 17:2392-2400(1978).
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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McKean D.J., Potter M., Hood L.E.;
"Mouse immunoglobulin chains. Pattern of sequence variation
kappa chains with limited sequence differences.";
Eicchemistry 12:760-771(1973).
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MCKean D.J., Bell M., Potter M.;
MKKean D.J., Bell M., Potter M.;
MCKean b.J., Bell M., Potter M.;
MCKean D.J., MCKean M., Potter M.;
MCKean D.J., MCKean M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M., Potter M
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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Match Length DB
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019760; AAM19760.1; -.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; 1g; 2.
SMART; SM00406; IG_MHC; 1.
PROSITE; PS00090; IG_MHC; 1.
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Q8VCI6;
01-MAR-2002
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                                                                                                                                                                                       streptococcal polysaccharide, N-act with cardiac myosin."; Infect. Immun. 68:5803-5808(2000). EMBL; AF206024; AAF69322.1; -. HSSP; P01607; IREI.
                                                                                                                                                                                                                                                                            MEDLINE-20448942; PubMed=10992488;
MEDLINE-20448942; PubMed=10992488;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"T-Cell-dependent antibody response to the dominant streptococcal polysaccharide, N-acetyl-glucosamine,
                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00466; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Fragment).
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2003 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 26.2 kDa protein.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                               PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein. SEQUENCE 238 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VWMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKDGQSPXLLIYKVSNRFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVEDRESGSGSGTDETLKISRVEABDLGVYECSQSTHVEETEGGGTKLEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TremBirel. 15, Created)
(TremBirel. 15, Last sequence update)
(TremBirel. 23, Last annotation update)
immunoglobulin light chain variable reg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Chordata; ; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26224 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.4%; Score 536; DB 11;
90.2%; Pred. No. 4.9e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35EC08E3DE5414AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104
                                                                                                                                                                                                                                                                                                     Diamond B.; o the dominant
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Best Local S
Matches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ dat
EMBL; BC021781; AAH21781.1; -.

InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.

Pfam; PF00047; ig; 1.

R SMART; SM00406; IGv; 1.

R PROSITE; PS00290; IG_MHC; 1.

M Hypothetical protein.

M SEQUENCE 239 AA; 26303 MW; C16119CACA25C337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8VC55 PRELIMINARY; PRT; 239 AA.
Q8VC55;
Q8VC55;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 26; 3 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Strausberg R.;
Strausberg R.;
Submitted (PEB-2002) to the EMBL/GenBank/DDBJ
EMBL; BC022362; AAH22362.1; -.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                   Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                          QSTCD0;
                                                                                                              SEQUENCE FROM N.A.
TISSUE=Lung;
                                                                                                                                                                                NCBI_TaxID=9606;
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TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVPDXFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQSNHLPYTFGGGTKLEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQXPGQSPKLLIXKVSNRFSGVPDKFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSGSGTDFTLKISRVEAEDLGVXFCSQTTHVPYTFGGGTKLEIK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 AA;
                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.2%;
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91.3%;
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                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                 Created)
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Pred. No. 1.1e-46;
7; Mismatches 3
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Pred. No. 3.
                                                                                                                                                                                                      Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C16119CACA25C337
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                                                                                                                                                                                                                                                                                                                                                                                                239
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3.9e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11;
                                                                                                                                                                                                        Hominidae:
                                                               databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 239;
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RESULT 6
Q9ULBO
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Best Local S
Matches 89
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DR InterPro; IPR003596; Ig_v.

Pfam; PF00047; Ig; 2.

R SMART; SM00406; IGv; 1.

R PROSITE; PS00239; IG_LIKE; 2.

PROSITE; PS00299; IG_MHC; 1.

Hypothetical protein.

SEQUENCE 239 Ab.
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Best Local :
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PKELLALL

QSUL80;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAY-2003 (TrEMBLrel. 23, Last annotation update)
O1-MAR-2003 (Tremblirel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                               NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF035034; AAD56270.1; -
HSSP; P80362; NWTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Q8NEKO PRELIMINARY;
Q8NEKO;
01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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Similarity 78.8%;
89; Conservative 1:
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                                                                                                                                                                               GVPDKFSGSGSGTDFTLKISRVBAEDLGVYYCFQGSH-VPMTFGGGTKLEIKR
                                                                                                                                                                                                                                                          IVLTQSPLSLPVSIGDQASISCRSSQSIVHSNGNTYLEWYLQXPGQSPXLLIYXVSNRFS
                                                                                                                                                 VWMTQSPLSLPVTLRQPASISCRSSQSPVXSDGNTYLNWFQQRPGQSPRRLIXXVSNRDS
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                                                                                                                                                                                                                                                                                                                                                                                                                 114
114 AA;
                                           PRELIMINARY;
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; 12775 MW;
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77.7%;
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  Created)
                                                                                                                                                                                                                                                                                                                             Score 465.5; DB 4
Pred. No. 8.5e-43;
2; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 467;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                               070E31E210D1CB01 CRC64;
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                                             239
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ dat

EMBL; BC031498; AAH31498.1; -.

EMBL; BC031498; AAH31498.1; -.

Interpro; IPR002198; ADH short.

Interpro; IPR003599; Ig.

Interpro; IPR003597; Ig. G1.

Interpro; IPR003597; Ig. MHC.

R Interpro; IPR003596; Ig. MHC.

R Interpro; IPR003596; Ig.

R Ffam; PR000407; ig; 2.

R SMART; SM004007; ig; 2.

R SMART; SM004006; IGv; 1.

R SMART; SM004006; IGv; 1.

R SMART; SM00406; IGV; 1.

R SMART; SM00406; IGV; 1.

R PROSITE; PS00061; ADH SHORT; 1.

R PROSITE; PS00061; ADH SHORT; 1.
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Matches 86
                  Query Match
Best Local Similarity
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InterPro; IPR003597; Ig-cl.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 2.
SMART; SM00407; IGcl; 1.
SMART; SM00407; IGcl; 1.
SMART; SM00405; IGv; 1.
PROSITE; PS50835; IG-LIKE; 2.
PROSITE; PS50835; IG-MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8K0F8;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                          Hypothetical protein SEQUENCE 239 AA; ;
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Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
EMBL; BC030814; AAH30814.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAR-2003 (TrEMBLrel.
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Homo sapiens (Human).
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Similarity 76.8%; Pred. No. 2.4e-41;
86; Conservative 13; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVPDRFSGSGSGTDFTLKISKVEAEDVGIXYCMQGLQTFQTFGQGTKVEIKR
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239 AA; 26024 MW;
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                                                                                                          26366 MW;
72.7%; Score 431; DB 11; 72.3%; Pred. No. 1.2e-38; cive 14; Mismatches 17;
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                                                                                                          D7BE84398AA341F0
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Matches

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RESULT 10
Q920E9
ID Q920E9
AC Q920E9
DT 01-DE9
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ dat

EMBL; BC028925; AAH28925;1; -.

InterPro; IPR003599; Ig.

InterPro; IPR003599; Ig.

InterPro; IPR003006; Ig_MHC.

R InterPro; IPR003596; Ig_V.

R InterPro; IPR003596; Ig_V.

R InterPro; IPR003596; Ig_V.

R Pfam; PF00047; ig; 1.

R SMART; SM00409; IG; 1.

R SMART; SM00406; IGy; 1.

R PROSITE; PS50835; IG_LIKE; 1.
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Best Local Similarity
Matches 71; Conserv
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01-OCT-2002
01-MAR-2003
ARKIN J.D., lape A., Jennings I.G., Horaitis O

*Pocinition of the Idiotope of Pterin-Mimickin

in Mammalian Cells.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ

EMBL; AP307935; AAL09419.1;

InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                        Q920E9 PRELIMINARY; PRT; 111 AA.
Q920E9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Pterin-mimicking anti-idiotope kappa chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8K122
Q8K122;
                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein. SEQUENCE 148 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                       (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16345 MW;
                                                                                                             Jennings I.G., Horaitis O.,
diotope of Pterin-Mimicking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.6%; Score 383; DB 11; 71.7%; Pred. No. 1.1e-33;
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Last annotation update)
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                                                                                                                                           R.G.
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Q9UL78;
01-MAY-2000
01-MAY-2000
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NON TER
SEQUENCE
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BMBL; AF035036; AAD56272.1; -
HSSP; P80362; IWTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                  TGIPDRFSGSGGTDFTLTISRLEPEDCAVYYCQQYGSSPLTFGGGTKVEIKR
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                                                                                                                                                                                             SGVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR
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                                                                                                                                                                                                                                          EIVLTQSPGTLSLSPGERATLSCRASQSV----SSSYLAWYQQKPGQAPRLLIYGASSRA
                                                                                                                                                                                                                                                                                                                                                                                                                          109
109 AA;
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111 AA; 12046 MW;
                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          109
11646 MW; 5F675C52EC7EE197 CRC64;
                                                                                                                                                                                                                                                                                                                                                   62.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.1%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                  Score 368; DB 4; Length Pred. No. 3.1e-32; Indel 9; Mismatches 19; Indel
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Pred. No. 2.8e-32;
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Catarrhini; Hominidae;
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Q9UL77 Q9UL77; Q1-MAY-2000

(TrEMBLrel. 13,

Created)

PRELIMINARY;

PRT

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Q9JL80
Q9JL80
AC Q9JL8
AC Q9JL8
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AC Q9JL8
DT 01-QC
DT 01-MA
DE Anti-
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QS Mus m
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Best Local S
Matches 66
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PROSITE; PSO835; IG, IKE; 1.

NOW TER 1 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS TO THE 100 SPORTS T
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ENEL; AF035037, AAD56273.1; -.
HSSP; P01607; IREI.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003196; Ig_V.
PROSITE;
NON_TER
NON_TER
                                                                                                                                                                                      HSSP; P80362; IWTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003996; Ig_v.
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Q9JL80;
01-OCT-2000
01-OCT-2000
                                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE=20448942; PubMed=10992488;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"T-Cell-dependent antibody response to the dominant streptococcal polysaccharide, N-acetyl-glucosamine,
                                                                                                                                                                                                                                                                                                                                                                     Infect. Immun. 68:5803-5808(2000).
EMBL; AF206026; AAF69324.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                     with cardiac myosin.";
Infect. Immun. 68:5803
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01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2003 (TrEMBLrel. 23,
Anti-myosin immunoglobulin ]
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01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *** P. Van der Merwe P.L.,

*** P. Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wu X., Liu B., Van der Young D.C.;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myosin-reactive
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                                                                              PS50835; IG_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
ive immunoglobulin light chain variable
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Rođentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11738 MW;
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Primates;
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58.9%;
                                                                                  LIKE; 1.
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light
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Pred. No. 3.7e-29;
5; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87:184-192 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local S
Matches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody V region genes.",
J. Immunol. 161:2020-2031(1998).
EMBL; U96396; AAB68785.1; ...
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                        Q9UL86;
Q9UL86;
01-MAY-2000
01-MAY-2000
01-MAR-2003
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NON_TER
SEQUENCE
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                              01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin kappa chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa lyariable region (Fragment).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Immanialia, Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q96SA9;
Q96SA9;
                                                                                          (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                               GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC-QQSYSTLTFGGGTKVEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                       IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
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                                                                                                                                      ) (TrEMBLrel 13, ) (TrEMBLrel 13, ) (TrEMBLrel 23,
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107 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 337;
Pred. No. 6
                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4BB43E9C5B577F16 CRC64;
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                                                                                                                                                                                                                                     109
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Homo.
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Result
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                  Score
             563
563
563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Geneseq 19Jun03:*

| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1107863 seqs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*
                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                  BG
                                                                                                                                                       AAB20434
AAP80154
AAP81364
       AAB62301
AAR21262
AAE15704
AAW03199
AAY21545
AAY95258
                                                                                                                                                                                                                                                                                                                                          SUMMARIES
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Chimeric Fv (BABS)
pscFvNQll encoding
Mouse monoclonal a
Anti-idiotype mono
Monoclonal antibod
WOW-1 Fab light ch
                                                                                                                                                       Anti-FIX/FIXa anti
Biosynthetic antib
Light chain variab
                                                                                                                                                                                                                                                             Description
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ligh ligh SC1	AAY25399 AAW68492 ABP57967 ABP52311	224	122 140 114	 សលសល 4444 ស្លេ4
Murine KC-4 immuno Murine KC-4 immuno VI sequence of ant Amino acid sequenc Chimeric MAb light BR55-2 light chain	AAR52772 AAR52790 AAR70457 AAW53598 AAR32241 AAR31587	144	131 131 131 131 131	 55447 4467
0.5 5 2 2 6	AAR75248 AAR75248 ABJ10398 AAR56240 AAR92995 AAR92993	16 17 17	112	 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
H and L chain FV r H and L chain FV r Heavy and light ch Hypercalcaemia age Mouse antibody 4D4 Antibody 3S193 lig	AAR32091 AAR32090 AAR32213 AAR27011 ABG74246 AAR82961	14 17 13 16	247 249 249 113 132	 55555555555555555555555555555555555555
MAb 1A7 light chai Light chain variab Vh-(Lk)-Vl of anti Vh-(Lk)-Vl of anti Fv region SC100 an Light chain variab Mouse immunoglobul Testosterone bindi MAb B3 light chain B3 immunoglobulin h66-118/h13-65/11-	AAY49209 AAY28468 AAY28470 ABP52310 AAY17416 AAY17416 AAY17416 AAY05239 AAR68741 AAR95217 AAR56235	1176 200 1176	149 149 263 109 112 238 112 112 219	 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5

## ALIGNMENTS

RESULT 1 AAB20434

AAB20434;

AAB20434 standard; Protein; 249 AA

Anti-FIX/FIXa antibody 193/K2 scFv.

21-JUN-2001 (first entry)

ŝ Chimeric - Mus musculus. Chimeric - Synthetic. Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse. Region Protein Peptide Region Protein 98..110 /label= CDR3 122..135 /label= Linker Location/Qualifiers 230..238 /label= CDR3 /label= VH 36. 249 abel= VL

22-MAR-2001. WO200119992-A2.

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RESULT 2
AAP80154
ID AAP8
XX AAP8
XX AAP8
XX AAP8
XX Bios
DT 01-J
XX Bios
XX Bios
XX mult
XX mult
XX Woss
XX Woss
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XX I Woss
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XX I Woss
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XX I J-V
XX I J-V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of a single chain Fv (scFv) derivative of antibody 193/K2, comprising the heavy (vH) and light (VL) chain variable regions of 193/K2 joined by an artificial, flexible linker peptide. The scFv was obtained by PCR amplification of cDMAs for 193/K2 vH and VL regions and cloning in vector pDAP2. 193/K2 is can example of anti-human Factor IX (FIX)/activated Factor IX (FIX) antibodies of the invention. Anti-FIX/FIX and their derivatives, concluding scFv and CDR3 fragments, have Factor VIIIa (FVIIIa) cofactor activity or FIXa activating activity. Administration leads to an increase in the proceagulant activity. Administration leads to an increase in the proceagulant activity of FIXa, even in the presence of FVIII or FVIIIa, and in the case of FVIII or FVIII or FVIII and the case of FVIII or FVIII and the the case of FVIII or FVIII and the case of FVIII or FVIII and derivatives are used in a claimed pharmaceutical composition for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 113; Conserv
                                                                                                                                                                                                                                                          31-OCT-2002
01-JAN-1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
                  19-MAY-1988;
                                                    01-DEC-1988
                                                                                                                     Synthetic.
                                                                                                                                                                        multifunctional
                                                                                                                                                                                      Biosynthetic
                                                                                                                                                                                                                         Biosynthetic
                                                                                                                                                                                                                                                                                                            AAP80154;
                                                                                                                                                                                                                                                                                                                                         AAP80154 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diathesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-290358/30.
                                                                                   WO8809344-A
                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QIVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQXPGQSPKLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                             SGVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QIVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 593; DB 22; llarity 100.0%; Pred. No. 1.5e-44; Conservative 0; Mismatches 0;
                                                                                                                                                                   antibody binding site; nal protein.
                                                                                                                                                                                                                       antibody binding site.
                                                                                                                                                                                                                                                        (updated)
(first entry)
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                  88WO-US01737
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                                                                                                                                                                                                                                                                                                                                             249
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                                                                                                                                                                                 framework region; assay; imaging
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RESULT 3
AAP81364
ID AAP8
XX AAP8
AC AAP8
XX II-C
DT 31-C
DT 17-C
XX Ligh
XX Ligh
XX Mus
OS Mus
OS Synt
XX WOSE
PN WOSE
PN WOSE
PN 19-D
XX 11-D
PR 11-D
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Best Local Simi
Matches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and the complementarity determining region from G-loop-4 heavy chain variable region and has lysozyme specificity. The effector protein is an enzyme, toxin, receptor, binding site, growth factor, cytokine or antimetabolite. The sequence capable of sequestering an ion is calmodulin or metallothionein. The sequence capable of binding to solid support is streptavidin or a protein A fragment. The protein may be used for, eg specific binding assays, affinity purificn., biocatalysts, drug targetting, imaging and immunological treatment of oncogenic etc. diseases. The protein offers fewer cleavage sites to circulating proteolytic enzymes and have improved stability. They reach target organs rapidly and are cleared quickly from the body. They also have reduced
21-MAY-1987;
                                19-MAY-1988;
                                                                01-DEC-1988
                                                                                                                                                                                             Light chain variable domain; biosynthetic antibody binding domain.
                                                                                                                                                                                                                            Light chain variable domain of biosynthetic antibody binding domain.
                                                                                                                                                                                                                                                               31-OCT-2002
17-OCT-1990
                                                                                                                                                                                                                                                                                                               AAP81364;
                                                                                                                                                                                                                                                                                                                                             AAP81364 standard; protein; 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           multifunctional protein which also comprises an effector protein, an AA acid sequence capable of sequestering an ion, or a sequence capable of binding to a solid support. The BABS comprises the framework region from murine anti-digoxin monoclonal antibody 26-10 heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant multifunctional protein - having antibody binding sequence for biological activity, ion sequestering or binding
                                                                                               W08809344-A
                                                                                                                                Synthetic.
                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The biosynthetic antibody binding site forms part of a recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page ?; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 solid support.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huston JS, Oppermann H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAY-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CREA-) CREATIVE BIOMOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Updated on 31-OCT-2002 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .mmunogenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAN80180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKAGQSPKLLIYKVSNRFS
                                                                                                                                                                                                                                                                                                                                                                                                                              GVPDRFSGSGSGTDFTLKISRVEAEDLGIYYCFQGSHVPWTFGGGTKLEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                             (updated)
(first entry)
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87US-0052800
                                88WO-US01737.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 570; DB Pred. No. 1.6e 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .6e-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 9;
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to a
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RESULT 4
AAB62301
ID AAB6
XX AAB
AC AAB6
XX AB6
XX Bioc
AC Chin
XX Bioc
KW Bioc
KW infe
KW anti
XX Mus
XX US61
XX IS61
XX AT IS61
XX AT IS61
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XX IS62
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Best Local :
21-MAY-1987;
12-MAR-1992;
19-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biosynthetic protein. The protein also comprises an effector molecule with biological activity (eg an enzyme, receptor binding site, growth factor, lymphokine, cytokine or antimetabolite), an amino acid sequence capable of sequestering an ion (eg calmodulin or metallothionein), or an amino acid sequence capable of selective binding to a solid support (eg streptavidin or a fragment of protein A). The protein can be used for specific binding assays, affinity purificn, biocatalysts, drug targetting imaging and immunological treatment of oncogenic and infectious diseases. It offers fewer cleavage sites to circulating proteolytic enzymes, and improved stability. It reaches target tissues rapidly and is quickly cleared from the body. It also has reduced immunogenicity and its design facilitates binding to other moieties in drug targetting and imaging
                                                                                                                                                                                                                                                                                                                                            Blosynthetic; antibody binding site; binding assay; drug targeting; biocatalysis; imaging; affinity purification; immunological; oncogenic; infectious disease; murine; monoclonal 26-10; anti-digoxin; cytostatic; antimicrobial; monoclonal glp-4; anti-lysozyme; chimeric.
                                                                                                                   18-DEC-1995;
                                                                                                                                                                           27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric
                                                                                                                                                                                                                                      US6207804-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB62301 standard; Protein; 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB62301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The light chain variable domain comprises complementarity determining regions of glp4 and framework regions from multine antidigoxin monoclonal 26-10. The domain forms part of a single chain multi-functional biosynthetic protein. The protein also comprises an effector molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page ?; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant multifunctional protein - having antibody binding sequence for biological activity, ion sequestering or binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1988-353928/49
N-PSDB; AAN80173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huston JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Updated on 31-OCT-2002 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CREA-) CREATIVE BIOMOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVPDKFSGSGSGTDFTLKISRVBAEDLGVYYCFQGSHVPWTFGGGTKLBIKR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVPDRFSGSGSGTDFTLKISKVEAEDLGIYYCFQGSHVPWTFGGGTKLBIKK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vmtotplslpvslgdoasiscrssosivhsngntyldwylokagospkiliykvsnrfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oppermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BABS) light chain variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
87US-0052800.
92US-0850228.
93US-0139901.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ž
                                                                                                                   95US-0575724.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 567; DB
Pred. No. 1.3e
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9;
..3e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                       Matches
                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                             The invention relates to a biosynthetic antibody binding site that comprises disulfide bonded heavy, light variable region (HVR, LVR) defining single, complete antigen (Ag1) binding site. HVR, LVR have polypeptide domain having sets of complementarity determining regions (CDR) and framework (FR) amino acid sequences homologous to first and second immunoglobulin respectively. The biosynthetic antibody binding sites are useful in specific binding assays, affinity purification, biocatalysis, drug targeting, imaging immunological treatment of various oncogenic and infectious diseases. The present sequence represents the light chain variable domain of a chimeric Fv (BABS) comprising the CDRs of murine monoclonal glp-4 (anti-lysozyme) and FRS of murine monoclonal
                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 4D; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel biosynthetic antibody binding site having chimeric polypeptide which defines selective antigen binding region and has CDR and framework amino acid sequences homologous to different immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-280767/29.
N-PSDB; AAF57658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huston JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CURI-) CURIS INC
                                                                                                                                       105;
                                                                                                                                                                                                                                  (anti-digoxin).
      64
                                      82
                                                                   4
                                                                                                    N
                                                                                                                                                      Similarity
GVPDRFSGSGSGTDFTLKISRVEAEDLGIYYCFQGSHVPWTFGGGTKLEIKR
                        GVPDKFSGSGSGTDFT1KISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR
                                                              VVMTQTPLSLPVŠLGDQASISCRSSQSIVHSNGNTYLDWYLQKAGQSPKLLIYKVSNRFS
                                                                                 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLBWYLQKPGQSPKLLIYKVSNRFS
                                                                                                                                                                                                       115
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oppermann
                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0213671.
                                                                                                                                                   95.6%;
                                                                                                                                     ..
                                                                                                                                               Score 567; DB 22;
Pred. No. 1.3e-42;
                                                                                                                                 Mismatches
                                                                                                                                                                 22;
                                                                                                                                 1.
                                                                                                                                                               Length 115;
                                                                                                                                 Indels
                                                                                                                                0
 115
                                                                                                                                Gaps
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## RESULT 5 AAR21262 Pd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus; g3p; binding; adsorption; gene VIII; diverse repertoire; specific binding pairs; replicable genetic display package; immunoglobulin; ss. Protein Peptide Protein Synthetic. pscFvNQ11 encoding anti-oxazalone antibody. 21-MAY-1992 AAR21262; AAR21262 standard; Protein; 249 AA. (first entry) Location/Qualifiers 'label= linker /label = \1<u>.</u> ≖ VH

23-JAN-1992

WO9201047-A.

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RESULT 6
AAE15704
ID AAE1
XX AAE1
XX AAE1
XX AOUS
XX MOUS
XX MUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anti-oxazalone antibody. NQ11, has been described by E. Gheradi, R. Pannell, and C. Milstein, (J. Immunol. Method 126 61-68). A plasmid contg. the VH and VL genes of NQ11 was converted to the scrv form by inserting the BstEII/SacI fragment of scFvD1.3 myc (nucleotides 432-499 of AAQ21096) between the VH and VL genes to generate pscFvNQ11 (protein sequence shown here). This scFv was cloned into PdTPs/Xh (see AAQ21095) to generate pAb NQ11. The specific bindin of pAb NQ11 was confirmed by ELISA.

See also AAR21260-307, 309-311; AAR22450, 565-581.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAY-1991;
10-JUL-1990;
19-OCT-1990;
12-NOV-1990;
06-MAR-1991;
                                                                                                                                                                                                                            Mouse; humanised form; monoclonal antibody alpha 340; gene therapy; epidermal growth factor receptor; EGF; cancer; colorectal; lung; breas gastric; ovarian; immune response; cytostatic; cell growth; apoptosis;
                      Region
                                                                                        Region
                                                                                                                                                             Mus sp
                                                                                                                                                                                                                                                                                                                          Mouse monoclonal antibody alpha 340 light chain variable (VK) region.
                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE15704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE15704 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                               inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxazalone is a hapten used for studying the immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing members of specific binding pairs - by expression recombinant host cells with a secreting replicable genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McCafferty J,
Jackson RH, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 9; Fig 13; 209pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CAMB-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-056862/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUL-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAMBRIDGE ANTIBODY.
MED RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holliger KP,
                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91GB-0010549.
90GB-0015198.
90GB-0022845.
90GB-0024503.
91GB-0004744.
                      /note= "Complementarity determining region
55..68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91WO-GB01134.
                                                                                                            Location/Qualifiers
                                                                 /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.6%;
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, Marks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 567; DB 13;
Pred. No. 2.9e-42;
3; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specific binding
                                                                                                                                                                                                                                                   therapy;
lung; breast;
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AAW03199
ID AAW
XX
AC AAW
AC AAW
DT 25-b
DT 26-E
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XX
Muri
KW Muri
KW vari

25-MAR-2003 26-FEB-1997 AAW03199;

(updated) (first en

entry)

AAW03199

standard; Protein; 149

8

61

Murine; mouse; variable light

Anti-idiotype monoclonal antibody 1A7 variable light chain.

anti-idiotype; monoclonal antibody; MAb; 1A7; chain; ganglioside 2; GD2; 14G2a; neuroblasto

14G2a; neuroblastoma;

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a humanised form of the antibody 340 (a C mouse monoclonal antibody which binds to epidermal growth factor (EGF) receptor and inhibits binding of EGF), obtainable from the cell line composited with the ECACC under accession number 97021428. The humanised CC manufacture of a medicament for treatment or prophylaxis of cancer. The invention is useful for treatment or prophylaxis of cancer after composition and the composite of cancer after composition and the composition of the action of the recurrence of cancer after composition cancers or also for preventing the recurrence of cancer after composition in the invention is also useful for enhancing a protective immune response against cancer by optimised immunisation composition of the antibody 340 has reduced immunogenicity but shows similar binding to cells expressing EGF conceptor, as the original murine antibody and has increased ability to inhibit the growth of EGF receptor expressing cells. The invention is cused as cell growth and apoptosis inhibitor. The present sequence is mouse monoclonal antibody alpha 340 light chain variable (VK) region.
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful
cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New humanized form of mouse monoclonal antibody 340 which binds to epidermal growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor and inhibits binding of growth factor receptor receptor and inhibits binding of growth factor receptor rece
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24-AUG-2000; 2000GB-0020794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ellis JRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAY-2001; 2001WO-GB02226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ($CAN-) SCANCELL LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-062384/08.
                                                                                              52
                                                                                                                                                        62
                                                                                                                                                                                                                  2 VIMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKBGQSPKLLIYKVSNRFS
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                             GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEI 111
                                                                                        GVPDRFSGSGSGTDFTLKISRVEAEDLGIYYCFQGSHVPWTFGGGTKLEI 111
                                                                                                                                                                                                                                                                               IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig 2; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 AA;
                                                                                                                                                                                                                                                                                                                                                  Conservative
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95..102
/label= CDR3
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                                                                                                                                                                                                                                                                                                                                                                              Score 565; DB 23;
Pred. No. 1.9e-42;
                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 112;
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The present sequence is that of the murine anti-idiotype monoclonal cantibody (MAb) 1A7 variable light chain. MAb 1A7 was raised against the anti-ganglioside 2 (GD2) MAb 1432a, which binds an unique Ceptiope of GD2. As the glycosphingolipid GD2 is expressed at high Consisty by human neuroectodermal tumours, e.g. malignant melanoma, concerned the lung, MAb 1A7, or its cDNA, can be used to reduce the corporate success. They can also be used to reduce the crisk of recurrence of a clinically detectable tumour, and detect an cuti-GD2 Ab bound to a tumour cell.

Consist GD2, which comprises anti-GD2 Ab (humoral response) and cuti-GD2 which comprises anti-GD2 Ab (humoral response) and cuti-GD2 in a sample or measure the level of cellular anti-IA7 or anti-GD2 in a sample or measure the level of cellular anti-IA7 or anti-GD2 in a sample or measure the level of cellular anti-IA7 or anti-GD2 in a sample or measure the level of cellular anti-IA7 or
                     The cDNA can be used in expression systems for 1A7 prodm., and in the prepm. of probes and primers to respectively assay for 1A7 cDNA, and amplify desired polynucleotides for use in gene therapy (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                         Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                 Monoclonal antibody 1A7 polypeptide(s) - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chatterjee M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JAN-1995;
16-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JAN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glycosphingolipid; human; neuroectodermal; tumour; glioma; lung; malignant melanoma; soft tissue sarcoma; small cell carcinoma; vaccine; treatment; palliate; detection; diagnosis; recombinant production; purification; probe; primer; assay;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amplification;
                                                                                                                                                                                                                                                                                                                                                             ial antibody 1A7 and related polynucleotide(s) and
ide(s) - useful to treat or palliate a GD2-associated
e.g. melanoma and glioma
                                                                                                                                                                                                                                                                                                                                       Fig 1; 141pp; English.
                                                                                    activity.
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96US-0591196.
95US-0372676.
96US-0591196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chatterjee
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81..112
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59..73
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Best Local
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                The invention provides a method of treating of psoriasis by administering an antigen which has similar immunogenic properties to an antigen expressed on cells of psoriatic tissue so that an immunological response is elicited in the individual. The antigen stimulates the generation of anti-idiotype antibodies that neutralize the aberrant immune response causing the psoriasis. The method is used to treat psoriasis, especially chronic plaque, gluttate, pustular, plaque-type psoriasis or psoriatic arthritis. The compositions allow the individual's own immune system to act against psoriatic tissue. The present sequence represents the light chain variable region of monoclonal antibody 1A7.
                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 2; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chatterjee M,
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17-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Psoriasis; immunological response; anti-idiotype antibody; chronic plaque; pustular; plaque-type psoriasis; psoriatic monoclonal antibody; 1A7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monoclonal antibody 1A7 light chain variable region
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                                                                                                                                       IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNRGNTYLEWYLQKPGQSPKLLIYKVSNRFS
GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR
                            GVPDKFSGSGSGFDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
                                                                                                     VLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPNLLIYFVSNRFS
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                                                                                                                                                                                                                                                                                                                                 149 AA;
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97US-0065774.
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                                                                                                                                                                                                                Score 563; DB 20;
Pred. No. 3.8e-42;
5; Mismatches 2
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Pred. No. 3.8e-42;
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                                                                                                                                                                                                                                                                                                                                            Composition is present between the time train of more around to activated vitronectin receptor alpha-v beta-3. WOW-1 Fab was created by replacing the 19 amino acid heavy chain complementarity determining region 3 (CDR3) of PACI Fab with the 50 amino acid alpha-v integrin-binding domain from adenovirus type 2 penton base protein by splice-overlap PCR (see AAA27850-53). PACI is a known monoclonal cantibody which immunoreacts with platelet glycoprotein receptor. The modified PACI antibody (designated WOW-1) has been expressed as WOW-1 Fab is used in a claimed method for detecting the presence of activated vitronectin receptor alpha-v beta-3 in a tissue, and in a claimed method for detecting the presence of claimed method for delivery of an agent in a therapeutic composition to such a tissue ex vivo or in vivo, the tissue being selected from neovascular cells, smooth muscle endothelial cells, arterial cells, composition is preferably a biologically active compound, especially a gene, antisense nucleic acid or catalytic nucleic acid (claimed).
                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel monoclonal antibody that selectively binds activated vitronectin receptor useful for detecting the presence of activated vitronectin receptor in tissue and for delivering therapeutic composition to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   grug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of the light chain of WOW-1 Fab,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 18; Page 15; 42pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shattil SJ, Nemerow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-EXFINDUNGEN VERW GES MBH.
(SCRI ) SCRIPPS RES INST.
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GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
                                                          VLMTQTELSLPVSLGDQASIPCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
                                                                                                   IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61
                                                                                                                                                                                                                                                                                                          219 AA;
                                                                                                                                                                                       Conservative
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99US-0145458.
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                                                                                                                                                                                                         Score 562; DB 2
Pred. No. 7e-42;
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                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                     DB 21;
                                                                                                                                                                                                                                        Length 219;
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RESULT 10
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XX MAD 1
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XW NOUNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumor-associated antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAb 1A7 light
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monoclonal antibody; MAb; 1A7; GD2; immune response; melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
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The invention provides a monoclonal antibody (MAD) dusignated 1A7, which elicits an anti-GD2 (tumor-associated antigen) immunological response in humans. MAD 1A7 has defined light and heavy Chain variable region sequences. The MAD 1A7 and polypeptides can be used for eliciting an anti-GD2 immune response. The polypeptides can also be used for detecting or purifying anti-GD2 antibody. The products can be used for treating GD2 -associated disease, e.g. melanoma, neuroblastoma, glioma, soft tissue carcinoma, and small cell carcinoma. They can be used for palliating the disease or for reducing the risk of recurrence. The present sequence represents the light chain variable region of MAD 1A7.

Monoclonal antibody 1A7 which elicits an anti-GD2 immunological response, useful for the development of products for the detection treatment of cancers -

WPI; 1999-619711/53.

AAZ31365

Foon KA,

Chatterjee

SK,

Chatterjee

(KENT ) UNIV KENTUCKY

Claim 1; Fig 1; 74pp; English

Sequence 149 AA;

Query Match

Local

Similarity

94.6%;

DB 20;

Length 149;

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RESULT 11
AAY28468
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AC AAY28
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                                                                                                                                                      Matches
                   AAY28468 standard; Protein;
                                                                                                                                                      105;
                                                                       18
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                                                                                                              21
                                                                                                                       GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
                                                                                                           VFMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPNLLIYFVSNRFS
                                                                   GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR
                                                                                                                                                     Conservative
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Pred. No. 5.8e
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AAY28468;

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This polypeptide is the variable light chain region of monoclonal anti-idiotype antibody 1A7. The polypeptide has three CDRs (complementarity determining regions) and four frame work regions. When administered to an individual the 1A7 antibody induces an immune-response against ganglioside GD2. The heavy chain variable region of the 1A7 antibody (AAY28469) is also capable of eliciting an anti GD2 response in mammals. Both the heavy and light chain variable regions of the 1A7 antibody produce anti-GD2 T cell and antibody responses. The peptides and antibody produce anti-GD2 T cell and antibody responses. The peptides and antibody smay be useful for the modulation of ganglioside GD2, and particularly for the treatment of GD2-associated tumours e.g. melanoma neuroblastoma, glioma, soft tissue sarcoma, and small cell carcinoma
Sequence
                                                                                                                                                                                                            Anti-GD2 immunological peptides useful for the treatment of tumours especially melanomas and small cell carcinomas
                                                                                                                                                                                                                                                  N-PSDB; AAX89552.
                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                              WPI; 1999-457600/38.
                                                                                                                                                                                                                                                                                    Chatterjee M,
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                       (including
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                     euroblastoma, glioma, soft
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                                                                                                                                                                                   Fig 1; 84pp; English.
149 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         variable region of MAb 1A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 variable region; antibody 1A7; T cell response; melanoma; GD2; CDR; complementarity determining region; carcinoma.
                                                                                                                                                                                                                                                                                                              KENTUCKY
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95US-0372676.
96US-0591196.
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43..58
/label= "CDR 1"
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59..73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= "Constant region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= "mature peptide"
/note= "light chain variable region of Ab 1A7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label= "Framework 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label= "Framework
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                      soft tissue sarcoma, and lung cancer).
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RESULT 12
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Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                                                                                                              This polypeptide is the product of PCR amplification and the joining of PCR products, creating Vh-(Lk)-Vl of antibody 1A7. Both the heavy and light chain variable regions of the 1A7 antibody produce anti-CD2 T cell and antibody responses. The peptides and antibodies may be useful for the modulation of ganglioside GD2, and particularly for the treatment of GD2-associated tumours e.g. melanoma, neuroblastoma, glioma, soft tissue sarcoma, and small cell carcinoma (including small cell lung cancer).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-NOV-1996;
17-JAN-1995;
16-JAN-1996;
                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-GD2 immunological peptides useful for the treatment of tumours especially melanomas and small cell carcinomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vh-(Lk)-Vl of antibody 1A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 7; Fig 15; 84pp; English.
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                         GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                              VLMTQTPLSLPVSLGDQAS:
                                                                                                                       IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK
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95US-0372676.
96US-0591196.
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                                                                                                                                                                                       Score 558; DB 20;
Pred. No. 1.9e-41;
5; Mismatches 2;
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Pred. No. 5.8e-42;
4; Mismatches 3
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                                                                                                                                                                                                                                   CC The present invention describes the use of a polypeptide (I) in the CC manufacture of a medicament for stimulating a cytotoxic T cell response, CC where (I) comprises a first portion comprising the part of human PC that CC binds to CD64 and a second portion comprising one or more heterologous CC T cell response in a patient such as a mammal, preferably human, by CC administering (I) to the patient. (I) has cytostatic activity and can be used in vaccine production. (I) and the nucleic acid encoding (I) are CC useful in the manufacture of a medicament for stimulating cytotoxic T CC cell response. The medicament is useful for preventing and/or treating CC cancer, e.g. colorectal, lung, breast, gastric or ovarian cancer. The CC medicament stimulates cytotoxic and helper T cell responses. The colorectal as vaccines to stimulate helper and cytotoxic T CC cell responses. The polypeptides and nucleic acids are useful in CC optimising immunisation schedules for enhancing a protective immune response against cancer. The present sequence represents an Fv region CC con example from the mresent inventor
                                                                                                                            Matches
                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of polypeptides and nucleic acids encoding the polypeptides, in manufacturing medicament for stimulating a cytotoxic T cell response and for preventing or treating cancer, e.g. colorectal, lung, breast ovarian cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 11; Page 38; 87pp; English
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Synthetic.
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                                                                                                                                                                                                                              example
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                                                                                     2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
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                    GVPDKFSGSGSGTDFTLKISRVEABDLGVYYCFQGSHVPWTFGGGTXL
GVPDRFSGSGSGTDFTLXISRVEAEDLGIYYCFQGSHVPWTFGGGTKL
                                                              VLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
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                                                                                                                                                                                                                              present invention.
                                                                                                                                               93.8%;
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                                                                                                                                             Score 556; DB 23;
Pred. No. 1.1e-41;
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RESULT 14

Mouse; immunoglobulin E; IgE; allergy; transgenic animal.

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Best Local
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                                                                                Mouse immunoglobulin E light chain.
                                                                                                                                                                                                     AAY17416;
                                                                                                                                                                                                                                                     AAY17416 standard; Protein;
                                                                                                                                            26-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monoclonal antibody 1A7 which elicits an anti-GD2 immunological response, useful for the development of products for the detection
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                                                                                                                                                                                                                                                                                                                                                                                                                            62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                              GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLBWYLQXXGQSPXLLIYFVSNRFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 AA;
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                                                                                                                                                                                                                                                       238
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Pred. No. 1.4e-41;
5; Mismatches 2
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                                                                                                                       Query Match 93.6%; Score 555; DB 20; Length 238; Best Local Similarity 92.9%; Pred. No. 3.2e-41; Matches 104; Conservative 6; Mismatches 2; Indels
                                                                                                                                                                                                              The present invention describes a transgenic, non-human animal with its genome altered to constitutively express a molecule having a constant region which can bind an IgE receptor on mast cells in the animals, the molecule having an immunoglobalin structure and being further capable of specifically binding a predetermined antigen. The transgenic animal is useful as a model for evaluating the activity and the ability of substances i.e. with antiallergic activity, to affect any allergic reaction caused in the animal by the administration of the antigen to the animal, and applying the substance to be evaluated. The present sequence is the mouse immunoglobulin E (IgE) light chain, given in the present invention.
                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-315404/27.
N-PSDB; AAX61085.
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 28; Page 30-32; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Transgenic non-human animal allergy models
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Karasuyama H, Matsuoka K, Taya C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-NOV-1997;
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(TOKM-) TOKYO METROPOLITAN INST MEDICAL SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP921189-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
21 VLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 80
                                                                               2 IVLTQSPISLEVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61
                                                                                                                                                                                      238 AA;
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/1abel= signal
20..238
/label= immunoglobulin_B_light_chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yonemawa H;
                                                                                                                         0;
                                                                                                                       Gaps
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Search completed: November 7, 2003, 07:27:01 Job time : 49.7303 secs

Scoring table:

Sequence 6, Appli sequence 5, Appli sequence 4, Appli sequence 4, Appli sequence 4, Appli sequence 4, Appli sequence 4, Appli sequence 32, Appli sequence 32, Appli sequence 3, Appli sequence 4, Appli sequence 4, Appli sequence 4, Appli sequence 4, Appli sequence 4, Appli sequence 2, Appli sequence 2, Appli sequence 2, Appli sequence 1, Appli sequence 1, Appli sequence 1, Appli sequence 1, Appli sequence 1, Appli sequence 1, Appli sequence 1, Appli sequence 1, Appli sequence 6, Appli sequence 6, Appli sequence 6, Appli sequence 6, Appli sequence 6, Appli sequence 6, Appli sequence 6, Appli sequence 6, Appli sequence 1, Appli sequence 6, Appli sequence 1, Appli sequence 2

Perfect score:

OM protein

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Post-processing: Minimum Match 0% Maximum Match 10
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Maximum DB seq length: 200000000
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12:
13:
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                          BLOSUM62
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195.799 Million cell updates/sec
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593
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                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
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              14
9 9 10
112
113
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           11 US-09-995-529-10
US-09-990-205-2
US-10-153-401-6
US-10-153-401-15
US-10-153-401-15
US-10-153-401-15
US-10-153-401-15
US-10-153-401-15
US-10-205-73-15
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US-09-341-894-4
US-09-341-894-4
US-09-796-794-16
2 US-10-231-452-64
2 US-10-231-452-64
2 US-10-231-452-64
2 US-09-948-049-2
10 US-09-948-049-2
10 US-09-948-039-95
0 US-09-9887-833-4
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     Sequence 10, Appli Sequence 2, Appli Sequence 2, Appli Sequence 15, Appl Sequence 15, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 18, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 27, Appli Sequence 27, Appli Sequence 28, Appli Sequence 29, Appli Sequence 29, Appli Sequence 24, Appli Sequence 24, Appli Sequence 24, Appli Sequence 24, Appli Sequence 24, Appli Sequence 24, Appli
                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                        Sequence 10, Application US/0999529
Publication No. US20030099655A1
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
APPLICANT: Huse, William D.
APPLICANT: Tang, Ying
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Related Methods
FILE REFERENCE: P-IX 4976
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOPTWARE: FastSEQ for Windows Version 4.0
EENGTH: 112
TYPE: PAT
ORGANISM: Mus musculus
US-09-995-529-10
RESULT 2
US-09-990-205-2
; Sequence 2, Application US/09990205
; Patent No. US20020150572A1
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US-09-995-529-10
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Best Local Similarity
Matches 106; Conserva
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494.5
487
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                                                                                                                                                   2 IVLTQSELSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQXPGQSPKLLIYKVSNRFS :::||:|||||||||||||||
                                                                                GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK
                                                                                                     GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                 96.3%; Score 571; DB 11;
95.5%; Pred. No. 1.9e-49;
tive 5; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 US-10-138-505-26
9 US-09-883-758-4
15 US-10-138-505-30
15 US-10-138-505-30
15 US-10-138-505-34
15 US-10-138-505-34
15 US-10-138-505-34
15 US-10-138-505-34
16 US-10-163-942-45
17 US-09-982-9928-4
18 US-09-726-258-42
18 US-09-726-258-42
19 US-09-726-258-42
10 US-09-726-258-42
10 US-09-726-258-42
10 US-09-726-258-42
10 US-10-231-452-13
11 US-09-726-258-45
12 US-10-231-452-14
13 US-10-231-452-14
14 US-09-733-452-14
15 US-09-733-452-14
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10 US-09-753-1452-14
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US-10-277-471A-5
US-10-138-505-6
US-10-138-505-30
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Result No.

Score

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Gaps

61 62 0

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US-10-153-401-2
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; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-990-205-2
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Best Local Similarity 93.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/990,205
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: U.S. 09/192,838
PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: U.S. 60/065,774
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: FOON, Kenneth A.
APPLICANT: CHATTERJEE, Malaya
APPLICANT: CHATTERJEE, Malaya
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
FILE REFERENCE: 304142000501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0
TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 813-5600
                                                                                                     APPLICATION NUMBER: US 09/293,533
FILING DATE: 1999-04-15
APPLICATION NUMBER: US 08/372,676
FILING DATE: 1995-01-17
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1996-01-16
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,401
FILING DATE: 27-Aug-2002
CLASSIFICATION: <Ukrown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FOOT, Kenneth A.
Chatterjee, Sunil K.
CIATTE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE
TREATMENT OF MELANOMA AND SMALL
                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Chatterjee, Malaya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 VLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPNLLIYFVSNRPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61
                                           REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 304142000202
                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                   NAME: Catherine M. Polizzi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: PALO ALTO
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Pred. No. 1.7e-48;
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SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-153-401-66
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US-10-153-401-66
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Publication No. US2003
GENERAL INFORMATION:
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                                                                                                               TELEX: 706141
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                 CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA;
APPLICATION NUMBER: US 09/293,533
FILING DATE: 1999-04-15
APPLICATION NUMBER: US 08/372,676
FILING DATE: 1995-01-17
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1996-01-16
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIF: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                    TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Foon, Kenneth A.
Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chatterjee, Malaya
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 VFMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPNLLIYFVSNRFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 IVLTQSPLSLFVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS ::||:||||||||||||||
                                                                                                                                                                                                                                     NAME: Catherine M. Polizzi
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 304142000202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/10/153,401 FILING DATE: 27-Aug-2002
                                                                                            LENGTH: 263 amino acids
                                                                                                                                                                                TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: CA
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                                                                                                                                                                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
ULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 149 amino acids
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to. US20030114398A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DORESSEE: MORRISON & FOERSTER
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Pred. No. 2.6e-48;
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RESULT 5
US-10-153-401-15
/ Sequence 15, Application US/10153401
/ Publication No. US20030114398A1
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INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/153,401
FILING DATE: 27-Aug-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION; SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC computible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Chatterjee, Sunil K.

TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 813-5600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 263
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                                                                                104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 09/293,533
FILING DATE: 1999-04-15
APPLICATION NUMBER: US 08/372,676
FILING DATE: 1995-01-17
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1996-01-16
VLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKKGQSPKLLIYFVSNRFS 61
                                                                                                                                                                                                                                                                    TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 304142000202
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Catherine M. Polizzi
REGISTRATION NUMBER: 40,13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: CA
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                                                                                                                                                                                                                                                STRANDEDNESS: single
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                                                                                               93.6%;
93.7%;
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93.7%;
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                                                                                  5; Mismatches
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                                                                                               Score 555; DB 15; Length 112; Pred. No. 7.5e-48;
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                                                                                Indels
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US-09-217-268B-27
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                                                                                                                                                                                                                               US-09-217-268B-27
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LENGTH: 13
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APPLICANT: Junghans, Richard P.
TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tu
                                                                                                                                                                                                                                                                                                                                             SOPTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                            Matches
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                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mateo de Acosta del Rio, Christina M
APPLICANT: Rodriquez, Rolando P
APPLICANT: Rrias, Ernesto M
TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recogni
TITLE OF INVENTION: Growth Factor Receptor (EGF-R); Diagnostic and Therapeut
FILE REFERENCE: 2720.1US
CURRENT SPLICATION NUMBER: US/09/217,268B
CURRENT FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/006,773
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: 60/250,089
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 19
SOFTMARE: PatentIn version 3.1
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                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: MISC_FEATURE
OTHER INFORMATION: Deduced amino acid sequence of VK of murine R3 antibody
                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Murine R3 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mus sp.
                                                                                                                                                                    Local
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62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVFWTFGGGTKLEIKR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 GVPDKFSGSGSGTDFTLXISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
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                                                                                        2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61
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                                                                2 VLMTQIPLSLPVSLGDGASISCRSSQNIVHSNGWTYLDWYLQKPGQSPNLLIYKVSNRFS
                                                                                                                                                                Similarity
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                                                                                                                                          91.2%; Score 541; DB 9; Length 114; 90.2%; Pred. No. 1.9e-46; tive 6; Mismatches 5; Indels
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Pred. No. 2.3e-47;
8; Mismatches 1
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; LENCTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-796-744-16
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                                                                                 SOFTWARE: Patentin
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Piechaczyk, Marc
APPLICANT: No. US20020168339A11, Daniele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 101;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09341894
Patent No. US20020168339A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEATURE:

NAME/KEY: misc feature

LOCATION: (1). (420)

OTHER INFORMATION: Seque

OTHER INFORMATION: ain
                                                                                                                                                APPLICANT: SHIBATA, KENJI
APPLICANT: YAMASAKI, MOTOO
TITLE OF INVENTION: GREE RECOMBINANT ANTIBODY AND ANTIBODY FRAGMENT THEREOF
FILE REFERENCE: 249-170
CURRENT APPLICATION NUMBER: US/09/796,744
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: JP 2000-59508
PRIOR APPLICATION NUMBER: JP 2000-401563
PRIOR APPLICATION NUMBER: JP 2000-401563
PRIOR APPLICATION NUMBER: JP 2000-401563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. US20020098527A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/341,894
CURRENT FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: FR97/00540
PRIOR FILING DATE: 1997-01-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
                                                                                                                             PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SHITARA, KENYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Biological material for treating a mammal by antibody gene transf
TITLE OF INVENTION: pharmaceutical composition containing same
FILE REFERENCE: 19904-002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Mus musculus
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SHOJI, EMI
SAKURADA, MIKKIKO
FURUYA, AKIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVPDRFSGSGSGTDFTLKISKVEAEDLGLYYCFQGSHIPFTFGSGTKFEIKR 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09796744
                                                                                                                                                                                                                                                                                                                                                                             NIWA, RINPEI
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90.2%;
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Pred. No. 2.4e-46;
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GENERAL INFORMATION:

APPLICANT: SHITARA, KENYA

APPLICANT: NAKAMURA, KAZUYASU

APPLICANT: HOSAKA, EMI

APPLICANT: TANAKA, AKIXO

APPLICANT: TOSAKA, EMI

APPLICANT: KOIKE, MASAMICHI

TITLE OF INVENTION: HUMAN COR GRAFTED ANTIBODY AND

FILE REPERENCE: 249-273

CURRENT APPLICATION NUMBER: US/10/231,452

CURRENT FILING DATE: 2003-04-18

PRIOR APPLICATION NUMBER: JP 2001-265144

PRIOR PILING DATE: 2001-08-31

NUMBER OF SEQ ID NOS: 78

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 64

TENCTUR. 130
                                                                                                                      APPLICANT: Basi, Guriq
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Ted
ITILE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
TITLE OF INVENTION: BETA AMYLOID PEPTIDE
FILE REFERENCE: ELN-002
CURRENT APPLICATION NUMBER: US/10/010,942B
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: US 60/251,892
PRIOR PILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                            SEQ ID NO 14
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Publication No.
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Best Local (
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Best Local :
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Publication No. US20030175273A1
PEATURE:
NAME/KEY: SIGNAL
                                       LENGTH: 131
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 132
TYPE: PRT
ORGANISM: Mus musculus
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No. US20030165496A1
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Pred. No. 8.8e-46;
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RESULT 13
US-09-518-737-4
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US-09-948-049-2
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GENERAL INFORMATION:
APPLICANT: Nicolau, Yves Claude
TITLE OF INVENTION: Methods and Compositions for Diseases Associated with Amyloidosis
FILE REFERENCE: 14723-0112 49055-261163
CURRENT APPLICATION NUMBER: US/09/948,049
CURRENT FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US 60/255,033
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: US 60/230,391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-010-942B-14
                                                        SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09518737
Publication No. US20030008321A1
                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 111
                                                                      CURRENT APPLICATION NUMBER: US/09/518,737
CURRENT FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: UP 1999-250209
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                 APPLICANT: FUKUI, YASUHISA
APPLICANT: NAGATA, SATOSHI
APPLICANT: SHIRAI, RYUICHI
APPLICANT: SHIRAI, RYUICHI
APPLICANT: SAITO, NAOAKI
TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3,4-DIPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
                                                                                                                                                                                            FILE REFERENCE: 1965/49618
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Murinae gen. sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1) ... (19)
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                      H: 112
PRT
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87.4%;
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Pred. No. 1.8e-45;
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Pred. No. 1.1e-45;
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; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 95:
US-09-947-839-95
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                        Query Match
Best Local (
          Matches
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Best Local :
                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/947,839
FILING DATE: 06-Sep-2001
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/976,288
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: 08/976,288
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: 07/977,696
FILING DATE: NO. US20030138428Alember 16, 1992
ATTORNEY/ACENT INFORMATION:
NAME: VILLED TOWNS NO. US20050138428Alember 16, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                     NAME: Viviana Amzel Ph.D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P6639938
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEPAX: (213) 489-4210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: do Couto Dr., Fernando J.R.

Ceriani Dr., Roberto L.

Peterson Dr., Jerry A.

Padlan Dr., Eduardo.

TITLE OF INVENTION: Analogue Peptides With Broad Carcinoma Specificity, and K.

Diagnostic Vaccination and
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                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VWMTQTPLSUPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFS
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                                                                                                                                   LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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ZIP: 90071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
88.5%; Score S25; DB 12;
87.4%; Pred. No. 8.7e-45;
cive 11; Mismatches 3;
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Pred. No. 5.8e-45;
9; Mismatches 4;
                                    Length 131;
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  Indels
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Search completed: November 7, 2003, 08:16:52 Job time: 100:12 secs
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/09/887,853
FILING DATE: 21-Um-2001
CLASSIFICATION NUMBER: US/09/887,853
FILING DATE: 21-Um-2001
CLASSIFICATION NUMBER: US/08/133,804
FILING DATE: E1-Uncown>
APPLICATION NUMBER: US/08/133,804
FILING DATE: 4Unknown>
APPLICATION NUMBER: US/08/133,804
FILING DATE: 4Unknown>
APPLICATION NUMBER: US/08/133,804
FILING DATE: 4Unknown>
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                US-09-887-853-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-09-887-853-4
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                                                                                                                                                                                                                                                                 Query Match 88.5%; Score 525; DB 10; Length 252; Best Local Similarity 88.4%; Pred. No. 1.8e-44; Matches 99; Conservative 8; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09887853
Patent No. US20020168375A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault/Patent Department
STREET: Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oppermann, Hermann
Houston, L. L.
Ring, David B.
RING, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Huston, James S.
                                                                                    62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
                                                                                                                                                                     21 VLMTQTPLSLPVTPGEPASISCRSSQSIVHSNGNTYLEWYLQXPGQSPQLLIYXVSIRFS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Imaging
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein search, using sw model
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Match
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593
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2: /cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
2: /cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
3: /cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/1/iaa/FCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/1/iaa/backfiles1.pep:*
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      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                            US-09-192-838B-2
US-09-324-151-2
US-08-331-398A-67
US-08-331-398A-66
US-08-752-844-2
US-08-752-844-66
US-08-752-844-15
US-08-752-844-15
US-08-752-844-15
US-08-752-844-15
US-08-752-844-48
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US-08-752-844-48
US-08-752-844-48
US-08-752-844-48
US-08-752-844-48
US-09-022-753A-3
US-09-227-693-48
US-09-227-693-34
      US-08-331-398A-34
US-08-331-397B-34
US-08-759-804A-34
US-08-859-649-19
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Sequence 2, Appli
Sequence 67, Appli
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RESULT 2 US-09-324-191-2 US-09-324-191-2 ; Sequence 2, Application US/09324191 ; Patent No. 6562798 ; GENERAL INFORMATION: ; APPLICANT: THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION ; APPLICANT: CHATTERJES, MALAYA ; APPLICANT: COON, KENTHODS AND COMPOSITIONS FOR THE TREATMENT OF PSOIN FOR THE TREATMENT OF THE TREATMENT OF THE TREATMENT OF THE TREATMENT OF THE TREATMENT OF THE TREATMENT OF THE TREATMENT OF THE TREATMENT OF THE TREATMENT OF THE TREATMENT OF THE TREATMENT OF THE TREATMENT OF THE TREATMEN	2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQXDGQSPXLLIYKV 2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQXDGQSPXLLIYKV 2:::  :	THE TREATMENT OF	546 92.1 131 1 US-08-053-171-5 Sequence 5, 546 92.1 131 1 US-08-053-171-5 Sequence 5, 546 91.6 238 2 US-08-224-591-12 Sequence 12, 543 91.6 238 2 US-08-392-338A-21 Sequence 21, 543 91.6 238 2 US-08-926-789-12 Sequence 21, 543 91.6 238 3 US-09-166-790-21 Sequence 21, 543 91.6 238 3 US-09-166-093-21 Sequence 21, 543 91.6 238 3 US-09-166-093-21 Sequence 21, 543 91.6 238 3 US-09-166-094-21 Sequence 21, 543 91.6 238 3 US-09-172-019-21 Sequence 21, 543 91.6 238 3 US-09-146-094-21 Sequence 21, 543 91.6 238 4 US-09-443-213-21	550 92.7 112 2 US-08-859-649-29 Sequence 29, 550 92.7 112 4 US-08-207-861-19 Sequence 19, 550 92.7 112 4 US-08-207-861-29 Sequence 29, 550 92.7 112 4 US-08-859-648-19 Sequence 19, 550 92.7 112 4 US-08-859-648-29 Sequence 19, 549 92.6 112 2 US-08-889-366-16 Sequence 26, 548 92.4 114 2 US-08-560-5588-27 Sequence 27, 549 92.4 114 2 US-08-560-5688-27 Sequence 27, 549 92.4 114 92.4 114 92.4 114 92.4 114 92.4 114 92.4 114 92.4 114 92.4 11
F PSORIASIS	Gaps 0; KVSNRFS 61        FVSNRFS 80 113	F PSORIASIS	222222222222222222222222222222222222222	29, App 19, App 29, App 19, App 19, App 16, App 16, App 18, App

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US-08-331-398A-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                            TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-5600
TELEPHONE: (415) 543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/331,398A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC comparible
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0'
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 30-SEP-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins TITLE OF INVENTION: and Their Uses (as amended) NUMBER OF SEQUENCES: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
NAME/KEY: Region LOCATION: 1..125 OTHER INFORMATION: OTHER INFORMATION:
                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                       NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 28
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew STREET: One Market Plaza, Steuart Street Plaza
                                                                                                            TOPOLOGY:
                                                                                                                            STRANDEDNESS:
                                                                                                                                                             LENGTH: 125 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67,
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                                                                                                                                               amino acid
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FitzGerald, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pastan,
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                                                                                                            linear
                                                                                       protein
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/note= "Mouse monoclonal antibody B5 Fv
Light chain region"
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Pred, No. 1.1e-47;
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US-08-331-397B-67
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Patent No. 5
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                                    Query Match
Matches 106; Conservative
                                                                                                                                                                                                                                                                      IRLEFAX: (415) 543-504
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Pastan, Ira
APPLICANT: Benhar, Itai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/767,331 FILING DATE: 30-SEP-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                        NAME/KEY: Region
LOCATION: 1..125
CITHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                     TELEPHONE: (415)
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                             NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 28-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                   Match 94.8%;
Local Similarity 94.6%;
                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                         ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T: One Market Plaza, Steuart Street Plaza San Francisco
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Similarity 94.6%;
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381726
                                                                                                                                                                                                                                                       125 amino acids
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                                                                                                                                                                                                     linear
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) 543-5043
Q ID NO: 67:
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Specific Antibody Fragments, Fusion Proteins,
Thereof
                                                                                        /note= "Mouse monoclonal antibody B5
Light chain region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/331,397B
                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 07/596,289
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                   Score 562; DB 2; Length 125; Pred. No. 1.2e-47;
                                                                                                                                                                                                                                                                                                                                                                   015280-126120US
 5; Mismatches
 Indels
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US-08-759-804A-66
                                                                                                                 US-08-759-804A-66
                            Query Match
Best Local Similarity 94.6
Matches 106; Conservative
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                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 576-0300
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL
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FILING DATE: 03-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-CCT-1994
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TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                               LOCATION: 1..125
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                      NAME/KEY: Region LOCATION: 1..125
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                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                       TYPE: amino acid
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2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61
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FitzGerald, David J.
Brinkmann, Ulrich
                                                                                                                                                                                                                                                                                                        125 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                    (415) 576-0200
                                                                                                                                                                                                                              protein
                                                     94.8%;
94.6%;
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                                                                                                                               /note= "Mouse monoclonal antibody B5
Light chain region"
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                                                       Score 562;
Pred. No. 1
                                       Mismatches
                                                                          DB 2; Length 125;
                                  Indels
                                     0
                                Gaps
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; Sequence 2, Applic
; patent No. 597/316
; GENERAL INFORMATI
; APPLICANT: Cha
; APPLICANT: Poo
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GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 494-079
TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chatterjee, Malaya
APPLICANT: Foon, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCIONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 66
APPLICANT: Chatterjee, Malaya
APPLICANT: Foon, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/752,844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                 ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                 105;
                                                                         INFORMATION:
                                                                                                                                                                                                                                   62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 113
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                                                                                                                                                                                                            81 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIKR 132
                                                                                                                                                                                                                                                                                     21 VFMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPNLLIYFVSNRFS
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                                                                                                                                                                                                                                                                                                            H: 149 amino acide
amino acid
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                                                                                                               Application US/08591196
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                                                                                                                                                                                                                                                                                                                                                            ; Score 561; DB 2; Length 149; 
; Pred. No. 1.8e-47; 
4; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
COUNTRY: USA

COUNTRY: USA

219: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1

CURRENT APPLICATION NUMBER: US/09/293,533

FILING DATE:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                    APPLICANT: Chatterjee, Malaya
APPLICANT: Foon, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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NAME: SChiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPHANE: (415) 8494-0792
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
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                                                                                                                                                                                                               CITY: PALO ALTO
                                                                                                                                                                                                                                     STREET:
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CLASSIFICATION: 424
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    Application US/09293533

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVXYCFQGSHVPWTFGGGTKLEIKR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 VFMTQTPLSLEVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPNLLIYFVSNRFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRPS 61
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US-08-752-844-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                         TELEFAX: (415) 494-079;
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, ve
CURRENT APPLICATION DATA;
APPLICATION UNMBER: US/08/752,844
FILING DATE:
CLASSIFICATION: 424
                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 3041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chatterjec, APPLICANT: Chatterjee, Sunil K.
APPLICANT: Foon, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
APPLICANT: Chatterjee, Sunil K.
APPLICANT: Chatterjee, Sunil K.
APPLICANT: Chatterjee, Sunil K.
APPLICANT: POON CONTROL ANTIBODY 1A7 AND USE FOR THE APPLICANT OF MELANOMA AND SMALL CELL CARCINOMA
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
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NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
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APPLICATION NUMBER:
                                                                                              TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 494-0792
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ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 149 amino acids TYPE: amino acid TOPOLOGY: linear
POPOLOGY:
        ENGTH: 263 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66, Application US/08752844
o. 5935821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 VEMTQTELSLEVSIGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPNLLIYFVSNRFS
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93.8%;
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Pred. No. 1.8e-47;
                                                                                                                                                                                                                                                                                                                                Version #1.30
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Foon, Kenneth A.
APPLICANT: Foon, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
APPLICANT: Chatterjee, Sunil K.
APPLICANT: CHATTEN MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
                                                                                                                                                              Matches
                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 66,
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                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                               LENGTH: 263 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 755 PAGE CITY: PALO ALTO
                                                                                                                                                                             Match 94.1%;
Local Similarity 93.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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213 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 263
                                                                            153 VLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPNLLLIYFVSNRFS 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 VLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPNLLIYFVSNRFS 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104;
                          62 GVPDKFSGSGSGIDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                              104; Conservative
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                                                                                                            2 IVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLBWYLQKPGQSPKLLIYKVSNRFS 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.1%; Score 558; DB 2; Length 263; 93.7%; Pred. No. 6.6e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/752,844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40,253
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                                                                                                                                                              5; Mismatches
                                                                                                                                                                             Score 558; DB 4;
Pred. No. 6.6e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30414-20002.21
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                                                                                                                                                                                                   DB 4; Length 263;
                                                                                                                                                            2; Indels
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TOPOLOGY: li

; MOLECULE TYPE:

US-08-752-844-15
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US-08-752-844-15
                                                                                                                                                                                              ; Sequence 15, Application US/08591196; Patent No. 5977316; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 494-0797
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Chatterjee, Malaya
APPLICANT: Foon, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                             APPLICANT: Chatterjee, Malaya
APPLICANT: Foon, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CAR
NUMBER OF SEQUENCES: 57
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NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,
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ADDRESSEE: MORRISON & FOERSTER
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) --- (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/752,844
FILING DATE:
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKKGQSPKLLIYFVSNRFS
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93.7%;
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Pred. No. 5e-47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 112;
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                                                                                          CARCINOMA
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TELEX: 706141
INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Appli
Patent No. 6509016
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Best Local Similarity
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APPLICANT: Chatterjee, Malaya

APPLICANT: Foon, Kenneth A.

APPLICANT: Chatterjee, Sunil K.

APPLICANT: Chatterjee, Sunil K.

TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE

TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CAP

TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CAP

TOTAL OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CAP

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                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ORBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
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NAME: SCHLIf, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPAX: (415) 494-0792
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PACEDIS PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 755 PAGE MILL ROAD CITY: PALO ALTO
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CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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    US/08/752,844
                                                                                                                                                             US/09/293,533
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Pred. No. 5e-47;
5; Mismatches
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RESULT 15
US-08-331-398A-48
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; ORGANISM: Artificial Sequence; PEATURE: Description of Artificial Sequence: Designed heavy US-09-192-545-4
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                               Sequence 48, Application US/08331398A Patent No. 5608039
                 Patent No.
GENERAL I)
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09192545
Patent No. 6118044
                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/192,545
CURRENT FILING DATE: 1998-11-13
EARLIER APPLICATION NUMBER: JP HEI 9-313989
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 12
SOFTMARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Karasuyama, Hajime
APPLICANT: Yonekawa, Hiromichi
APPLICANT: Taya, Choji
APPLICANT: Matsuoka, Kunie
TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their U
FILE REFERENCE: 799P79570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 706141
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
APPLICANT:
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TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. michael
REGISTRATION NUMBER: 40,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                             104;
                 INFORMATION:
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                                                                                                                                                                 62 GVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCCFQGSHVPWTFGGGTKLEIKR 113
                                                                                                                                                                                                                  21 VLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS
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                                                                                                                                                                                                                                            2 IVLTQSplslpvslgdqasiscrssqsivhsngntylewylqkpgqspklliykvsnrfs
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                                                                                                                                             GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPLTFGAGTKLELKR 132
                                                                                                                                                                                                                                                                                               Conservative
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93.7%; Pred. No. 5e-47;
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Pred. No. 1.2e-46;
                                                                                                                                                                                                                                                                                               Mismatches
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COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/331,398A
FILING DATE: 28-CCT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
FRIOR APPLICATION NUMBER: US 07/596,289
FILING DATE: 10-CCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: HUNTER: 12-CCT-1990
ATTORNEY/AGENT INFORMATION:
REGESTRATION NUMBER: 015280-126110US
TELEPHONE: (415) 543-5000
TELEPAX: (415) 543-5000
TELEPAX: (415) 543-5000
TELEPAX: (112 amino acids
TYPE: amino acids
Search completed: November 7, 2003, 07:30:09 Job time : 17.5955 secs
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                                                                                                                                                                                                                                       Query Match 93.1%; Score 552; DB 1; Length 112; Best Local Similarity 93.7%; Pred. No. 9.7e-47; Matches 104; Conservative 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Pai, Lee
APPLICANT: Pai, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
                                                                                                                                                                                                                                                                                                                                                                                              PEATURE:
NAME/KEY: Protein
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APPLICANT:
APPLICANT:
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OTHER INFORMATION:
OTHER INFORMATION:
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STRANDEDNESS:
TOPOLOGY: linear
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CITY: San Francisco
STATE: California
                                                                                 62
                                                                                                62 GVPDKFSGSGGTDFTLKISRVEAEDLGVYYCFQQSHVPMTFQGGTKLEIK 112
                                                                                                                                                     GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPFTFGSGTKLEIK 112
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FitzGerald, David
Brinkmann, Ulrich
                                                                                                                                                                                                                                                                                                                                   /note= "Mouse monoclonal antibody B3
Variable Light chain (V-L)"
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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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    22222222222222222
24236242222222222
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BB
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484.5
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492.5
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487
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length: 2000000000
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644
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                      Match
                                                                                                                                                                                                                                                                                                                                                                      PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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742.581 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283308 segs, 96168682 residues
   EVQLQESGGGLVKPGGSLKL.....FTVNWYFDVWGAGTLVTVSA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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   띯
                                                                                                                                 S55538
PH0098
C27888
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S26327
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 Description
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472.5	472.5	473	475	477	477	477.5	477.5	480	480.5	480.5	482	482.5	483	483.5	484
73.4	73.4	73.4	73.8	74.1	74.1	74.1	74.1	74.5	74.6	74.6	74.8	74.9	75.0	75.1	75.2
119	111	106	147	112	108	142	119	123	124	108	121	118	121	111	121
N	N	N	N	Ŋ	N	N	N	N	Ŋ	N	N	N	N	N	N
C36005	\$40090	PH1008	I37780	A27889	PL0248	C34903	B34353	G27888	127888	PH1006	S55540	S20641	D27888	PH1007	B27888
Ig heavy chain V r	Ig heavy chain - m	Ig heavy chain V r	Ig variable region	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain pre	anti-peptide Fab'	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r		Ig heavy chain V r	_		Ig heavy chain V r

## ALIGNMENTS

Ig heavy chain V region (H35-C6) - mouse C;Species: Mus musculus (house mouse) C;Deceies: Mus musculus (house mouse) C;Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996 C;Accession: E27888 R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W. BMBO J. 5, 1577-1587, 1986 MBO J. 5, 1577-1587, 1986 A;Reference number: A91043; MUID:86300658; PMID:2427335 A;Accession: E27888

A; Molecule type: DNA A; Residues: 1-122 < CAT>

A; Experimental source: strain Balb/c

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R;Stark, S.B.; Caton, A.J.

1. Exp. Med. 174, 613-624, 1991

A;Title: Antibodies that are specific for a single amino A;Reference number: S26309; MUID:91341421; PMID:1908510

A;Accession: S26327
                                                                                                                                                                                Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C;Accession: $26327
                                                                                                                                                                                                                                                                    RESULT 2
S26327
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A;Molecule type: mRNA
A;Residues: 1-112 <STR>
A;Cross-references: EMBL:X59192
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTFEKRLEWVATISSGGSSTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Pred. No. 6.5e-41;
6; Mismatches 10
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-119 <CAT>
A; Residues: 1-119 <CAT>
A; Residues: 1-119 <CAT>
A; Rote: this sequence was determined from the germline gene
C; Comment: This chain was isolated from a hybridoma protein that
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R/Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, J. Exp. Med. 171, 265-297, 1990
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0249
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PL0249
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F;31-35/Region: complementarity-determining
F;36-49/Region: framework 2
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F;9-91/Domain: immunoglobulin homology <IM</pre>
                                                                                                                                                                                    A;Title: Structural and functional implications of a restricted A;Reference number: A91043; MUID:86300658; PMID:2427335 A;Accession: F27888
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                                                                                                                                                                                                                                                                                                     C;Accession: F27888
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A; Residues: 1-117 < SHL>
                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain
                                                                                                                                                                                                                                                                                                                     g heavy chain V region (H158-89H4) - mouse
;Species: Mus musculus (house mouse)
;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;109-117/Region: framework
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Pred. No. 4.7e-39;
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RESULT 6

$55537

Ig heavy chain V region pe21 - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999

C:Accession: $55537

C:Accession: $55537
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A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-120 <-BOS>
A,Residues: 1-120 <-BOS>
A,Cross-references: EMBL:X82589; NID:g854304; PIDN:CAA57925.1; PID:g854305
A,Cross-references: EMBL:X82589; NID:g854304; PIDN:CAA57925.1; PID:g854305
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin homology <-IMM>
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S55536
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R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibod utations in the variable region genes.

utations in the variable region genes.
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A;Residues: 1-120 <BOE>
A;Cross-references: EMBL:X82590; NID:g854306; PIDN:CAA57926.1; PID:g854307
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
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A, Accession: S55537
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Best Local Similarity
Matches 102; Conserv
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Best Local :
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Pred. No. le-38;
4; Mismatches 1
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Pred. No. 7.6e-39;
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Ig heavy chain V region precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
C;Accession: S09258
R;Hamada, H; Maezawa, K.; Tsurro, T.
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              A;Molecule type: DNA
A;Residues: 1-121 <CRT>
A;Residues: 1-121 <CRT>
A;Resperimental source: strain Balb/c
A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                A;Title: Structural and functional implications of a restricted A;Reference number: A91043; MUID:86300658; PMID:2427335 A;Accession: I27887
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A;Residues: 1-138 <HAM>
A;Cross-references: EMBL:X51719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Nucleotide sequences of the variable regions of A; Reference number: $09258; MUID:90245594; PMID:2110659 A; Accession: $09258
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                                                                                                                                                                                                                                                 Ig heavy chain V region (H37-45) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change
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C; Superfamily: immunoglobulin V region; im C; Keywords: heterotetramer; immunoglobulin
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Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords; heterotetramer; immunoglobulin
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Pred. No. 1e-38;
3; Mismatches 14;
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Pred. No. 1.
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RESULT 9
FU0252
Ig heavy chain V region (anti-DNA, clones 2E3VH, 6B8VH, and 3G9VH) - mouse (fragging heavy chain V region (anti-DNA, clones 2E3VH, 6B8VH, and 3G9VH) - mouse (fragging heavy chain V region (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence revision 16-Sep-1992 #text_change 16-Aug-1996
C;Accession: PLO252; PLO251; Maccelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Roth R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Roth J. Exp. Med. 171, 265-297, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-49/Region: framework 2
F;50-66/Region: complementarity-determining 2
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C;Accession: D27889

R;Catcn, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A;Title: Structural and functional implications of a restricted A;Reference number: A91043; MUID:86300658; PMID:2427335

A;Accession: D27889
                                                                                                                                                                                                    RESULT 10
D27889
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A; Residues: 1-117 <SH
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                                                                                                                              Ig heavy chain V region (H36-2) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_
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Pred. No. 1.2e-38;
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Pred. No. 2.3e-38;
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A;Experimental source: strain Balb/c
A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that
C;Superfamily: immunoglobulin V region; immunoglobulin homology

binds

influenza

antibody respons

A;Residues: 1-119 <CAT> A:Molecule type:

Fr:

Nov

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Ig heavy chain V region pe24 - mouse (fragment)
C,Species: Mus musculus (house mouse)
C,Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
C;Accession: S55539
R,Boettger, V; Boettger, A.; Lane, E.B.; Spruce, B.A.
J.Mol. Biol. 247, 932-946, 1995
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S55539
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F;15-98/Domain: immunoglobulin homology <IMM>
Ig heavy chain V region (H37-40) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15.Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C;Date: 18.Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C;Accession: H27888
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
RMEO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a.
A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: H27888
A;Molecuie type: DNA
A;Residués: 1-121 <CAT>
A;Residués: 1-121 <CAT>
A;Residués: 1-121 <CAT>
A;Residués: 1-121 <CAT>
A;Rote: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus
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A; Accession: S55539
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A;Reference number: S55528; MUID:95239763; PMID:7536850
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A;Molecule type: mRNA
A;Residues: 1-120 <BOE>
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Pred. No. 3.1e-38;
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Pred. No. 3.5e-38;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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S55538
                                                                             Ig heavy chain V region (anti-cyclosporin G) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 16-Aug-1996
C;Accession: PH0098
R;Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesniaux, Mol. Immunol. 27, 1029-1038, 1990
A;Title: Analysis of the structural diversity of monoclonal antibodies to cycle A;Reference number: PH0087; MUID:91042649; PMID:2122240
A;Accession: PH0098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X82591; NID:g854308; PIDN:CAA57927.1; PID:g854309 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;14-97/Domain: immunoglobulin homology <IMM>
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A;Reference number: S55528; MUID:95239763; PMID:7536850
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C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: $55338
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A; Residues: 1-120 < BOE>
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J. Mol. Biol. 247, 932-946, 1995
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A;Residues: 1-119 <SCH>
A;Residues: 1-119 <SCH>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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Pred. No. 3.9e-38;
6; Mismatches 16
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A;Molecule type: DNA
A;Residues: 1-124 <CAT's
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A;Residues: 1-124 <CAT's
A;Residues: 1-124 <CAT's
A;Residues: 1-124 <CAT's
A;Residues: 1-124 <CAT's
A;Resperimental source: strain Balb/c
A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus
C;Comment: immunoglobulin Yegion; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM's
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C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C;Accession: C27888
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C27888
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Search completed: November 7, 2003, 07:36:20 Job time: 16.8997 secs
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Best Local Similarity 79.5
Conservative
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Best Local Similarity
Matches 98; Conservat
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61 PDSVKGRFTISRDNAKNTLYLQMSSLQSEDTAVYYCT-----IPSNWGVDYWGQGTTLTV 115
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79.5%;
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Pred. No. 1.8e-37;
7; Mismatches 13
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Pred. No. 1.9e-37;
8; Mismatches 15;
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Sequence:

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HV30 MOUSE HV37 MOUSE HV31 MOUSE HV31 MOUSE HV31 HUMAN HV31 HUMAN HV3H HUMAN HV3H HUMAN HV3H HUMAN HV2B MOUSE HV2D MOUSE

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ALIGNMENTS

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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InterPro; IPR00306; Ig_MHC.
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Pfam; PF00047; ig; 1.
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SMART; SM00406; IGv; 1.
PROSITE; PS50838; IG_LIKE; 1.
Immunoglobulin V region; Signal.
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STRAIN-BALB(CJ;

MEDLINE=89279149; PubMed=2499654;

Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;

Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;

"Early onset of somatic mutation in immunoglobulin VH genes durin

"Early onset of somatic mutation in immunoglobulin VH genes durin

"Early Med. 169:2007-2019(1999).

J. Exp. Med. 169:2007-2018 SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region 345 precursor.
Mus musculus (Mouse).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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HSSP; P01810; 2FBJ.
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IG HEAVY CHAIN V REGION 345.
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
BY SIMILARITY.

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Length 117; Indels

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J. Exp. Med. 169:2007-2019(1989)
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15-UUL-1999 (Rel. 38, Last amnotation update)
19 heavy chain V region 5-84 precursor.
Mus musculus (Mouse)
                          MEDLINE=89279149; PubMed=2499654; Levy N.S., Malipiero U.V., Lebecque "Early onset of somatic mutation in the primary immune response."; J. Exp. Med. 169:2007-2019(1989).
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15-SEP-2003 (Rel. 42, Last am
Ig heavy chain V region 6.96.
Mus musculus (Mouse)
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SMART; SM00406; IGv; 1.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Mammalia; Butheria; Rodentia;
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Mammalia; Eutheria; Rodentia;
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HSSP; P01810; 2FBJ.
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(Rel. 16, Last sequence up
(Rel. 42, Last annotation
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  THIS SEQUENCE BELONGS
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5; Mismatches
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Pred. No.
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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BY SIMILARI
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                                                                                S.G., Gearhart immunoglobulin
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  THE VH7183 SUBFAMILY.
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Best Local S
Matches 90
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Interpro; Ir...
Interpro; IPR0035>~.
Interpro; IPR0035>~.
Interpro; IPR0047; ig; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IG LIKE; 1
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SEQUENCE 98 A
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIJINE=89279149; PubMed=2499654;
Levy N.S., Malipiero U.V., Lebecque
"Early onset of somatic mutation in
the primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
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01.NOV-1990 (Rel. 16, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain v region 914.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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SMART; SM00406; IGV;
PROSITE; PS50835; IG
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HSSP; P01810; 2FBJ.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus (Mouse)
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Immunoglobulin V region.
DOMAIN 1 >97
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO
1- SIMILARITY: Contains 1 immunoglobulin-li
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PDSVKGRFTISRDNARNILYLQMSSLRSEDTAMYYCAR
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90.8%;
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3; Mismatches
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Pred. No. 4.8e-40;
                                                                                                                                                                                  Score 460.5;
Pred. No. 6.7
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immunoglobulin
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RESULT 5
HV58_MOUSE
ID HV58_MOUSE
P18529;
--NOV-199
RESULT 6
HV16 MOUSE
ID HV16 MOUSE
AC P01783;
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AC P01783;
BC P01783;
BC P01783;
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Matches 87
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NON TER
SEQUENCE
                                                                                                                                                                                   Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Exp. Med. 169:2007-2019(1989).
                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region MOPC 21 precursor (Fragment).
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                                MEDLINE=81234548;
Bothwell A.L.M., I
                                                                                                                                                  NCBI_TaxID=10090;
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HSSP; P01810; 2FBJ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region 5-76 precursor. Mus musculus (Mouse).
                                                                                       SEQUENCE FROM N.A.
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15-JUL-1999 (Rel. 38, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interPro;
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r; SM00406; IGv; 1.
ITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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                                   Paskind M.,
                                   PubMed=6788376;
Paskind M., Reth
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49
54
68
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117
                                                                                                                                                                                      Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 453; DB 1;
Pred. No. 4.8e-39;
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                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                   Imanishi-Kari
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                                Rajewsky K.,
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TAGE BOOOKS SOO
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HV53_MC
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InterPro; IPR003006; Ig_WHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; iGv; 1.
PROSITE; PSSAGGE
                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DISULFID
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=77100368; PubMed=401950; Adetugbo K., Milstein C., Secher D. "Molecular analysis of spontaneous
                                                                                  01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation updat
Ig heavy chain V region RF precursor.
                                                                                                                        P18524;
01-NOV-1990
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DOMAIN
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Cell 24:625-637(1981).
SEQUENCE FROM N.A. STRAIN=BALB/CJ;
                                NCBI_TaxID=10090;
                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                      Ig heavy chain V reg
Mus musculus (Mouse)
                                                                                                                                                             MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; E90809; G1MS21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 265:299-304(1977)
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InterPro; IPR007110;
                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                     120
                                                                                                                                                                                                               134
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                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                       PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNMY-FDVWGAGTLVT
                                                                                                                                                                                                                                                                                                                                    BVQLQESGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
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bbulin V region; s:
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                                                                                                                                                                                                                                                                                                                                                                                                              115
120
38
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89
115
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136 AA;
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                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                               136
                                                                                                                                                STANDARD;
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119
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72.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG HEAVY CHAIN V REGION MOPC D SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                          Score 441; DB 1;
Pred. No. 9.3e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JH4 SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                               2276A98DBDBF7016 CRC64;
                                                                                                                                                                                                                                                                                                                                                            Mismatches
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Best Local :
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89279149; PubMed=2499654;
Levy N.S., Malipiero U.V., Lebecque
"Early onset of somatic mutation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
1g heavy chain V region 7-39 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HV59 MOUSE
P18530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Exp. Med. 169:2007-2019(1989).
-!- MISCELLANEOUS: THIS SEQUENCE BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
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HSSP; P01810; 2FBJ.
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Levy N.S., Malipiero U.V., Lebecque
"Early onset of somatic mutation in
                                                                                                                                                                                                                                                                                                                                                                                             the primary immune response.",
J. Exp. Med. 169:2007-2019(1989).
-i- MISCELLANEOUS: THIS SEQUENCE
PIR: JT0507; HVMS39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49
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85.7%;
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
FRAMEWORK-2.
FRAMEWORK-3.
FRAMEWORK-3.
BY SIMILARITY.
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Pred. No. 5e-37;
                                        IG HEAVY CHAIN V REGION 7-39. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   BELONGS
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immunoglobulin VH genes during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TO THE VH7183 SUBFAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P.J.;
VH genes during
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STTTTT RESERVED BERREE BERREE BOOK COCCOCCERT TO SERVE BERREE BOOK BETTTE
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Query Match
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Matches 79;
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                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=81101090; PubMed=6450418; Matchyssens G., Rabbitts T.H.; "Structure and multiplicity of genes heavy chain variable region."; Proc. Natl. Acad. Sci. U.S.A. 77:6561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL 1986 (Rel. 01, Create
21-JUL-1986 (Rel. 01, Last s
15-SEP-2003 (Rel. 42, Last a
Ig heavy chain V-III region
                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HV3C
                                                                                                        Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal; 3D-structure.
                                                                                                                                                                                                           88
                                                                                                                                                                                                                                              EMBL; J00236; AAA53516.1; -.
EMBL; M35415; AAA58735.1; -.
PIR; A02047; H3HU26.
PDB; 1HOU; 23-DBC-99.
                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P01764;
                                                                                                SIGNAL
                                                                                                                                                         InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                     Genew; HGNC:5545; IGHV@.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                              GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding activ
GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 1 immunoglobulin-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80
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             Similarity
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85
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115
                                              12582 MW;
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83.7%;
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           65.1%;
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Last annotation update)
region VH26 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Score 419; DB 1;
Pred. No. 1.3e-35;
8; Mismatches 11
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                                                                       IG HEAVY
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InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig v.
InterPro; IPR003596; Ig v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Lehman D.W., Putnam F.W.;
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GO:0003823; F:antigen binding activity; NAS
GO:0006955; P:immune response; NAS.
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obulin V region; Pyrrolidone carboxylic
1 112 IG-LIKE.
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122 AA;
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Pred. No. 2.2e
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SMART; SM00406; IGv; 1.

PROSITE; PSS0835; IG LIKE; 1

Immunoglobulin V region.

DOMAIN 1 112

NON TER 119 119

SEQUENCE 119 AA; 13169 MM
               (protein WEA) with antibody activity against 3,4-pyruvylated galactose in Klebsiella polysaccharides K30 and K33,";
Proc. Natl. Acad. Sci. U.S. A. 80:4837-4841(1983).
-i- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH WALDENSTROM'S MACROGLOBULINEMIA.
-i- SIMILARITY: Contains 1 immunoglobulin-like domain.
-pir; A02046; M3HUWE.
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HSSP; P01810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
IntexPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                       SEQUENCE.

MEDLINE=83273707; PubMed=6410398;

MEDLINE=83273707; PubMed=6410398;

MODINE F., Frangione B.;

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Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
Rao D.N., Rudikoff S., Krutzsch H., Potter M.;

"Structural evidence for independent joining reglome independent independent independent in generating diversity in complementarity-determining regions.";

Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).

-- MISCELLANDOUS; THIS CHAIN WAS ISOLATED FROM AN IGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
15 heavy chain V-III region WEA.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata
Mammalia; Eutheria; Primates; Catarrhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P01763;
21-JUL-1986
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13169 MW;
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Pred. No. 2.7e-35;
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on update)
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MOD_RES
NON_TER
                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS)
MEDLINE=75065510; PubMed=4530984;
Segal D.M., Padlan B.A., Cohen G.H., 1
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-120.
MEDLINE=75017346; PubMed=4213527;
Rudikoff S., Potter M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-80199926; PubMed-6769593;
Early P., Huang H., Davis M., Calame K., Hood I
Farly P., Huang H., Davis M., Calame K., Hood I
Fan immunoglobulin heavy chain variable region
three segments of DNA: VH, D and JH.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region M603.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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SMART; SM00406; IGV; 1.
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                                                                                                                                                                                                                                                                                                                                                                          "Variable region sequence of the heavy binding myeloma protein."; Biochemistry 13:4033-4038(1974).
                                                                                                                                             "The three-dimensional structure of a phosphorylcholine-binding mouse immunoglobulin Fab and the nature of the antigen binding site."; broc. Natl. Acad. Sci. U.S.A. 71:4298-4302(1974).

-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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Immunoglobulin V region; Pyrrolidone carboxylic acid.
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                                                                      BINDS PHOSPHORYLCHOLINE.
SIMILARITY: Contains 1 immunoglobulin-like domain; B90795; AVMS63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ly P., Huang H., Davis
immunoglobulin heavy
ee segments of DNA: VI
l 19:981-992(1980).
                            IMCP; 15-JUL-92.
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  IPR007110; Ig-like
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                                                                                                                                                                                                                                                                   Padlan B.A., Cohen G.H., Rudikoff S., Potter M.,
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Pred. No. 5.1e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is generated from
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RESULT 14
HV3J_HUMAN
ID HV3J_H
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Best Local S
Matches 80
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGy; 1.
PR0SITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; 3D-st;
                                                                                                                                                                                                                                                                                                   STRAND
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SEQUENCE
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                        MBDLINE-79124695; PubMed-420800; Chiu Y.-Y.H., Lopez de Castro J.A., Po "Amino acid sequence of the VH region cryoimmunoglobulin IgG Hil."; Biochemistry 18:553-560(1979).
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                                                                                         Eukaryota;
Mammalia; I
                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V-III region HIL.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                    TURN
STRAND
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            -!- SIMILARITY: Contains
                                                                    SEQUENCE
                                                                                 NCBI_TaxID=9606;
                    PROTEIN
      A02054; G1HUHL.
                                                                                                                                                 HUMAN
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                                                                                                                                                                                   119 TVSS 122
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                                                                                                                                                                                                                                                                              Similarity
                                                                                       ; Metazoa;
Eutheria;
                                                                                                                                                                                                 TVSA 122
                                                                                                                                                                                                               EYSASVKGRFIVSRDTSQSILYLQMNALRAEDTAIYYCARNYYGST--WYFDVWGAGTTV
                                                                                                                                                                                                                       YYPDSVKGRPTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLV
                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       52
                                                                                                                                                                                                                                                                                                    13626 MW;
                                                                                                                                                                                                                                                                              64.5%;
                           CHAIN WAS ISOLATED FROM AN IGG1
             ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3D-structure.
                                                                                                                                                                                                                                                                       17;
            immunoglobulin-like
                                                                                                                                                                                                                                                                       Score 411; DB Pred. No. 8.8e
                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG-LIKE.
H-BOND WITH THE PHOSPHATE GROUP PHORYLCHOLINE.
H-BOND WITH THE PHOSPHATE GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHORYLCHOLINE
                                                                                                Craniata; Vertebrata; Euteleostomi;
                                                                                         Catarrhini;
                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                    BA2C864438B64F0F CRC64;
                                                     Poljak R.J
                                                                                                                           update)
                                                                                                                                                 121 AA
                                               숅
                                                                                                                    update)
                                                                                                                                                                                                                                                                              8.8e-35;
                                               human
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                                                                                         Hominidae;
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              domain.
                                               myeloma
                                                                                                                                                                                                                                                                                      Length
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                                                                                         Homo.
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                           MYELOMA
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1 EVKLBESGGGLVQPGGSMKLSCVASGFTFSNYMMMWVRQSPEKGLEMVAEIRLKSNNYAT

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                                                       Query Match 62.8%; Score 404.5; DB 1; Length 115; Best Local Similarity 63.7%; Pred. No. 3.8e-34; Matches 79; Conservative 19; Mismatches 15; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 79; Conserval
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GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_WHC.
InterPro; IPR003006; Ig_V.
R Pfam; PF00047; ig; 1.
R SMART; SM00406; IGY; 1.
R SMART; SM00406; IGY; 1.
R SMART; SM00406; IGY; 1.
R SMART; SM00406; IGY; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
DOMAIN
INTERPROPERTY ACTOR
                                                                                                                                                                          DISULFID
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                            BINDS INULIN.

-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; C92811; AVMS06.
HSSP; P01789; 1MCP.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PV32 MOUSE STANDARD; PRT; 115 AA. P01801; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 19 heavy chain V-III region J606.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOD_RES
NON_TER
SEQÜENCE
                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE.
MEDLINE=82099361; PubMed=6798111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      binding proteins.
J. Immunol. 128:3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Johnson N., Slankard J., Paul L., Hood L.; "The complete V domain amino acid sequences of two myeloma inulin-
                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
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| $$ 121
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EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATI--SSGGSST 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDSVKGRFTISRDNSKRTLYMZMNSLRTEDTAVYYCARDPDILTA-FSFDYWGQGVLVTV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVKLVQAGGGVVQPGRSLRLSCIASGFTFSNYGMHWVRQAPGKGLEWVAVIWYNGSRTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 128:302-307(1982)
                                                                                                                                                                          115 AA;
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121 AA; 13566 MW; 480FC53610BF5DAB CRC64;
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115
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                                                                                                                                                             98 BY SIMILARITY.
115
12810 MW; B67AD6638A121A5F CRC64;
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                                                                                                                                                                                                                                 IG-LIKE.
BY SIMILARITY.
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Search completed: November 7, 2003, 07:28:08 Job time: 8.79573 secs

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Result
No.
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Maximum Match 100%
Listing first 45 s
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
               521
493.5.5
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482.5
466.5
455.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPTREMBL 23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_hungi:*
4: sp_hunan:*
5: sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
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1 EVQLQESGGGLVKPGGSLKL....
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L Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; BC004786; AAH04786.1; -.

R HSSP; P01840; 2FBJ.

R InterPro; IPR003006; Ig-like.

R InterPro; IPR003996; Ig_wHC.

R InterPro; IPR003596; Ig_v.

R Pfam; pF00047; ig; 4.

R SMART; SM00406; IGv; 1.

R PROSITE; PS00835; IG LIKE; 4.

R PROSITE; PS00835; IG LIKE; 4.

R PROSITE; PS00290; IG_MHC; 2.

RR PROSITE; PS00290; IG_MHC; 2.

RR Hypothetical protein.
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Q99KA4;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 52.6 kDa protein.
Mus musculus (Mouse).
Mus musculus (Mouse).
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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   PDNVKGRFTISRDNAKNNLYLQMSHLKSEDTAMYYCARDMGGSPYGGYSRFDYWGQGTTI
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81.5%; Pred. No. 6.2e-45;
tive 5; Mismatches 16; Indels
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Q8NCC1
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submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AR307937; AAL09421.1; -...
InterPro; IPR003106; Ig-NHC.
InterPro; IPR003106; Ig_V.
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013556; AAH13556.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   Hypothetical 51.6 kDa protein.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata,
Mammalia, Butheria, Rodentia;
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
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Mammalia; Eutheria;
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01-DEC-2003 (TYEMBLYEl. 23, Last annotation update)
01-MAR-2003 (TYEMBLYEL 23, Last annotation update)
Ferin-mimicking anti-idiotope heavy chain variable region
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Larity 85.2%; Pred. No. 3.9e-45;
Conservative 3; Mismatches 12;
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Rodentia;
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Hotope of Pterin-Mimicking Antibodies Expressed
                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Best Local :
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Best Local S
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Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
SMOSITE; PS50835; IG_LIKE; 4
PROSITE; PS500290; IG_MHC; 2.
Hypothetical protein_
SEQUENCE 479 AA; 51603 MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ol-Mak-2007 (-)
Hypothetical protein.
Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;

Submitted (PEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; BC024289; AAH24289.1; .

InterPro; IPR007110; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.

Pfam; PF0047; ig; 4.

SMART; SM00406; IGv; 1.

SMART; SM00406; IG_MHC; 2.

PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8TC77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Spleen;
                                                                                                                       140
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                                                                                                                                                                                                                   80 ADSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCARDLRQLTSYWYRDLWGRGTLVTV
                                                                                                                                                                                                                                               61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV
                                                                                                                                                                                                                                                                                                                  20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 EVQLVESGGGLVKPGGSLKVSCAASGLTESNYAMSWVRQSPEKRLEWVAAINSNGGNTYY
                                                                                                                                                                                                                                                                                                                                                                                                              92;
                                                                                                                                                                                                                                                                                                                                                                1 EVQLQESGGLVKFGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
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                                                                                                                                                                                                                                                                                                               EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSMSSSSYTYY
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                                                                                                                       SS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               471 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51791 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     75.6%;
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77.9%;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 487; DB 4;
Pred. No. 1.8e-41;
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Pred. No. 3.9e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 471;
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PRELIMINARY;

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 Query Match
Best Local S
Matches 92
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Best Local S
Matches 93
                                              Pfam; PF00047; ig; 4.

SMART; SM0406; IGV; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 2.

Hypothetical protein.

SEQUENCE 486 AA; 52682 MW;
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Q91Z07;
01-DEC-2001 (TrEMBLrel. 19, Crea
01-DEC-2001 (TrEMBLrel. 19, Last
01-MAR-2003 (TrEMBLrel. 23, Last
Hypothetical 52.7 kDa protein.
Mus musculus (Mouse)
                                                                                                                Strausberg R.;
submitted (JUL-2001) to the EMBL/GenBank/DDBJ
EMBL; BC010324; AAH10324.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMEL; BC010798; AAH10798.1; -
InterPro; IPR007110; Ig_nHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Unknown (Protein for IMAGE:4224494) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 4.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIXE; 4.

PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Colon;
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 Similarity 71.
92; Conservative
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           72.4%;
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76.2%;
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  0.
 Score 466.5; |
Pred. No. 2.3e
10; Mismatches
                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                             Created)
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Pred. No. 5.3e-41;
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                                                 4FEF835125DA870B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20B9234EEF2B41ED CRC64;
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           3e-39;
                     DB 11;
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                       Length
 13;
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Gaps
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RESULT 8
Q91202
ID Q9121
AC Q9121
AC Q9121
AC Q9121
DT 01-D
DT 01-D
DT 01-M
DF Hypo
GN Hypo
GN Hypo
GN Hypo
GN Mus
GN Mus
OC NCLI
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ day
SMBL; BC015760; AAH15760.1; -
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS05035; IG_IKE; 5.
PROSITE; PS05035; IG_IKE; 5.
PROSITE; PS050290; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9
                                                                                                                                               Q91205 PRELIMINARY, PRT; 473 AA.
Q91205; Control (TrembLrel. 19, Created)
01-DEC-2001 (TrembLrel. 19, Last sequence update)
01-MAR-2003 (TrembLrel. 23, Last annotation update)
Hypothetical 51.9 kDa protein.
AU044919.
                                                                     Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
  SEQUENCE FROM N.A.
                               NCBI_TaxID=10090;
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TISSUE=B-cell;
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                                                               Chordata; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65039 MW; 4FCA3AD8ECE263D9 CRC64;
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                                                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.; "Cloming of cDWAs encoding for anti-white pine blister rust antibody (Mab 7, its light and heavy chains) and construction single chain antibody (scFV).";
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 3.
PF00047; ig; 3.
PF00047; SMART; SM00406; IGV I
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SMART; SM00406; IG
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Submitted
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:96446;
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Last annotation update)
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                                                                                                    Score 450; DB 1
Pred. No. 1e-37;
3; Mismatches
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Pred. No. 5.4e-38;
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Best Local :
                                                                                                 Q9UL91 PRELIMINARY; PRT; 118 AA.
Q9UL91;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Wyosin-reactive immunoglobulin heavy chain variable
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NON TER
SEQUENCE
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE;
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Q9UL71;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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MEDLINE-98277139; PubMed=9614934;
WH.X., Liu B., Van der Merwe P.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP, P01772; 2FB4.

InterPro; IPR007110; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.
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                                                                                        (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SA 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVOLVESGGGVVQPGGSLRLFCAASGFTFDGYAMHWVRQAPGKGLEWVSLISGDGGSTYY
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121 AA;
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     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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RESULT 12
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
SMBL; BCC020240; AAH20240.1; -.

InterPro; IPR007110; Ig-1ike.
InterPro; IPR00306; Ig_wHC.
InterPro; IPR003596; Ig_v.
R Ffam; PF00047; 1g; 5.
R Ffam; PF00047; 1g; 5.
R Ffam; PF00046; IGv; 1.
R SMART; SM00406; IGv; 1.
R SMART; SM00406; IGwHC; 3.
R PROSITE; PS00239; IG_WHC; 3.
R PROSITE; PS00290; IG_MHC; 3.
R PROSITE; PS00290; IG_MHC; 3.
R PROSITE; PS00290; IG_MHC; 3.
R SMOSITE; PS00290; IG_MHC; 3.
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Q8WUK1; 17:00
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2003 (TrEMBLrel. 20,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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MEDLINE=98277139; PubMed=9614934;

Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Myosin-reactive autoantibodies in rheumatic carditis and normal
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l Similarity 71.9%;
87; Conservative 12
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                                                                                               Conservative
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                                                                                                                      68.5%;
                                                                                            ; Score 441; DB 4;
; Pred. No. 1.3e-36;
14; Mismatches 15
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; Pred. No. 1.3e-37;
12; Mismatches 18
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Last sequence update)
Last annotation update)
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Best Local S
Matches 88
Hypothetical protein.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, C.
Mammalia, Eutheria, Primates, C.
NCBI TaxID=9606,
[1]
                                                                                                                                               Q8WU38;
Q8WU38;
01-MAR-2002;
01-MAR-2002;
01-MAR-2003;
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MEDLINE-98277139; PubMed=9614934;
Yan B. Van der Merwe P.L.,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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01-MAY-2000
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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HSSP; P01772; 2FB4.
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Myosin-reactive autoantibodies in rheumatic carditis and normal
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AF035021; AAD56257.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAMYYCA-GGGGLGLGY----WGQGTLVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYYP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 AA;
                                                                                                                                            (TrEMBLrel. 20, 12) (TrEMBLrel. 20, 13) (TrEMBLrel. 23, 13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.2%; Score 439.5; DB 4 (larity 72.7%; Pred. No. 2.3e-37; Conservative 10; Mismatches 18
                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                            Created)
Last sequence update)
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                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local S
Matches 85
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Best Local S
Matches 85
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021276; AMH21276.1; -.
R InterPro; IPR0070110; Ig-like.
R InterPro; IPR003006; Ig_MHC.
R InterPro; IPR003596; Ig_v.
R Pfam; PF00047; ig; 4.
R Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
R SMART; SM00406; IGv; 1.
R PROSITE; PS05035; IG_LIKE; 2.
R PROSITE; PS05035; IG_LIKE; 2.
R PROSITE; PS05035; IG_MHC; 2.
R PROSITE; PS05035; IG_MHC; 2.
SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;
                                                                                                                                                                                                                                                             Strausberg R.;
Strausberg R.;
Strausberg R.;
Sthmitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032249; AAH32249.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Verrebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NOBI TaxID=9806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8N5K4
QBN5K4;
QBN5K4;
Q1-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                  Pfam; PF00047; ig; 4.

SMART; SM00409; IG; 4.

SMART; SM00400; IGC1; 2.

SMART; SM00406; IGV; 1.

PROSITE; P850835; IG_LIKE; 4.

PROSITE; P8508290; IG_MHC; 1.

Hypothetical protein.

SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. TISSUE=Tonsil;
                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 TVSA 122
61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTRE----GGGFTVNWYFDVWGAG 115
                           , 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYF--DVWGAGTLV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 ADSVKGRFTISRDNAKNSLYLOMNSLRAEDTALYYCAKHGSGSYIGYYYGMDVWGQGTTV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY
                                                   1 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVOLOESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLSWVATISSGGSSTYY
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                                                                                      h 67.9%; Score 437.5; DB 4; Length 499;
Similarity 66.9%; Pred. No. 2.2e-36;
B5; Conservative 13; Mismatches 24; Indels 5
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                            TVSS 143
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Last sequence update)
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Search completed: November 7, 2003, 07:34:35 Job time : 40.3323 secs

Run on:

OM protein -

Scoring table: Sequence: Perfect score:

BLOSUM62

644

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Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than ox equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                               A_Geneseq_19Jun03:*

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        November 7, 2003, 07:21:17; Search time 52.6115 Seconds (without alignments) 368.069 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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              AAB20435
AAB20438
AAB20437
AAB20436
AAB20436
AAB20436
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                    Anti-FIX/FIXa anti
Anti-FIX/FIXa anti
Anti-FIX/FIXa anti
Anti-FIX/FIXA anti
Anti-FIX/FIXA anti
Murine antibody 14
Anti-FIX/FIXA anti
                                                                                                                         Description
Mouse antibody 2A4
Mouse antibody MB3
                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
AAB20435
ĕ
                                                                                                                                                                                             Chimeric - Mus musculus.
Chimeric - Synthetic.
                                                                                                                                                                                                                               Ractor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
Factor VIII cofactor; blood coagulation disorder; haemophilia A;
haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.
                      WO200119992-A2
                                                          Region
                                                                                   Protein
                                                                                                          Peptide
                                                                                                                                  Region
                                                                                                                                                                                                                                                                                  Anti-FIX/FIXa antibody 198/AB2 scFv.
                                                                                                                                                                                                                                                                                                                                   AAB20435;
                                                                                                                                                                                                                                                                                                                                                          AAB20435 standard; Protein; 249
                                                                                                                                                           Protein
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/label= CDR3
123..136
/label= Linker
                                                                                                                                                                      Location/Qualifiers
                                                          230..238
                                               label= CDR:
                                                                      /label= VL
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AAW66099
AAY32404
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AAX77513
AAG677513
AAG67393
AAG64775
AAB95208
ABJ95208
ABJ95208
ABJ72295
ABF72295
AAU76122
AAR20064
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ABB95197
ABJ36649
AAW57592
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AAU72801
AAW57576
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AAB76880
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AAW11917
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MRNISE monoclonal a MRKIS-H chain. Ch Humanised mouse TR Murine MAb SK48-E2 Mouse mAb 26-2F he Murine anti-PI-3,4 Mouse mAb 26-2F he anti-CD22 monoclon Mouse anti-verotox Heavy chain variab Human anti-DAF ant

Mouse humanised an Mouse antibody H c Amino acid sequenc Amino acid sequenc Amino acid sequenc House joint diseas Angiogenesis inhib Anti-Streptococcus Chimeric construct Chimeric construct Murine CBEII heavy Mouse monoclonal a Marti-Streptococlonal and Chimeric Chimeric Chimeric Construct Murine CBEII heavy Mouse monoclonal and Mouse monoclon

Peptide seq ID No:
Amino acid sequenc
Mouse anti-PTHrP mouse
Human PTHrP mouse
Human PTHrP mouse
Human PTHrP mouse
Angiogenesis inhib
Chimeric antibody

TRA-8 heavy chain. Chimeric H chain S Mouse humanised an

Humanised mouse

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :

Result No.

Score

Query Match

Length

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5337.5 537.5 537.5 537.5 537.5

100.0 96.9 96.9 94.6 83.6 82.7

22-MAR-2001.

Pred. No.

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ARESULT 2
ARB20442
ID ARB2
XX ARB2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of a single chain Fv (scFv) derivative co fantibody 198/AB2, comprising the heavy (VH) and light (VL) chain variable regions of 198/AB2 joined by an artificial, flexible linker peptide. The scFv was obtained by PCR amplification of cDNAs for 198/AB2 WH and VL regions and cloning in vector DARP2. 199/AB2 is an example of anti-human Factor IX (FIX)/activated Factor IX (FIXA) and their derivatives, concluding scFv and CDR3 fragments, have Factor VIIIa (FVIIIa) cofactor cactivity or FIXA activating activity. Administration leads to an increase in the procoagulant activity of FIXA, even in the presence of FVIII or FVIIIa, and in the case of FVIII or FVIIIa, and in the case of FVIII or FVIIIA, and in the case of FVIII or FVIIIA, and in the case of FVIII chibitor patients. The antibodies and derivatives are used in a claimed pharmaceutical composition for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic claimed coagulation disorders, especially haemophilia A and haemorrhagic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Simi
Matches 122;
                                Chimeric - 1
                                                                                                 Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
                Chimeric -
                                                                                    myc-tag.
                                                                                                                                                                      Anti-FIX/FIXa antibody 198/B1-myc-tag
                                                                                                                                                                                                         21-JUN-2001
                                                                                                                                                                                                                                            AAB20442;
                                                                                                                                                                                                                                                                             AAB20442 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scheiflinger F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BAXT ) BAXTER
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DB; AAF30725.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVQLQESGGGLVKPGGSLKLSCAASGFTPSSYIMSWVRQTPEKRLEWVATISSGGSSTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYIMSWVRQTPEKRLEWVATISSGGSSTYY
                  Escherichia coli
                                                   Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 644; DB 22; ilarity 100.0%; Pred. No. 1.4e-54; Conservative 0; Mismatches 0;
                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA:
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                                                                                                                                                                                                                                                                               294 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dorner
                                                                                                  therapy; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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23

82

Query Match Best Local S Matches 118

Similarity

96.98;

Score 624; DB 22; Pred. No. 1.5e-52; 2; Mismatches 2;

Length 2

294;

0

Conservative

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The present sequence is that of a fusion protein comprising: a PelB CC leader; a single chain Fv (scrv) derivative of antibody 198/B1 CC comprising the heavy (VH) and light (VL) chain variable regions of CC 198/B1 joined by an artificial, flexible linker peptide; a spacer; CC a Myc-tag peptide; a spacer; and a C-terminal fills affinity tail. CC 198/B1 is an example of anti-human Factor IX (FIX)/activated Factor IX (FIXA) antibodies of the invention. Anti-FIX/FIXA antibodies and CC their derivatives, including scFv fragmants, have FVIII a cofactor CC activity or FIXA activating activity. Administration leads to an CC increase in the procoagulant activity of FIXA, even in the presence CC in the absence of FVIII or FVIII or FVIII and inhibitors. This allows for rapid blood coagulation even in the absence of FVIII or FVIII and in the case of FVIII inhibitor CC patients. The antibodies and derivatives are used in a claimed CC pharmaceutical composition for treating patients with blood CC coagulation disorders, especially haemophilia A and haemorrhagic CC diathesis. The scFv-myc-tag fusion was expressed in B. coli. It
                                                                                                                                                                                                                                                                                                             New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Peptide
Sequence
                                                                                                                                                                                                                                                                                    Example 18; Fig 34; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 Scheiflinger F, Kerschbaumer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                               (BAXT ) BAXTER
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)B; AAF30732.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label= His_tag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               abel=Myc_tag
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   New factor IX/factor IXa antibodies and their derivatives useful for
                                WPI; 2001-290358/30.
N-PSDB; AAF30728.
                                                                            Scheiflinger F,
                                                                                                                                                                    13-SEP-2000;
                                                                                                                                      14-SEP-1999;
                                                                                                                                                                                                 22-MAR-2001.
                                                                                                                                                                                                                                                                      Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Factor IX, FIX, Factor IXa; FIXa; miniantibody, procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse; bivalent antibody; plasmid pZip-198AB2#102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB20438;
                                                                                                         (BAXT ) BAXTER AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                        /note= "encoded 181
                                                                                                                                                                                                                                                                                                                                                                                                                      166
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                                                                            Kerschbaumer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Linker
160..271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label= VH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Signal_peptide
/note= "PelB leader"
                                                                                                                                                                                                                                                                                                                                           label= Spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                         note= "encoded
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                                                                                                                                                                                                                                                                                    abel= Helix
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Best Local :
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                                                                                                                                                                                        Chimeric
Chimeric
Peptide
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                                                                                                                                             Peptide
                                                                                                                                                                                                                      Chimeric
                                                                                                                                                                                                                                                   alkaline
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                                                                                                                                                                                          Escherichia coli.
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increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic disthesis
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Example 16; Fig 28; 138pp; English.

The present sequence is that of a bivalent miniantibody comprising CC a PelB leader peptide, the single chain Pv (scPv) fragment of a PelB leader peptide, the single chain Pv (scPv) fragment of cantibody 198/B1 (subclone AB2), an amphipathic helical structure and a c-terminal GHIs tag. The protein was expressed in Scherichia coli from plasmid pZip198ABZ#102 (see AAF30728). Antibody 198/B1 is an example of anti-human Factor IX (FIX) Activated Factor IX (FIX) antibodies of the invention. CC (FIX)/Activated Factor IX (FIX) antibodies have FVIIIa cofactor activity or FIXa activating activity. Administration leads to an increase in the procoagulant activity of FIXa, even in the presence of FVIIIa inhibitors. This allows for rapid blood cogulation even in the absence of FVIII or FVIIIa, and in the case of FVIII inhibitors. The antibodies and derivatives are used in a colaimed pharmaceutical composition for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic distinct. The bivalent miniantibody exhibited FVIII-like

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121 ȘA 122
                                                                                                                                                                                        Similarity
                                                        PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV
                                                                                                   EVXLVESGGGLVKPGGSLKLSCAASGFTESSYTMSWVRQTPEXRLEWVATISSGGSSTYY
                                                                                                                        EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
                                 PDSVKGRFTISRDNAKNTLYLØMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTSVTV
                                                                                                                                                                     96.9%;
ilarity 96.7%;
Conservative
                                                                                                                                                                 Score 624; DB 22;
Pred. No. 1.6e-52;
2; Mismatches 2;
                                                                                                                                                                                                     Length 325;
                                                                                                                                                                       Indels
                                                                                                                                                                     0
                                                                                                                                                                   Gaps
                                                                120
                                                                                                   82
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                                                                                                                                                                       0
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AAB20437 standard; Protein; 732

Anti-FIX/FIXa antibody 198/B1-alkaline phosphatase fusion

Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse phosphatase. therapy; mouse;

c - Mus musculus.c - Synthetic.c - Escherichia cc

Misc-difference 23..144 /label= /note= "encoded by 145..159 /label= Mature\_protein 23..271 /label= Signal\_peptide 23..732 Location/Qualifiers /label= SCFV Æ GGN

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RESULT 5
AAB20436
ID AAB2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of a fusion protein comprising: a PelB Cleader; a single chain Fv (scFv) derivative of antibody 198/B1 comprising the heavy (VH) and light (VL) chain variable regions of comprising the heavy (VH) and light (VL) chain variable regions of the invention coli alkaline phosphatase; and a C-terminal 6His affinity tail. 198/B1 is an example of anti-human Factor IX (FIX)-activated Factor IX (FIXa) antibodies of the invention. Anti-FIX/FIXa antibodies and their derivatives, including scFv fragments, have FVIIIa cofactor activity or FIXa activating activity. Administration leads to an increase in the procagulant cativity of FIXa, even in the presence of FVIIIa inhibitors. This allows for rapid blood coagulation even in the absence of FVIII or FVIIIa, and in the case of FVIII inhibitor pattents. The antibodies and derivatives are used in a claimed pharmaceutical composition for treating pattents with blood coagulation disorders, especially haemophilia A and haemorrhagic diathesis. The colivity case of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the pr
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Best Local Similarity
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                          AAB20436 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 16; Fig 26; 138pp; English
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SS 144
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                                                                                                                                                                                                                                                                                SA 122
                                                                                                                                                                                                                                                                                                                                            PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTSVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVKLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    732 AA;
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/label=_Alkaline_phosphatase
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/label=_Spacer
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96.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 624; DB 22;
Pred. No. 4.2e-52;
2; Mismatches 2
                                  249
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Query Match
Best Local Similarity
Matches 114; Conserv

94.6%; llarity 93.4%; Conservative

Score 609; DB 22; pred. No. 3.4e-51; 5; Mismatches 3;

Length 249; Indels

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Gaps

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Sequence

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The present sequence is that of a single chain Fv (scFv) derivative of antibody 198/A1, comprising the heavy (VH) and light (VL) chain covariable regions of 198/A1 joined by an artificial, flexible linker peptide. The scFv was obtained by PCR amplification of cDNAs for coppide. The scFv was obtained by PCR amplification of cDNAs for peptide. The scFv was obtained by PCR amplification of cDNAs for complete of anti-human Factor IX (FIX)/activated Factor IX (FIX) and VL regions and cloning in vector pDRP2. 198/A1 is an example of anti-human Factor IX (FIX)/activated Factor IX (FIX) antibodies of the invention. Anti-FIX/FIXA and their derivatives, concluding scFv and CDR3 fragments, have Factor VIIIa (FVIIIa) cofactor activity or FIXA activating activity. Administration leads to an increase in the procagulant activity of FIXA, even in the presence of increase in the procagulant activity of FIXA, even in the presence of FVIII or FVIIIA, and in the case of FVIII in the absence of FVIII or FVIIIA, and in the case of FVIII in the absence of FVIII or FVIIIA, and in the case of FVIII composition for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic collabeled by a separate of the coagulation disorders, especially haemophilia.
                                                                                                                                                                                                                                                                                                                                                  New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                    Example 10; Fig 17; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scheiflinger F,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-FIX/FIXa antibody 198/A1 scFv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUN-2001
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/label= Linker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kerschbaumer R,
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                 The invention relates to a novel monoclonal antibody having the identifying characteristics of, or that is a monoclonal antibody 14F3. An antibody of the invention has osteopathic, antirheumatic, antiarthritic, antiinflammatory, cytostatic, antipsoriatic, antidiabetic, and neuroprotective activity. The polynucleotides encoding the antibodies of the invention may have a use in gene therapy. The antibodies and polypeptides are useful for treating or preventing osteopathic diseases, such as rheumatoid arthritis, osteoporosis, metastatic and primary bone
                                                                                                                                                                                                                                                                                                                                         New monoclonal antibody having the characteristics of a monoclonal antibody 14F3, useful for treating or preventing osteopathic diseases, e.g. rheumatoid arthritis, or osteoporosis, and immune diseases e.g. psoriasis, or diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sweet RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-156758/15.
N-PSDB; ABV99887.
                                                                                                                                                                                                                                                                                 Disclosure; Page 8; 51pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIK )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 multiple sclerosis; heavy chain variable region; complementary determining region; CDR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine antibody 14F3 heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse; monoclonal antibody; 14F3; osteopathic; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-2003
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SMITHKLINE
  wear debris induced osteolysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tornetta
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/label= CDR3
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                                                                                                                                                                                                                                                                                 English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic;
or osteoarthritis, and immune
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Best Local S
Matches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases such as psoriasis, insulin-dependent diabetes, inflammatory bowel disease or multiple sclerosis. The present sequence represents the heavy chain variable region of the murine monoclonal antibody 1473 of invention. The sequence contains three complementary determining regions.
                                                                                                                                                           14-SEP-1999;
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                                                                2001-290358/30.
DB; AAF30724.
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98..110
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                                                                                                       Kerschbaumer
                                                                                                                                                                                                                                                                   /label= CDR3
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                                                                                                                                                                                                                                                                                                                      'label= Linker
                                                                                                                                                                                                                                                                                                                                               label = CDR3
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Pred. No. 1.2e-44;
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New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 105
        26-MAY-2000; 2000US-207628P
                                                                                                                                                        Region
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                                                                                                                                                                                                                                                                                                                                       Mouse; antibody 2A4; heavy chain variable region; osteopathic; psoriasis; cytostatic; antiinflammatory; osteoporosis; bone cancer; immune disease; inflammatory bowel disease; multiple sclerosis; osteopenic disease;
                                   24-MAY-2001; 2001WO-US16865.
                                                                                                WO200191793-A1
                                                                                                                                                                                                                                                                                                                                                                                                 Mouse antibody 2A4 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE16426 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                            rheumatoid arthritis; diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                  /note= "Complementarity determining region"
                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                         'note= "Complementarity determining region'
                                                                                                                                           label = CDR
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                                                                                                                                                                                                                                                                                                                                                                  T-cell receptor; cytostatic; dermatological; neuroprotective; immunostimulant; GD3; ganglioside antigen; MB3.6; FSMA; tumour; 3D8; 4D4; 3E11; prostate-specific membrane antigen; zeta signalling chain; CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer; small cell lung cancer; heavy chain variable region; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to anti-RAMK monoclonal antibodies which has the identifying characteristics of monoclonal antibody 2A4. The antibody or polypeptide is useful for treating or preventing osteopenic diseases (e.g., rheumatoid arthritis, osteoporosis, metastatic and primary bone cancer, wear debris induced osteolysis or osteoarthritis) or immune diseases (e.g., psoriasis, insulin dependent, diabetes, inflammatory bowel disease or multiple sclerosis). The antibody is also useful for treating and diagnosing conditions mediated by the RANK ligand. The present sequence is mouse antibody 2A4 heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse antibody MB3.6 heavy chain variable region.
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SMITHKLINE BEECHAM PLC.
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Best Local Sim
Matches 103;
                                                                                                                                                                                                                                                                        Tumour necrosis factor-related apoptosis-inducing ligand receptor; TRAIL; TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation; autoimmune disease; systemic lupus erythematosus; Hashimoto's disease; rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia; Addison disease; scleroderma; Goodpasture's syndrome; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes; allerome.
                                                                                                   WO200183560-A1
                                     08-NOV-2001
                                                                                                                                                                                                                            allergy; arteriosclerosis; myocarditis; glomerular nephritis; cancer; antibody:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanised mouse TRA-8 anti-human DR5 antibody #4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 9; 35pp; English.
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82.4%;
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Pred. No. 1.4e-43;
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119 AA;

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necrosis factor (TNF)-related apoptosis-inducing ligand (TRAII) receptor CC DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing CC activity to a cell expressing DR5 in vivo. It is also useful for CC preparing a therapeutic for selective apoptosis of abnormal or CC dysregulated cells, and for inhibiting cell proliferation in a cell, CC preferably a human breast, ovary, colon, haematopoietic, prostate, CC lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may CC also be administered e.g. paclitaxel, taxol or cycloheximide. The CC antibody is used to treat an autoimmune disease, systemic lupus CC erythematosus, Hashimoto's disease, rheumatoid arthritis, CC graft-versus-host disease, Sjogren's syndrome, Chron's disease, syndrome, CC graftous anaemia, Addison disease, scleroderma, Goodpasture's syndrome, CC graft-versus-host disease, insulin-dependent diabetes mellitus, CC allergy, atopic disease, arteriosclerosis, myosathenia gravis, multiple CC sclerosis, Basedow's disease, insulin-dependent diabetes mellitus, CC allergy, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy, CC glomerular nephritis, hypoplastic anaemia, rejection after organ CC transplantation, and numerous malignancies of lung, prostate, liver, CC ovary, lymphatic or breast tissue. This sequence shows one of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel antibody specific for tumour necrosis factor-related apoptosis-inducing ligand, useful for inhibiting cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-2000; 2000US-201344P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAY-2001; 2001WO-US14151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UABR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention describes a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26; Page 212-213; 229pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UAB RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ichikawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kimberly RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody which
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 118
                     121 SA 122
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                                                                                                                           Similarity 83.0
02; Conservative
|:
| 119
                                                     PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV
                                                                                  EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTPEKRLEWVATISSGGSYTYY
                                         PDSVKGRFTISRDNAKNTLYLOMSSIRSEDTAMYYCARRGDSMITT---DYWGQGTTLTV
                                                                                                EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
                                                                                                                                     80.7%;
                                                                                                                          2;
                                                                                                                          Score 519.5;
Pred. No. 7.1e
2; Mismatches
                                                                                                                         7.1e-43;
hes 15;
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RESULT 11 AAU72801

AAU72801 standard; Protein; 464 AA.

AAU72801;

26-FEB-2002

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Tumour necrosis factor-related apoptosis-inducing ligand receptor; TRAIL; TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation; autoimmune disease; systemic lupus erythematosus; Hashimoto's disease; rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia; Addison disease; scleroderma; Goodpasture's syndrome; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes; allergy; arteriosclerosis; myocarditis; cardiomyopathy;

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RESULT 12
AAW57576
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AC AAW57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes a novel antibody which recognizes a tumour concerns factor (PNF)-related apoptosis-inducing ligand (PRAIL) receptor DRS (located on chromosome Bp21-22). The antibody has apoptosis-inducing activity to a cell expressing DR5 in vivo. It is also useful for preparing a therapeutic for selective apoptosis of abnormal or dysregulated cells, and for inhibiting cell proliferation in a cell, preferably a human breast, ovary, colon, haematopoietic, prostate, lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may also be administered e.g. paclitaxel, taxol or cycloheximide. The aniso be administered e.g. paclitaxel, taxol or cycloheximide. The aniso be administered e.g. paclitaxel, taxol or cycloheximide of the cantibody is used to treat an autoimmune disease, systemic lupus graft-versus-host disease, sleenoderma, Goodpasture's gyndrome, chron's disease, graft-versus-host disease, sleenoderma, Goodpasture's syndrome, cutoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple solerosis, Basedow's disease, insulin-dependent diabetes mellitus, allerosis, basedow's disease, insulin-dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      allergy, atopic disease, artériosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, rejection after organ transplantation, and numerous malignancies of lung, prostate, liver, ovary, lymphatic or breast tissue. Peptides used to design primers for isolating heavy and light chain cDNA of the mouse TRAIL (AAU72801 and AAU72802), TRA-8 are shown in AAU72799 and AAU72800.
 03-SEP-1998
                                                                    AAV57576 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel antibody specific for tumour necrosis factor-related apoptosis-inducing ligand, useful for inhibiting cell proliferation
                                    AAW57576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UABR-)
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                                                                                                                                                               137
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102; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26; Page 198-199; 229pp; English.
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                                                                                                                                                             SS 138
                                                                                                                                                                                                                                                           PDSVKGRFTISRDNAKVTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
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                                                                                                                                                                                                                                                                                                                               EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
                                                                                                                                                                                                                                    PDSVKGRFTISRDNAKNTLYLOMSSLRSEDTAMYYCARRGDSMITT----DYWGQGTTLTV
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llarity 83.6%;
Conservative
(first entry)
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                                                                      protein; 118
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Pred. No. 3.5e-42;
2; Mismatches 15
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RESULT 13 AAW89627

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117

SA 118

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AAW89627; 14-APR-1999

(first entry)

AAW89627 standard; Protein; 118

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Matches 102;
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Chimeric - |
Chimeric - |
                                                                                                                                                                                                                                               New antibodies have been developed which are specific for human parathormone related peptides (hPTRP). The antibodies comprise chimeric L and/or H chains, where the C region is of human and L region of mouse, origin. The present sequence represents a specifically claimed region of an antibody of the invention. Host cells, transformed with vectors containing DNA encoding antibodies of the invention, can be used to produce the antibodies. The antibodies may be used to treat hypercalcaemia, especially that due to a malignancy, e.g. cancers of pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver, breast, kidney, bladder, womb or prostate or malignant lymphoma. They may also be used for treatment of hypophosphaemia such as that due to pathogens or to vitamin D resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New chimeric antibodies against human parathormone related peptide(s) - useful for, e.g. treatment of hypercalcaemia disorders caused by malignant neoplasm(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypophosphaemia; pathogen; humanised.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric; antibody; human parathormone related peptide; hPTRP; L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; C hypophosphaemia; pathogen; vitamin D resistance; V region; C re
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 111-112; 182pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-230640/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sato K, Wakahara Y,
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26-SEP-1996;
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        121
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                                                                                                                                                                            Similarity
    SA 122
                                 PDSVKGRFISRDNAKNTLYLQMSSLKSEDTAMFYCARQ----TIMTYFAYMGQGTLVTV
                                                   PDSVKGRFTISRDNAKVILYLOMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
                                                                                                                EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYIMSWVRQTPEKRLEWVATISSGGSSTYY
                                                                                                EVQLVESGGDLVKPGGSLKLSCAASGFTFSSYGMSWIRQTPDKRLEWVATISSGGSYTYY
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o sapiens.
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96JP-0255196
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                                                                                                                                                                          80.6%;
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                                                                                                                                                          Score 519; DB
Pred. No. 7.9e
5; Mismatches
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                                                                                                                                                                          DB 19;
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RESULT 14
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  active component. This substance may be an antagonist to the receptor, or an antibody (preferably monoclonal) or antibody fragment, recognising PTHrP. The antibody is preferably humanised or chimeric. The present invention also describes a humanised antibody prepared by hybridoma 23-57-137-1 (FERM BP-5631). The composition is used for the treatment of cachexia arising in connection with diseases such as cancer, thereby improving the quality of life of the patient. The present sequence represents mouse humanised antibody heavy chain from #23-57-137-1 from the present invention.
             Hypercalcemic crisis; parathyroid hormone related peptide; PTHrP;
                                                                    26-APR-2000
                                                                                                AAY77502
                                                                                                                        AAY77502 standard; Protein; 118 AA
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes compositions for the treatment cachexia containing a substance which inhibits the binding of a parathyroid hormone related peptide (PTHrP) to its receptor, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 72-73; 125pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibitors of binding of parathyroid hormone related peptide to its receptor - useful for, e.g. treatment of cachexia arising from cancer or other diseases
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15-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHUS ) CHUGAI SEIYAKU KK.
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inhibitor; humanised.
                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                        seq ID
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                                                                                                                                                                                                SA 118
                                                                                                                                                                                                                                                                       PDSVKGRFTISRDNAKWTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
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                                                                                                                                                                                                                                                      PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMFYCARQ----TTMTYFAYWGQGTLVTV
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                                                                                                                                                                                                                                                                                                                                                                                                                          118 AA;
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                                         No: 46.
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97JP-0125505
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                                                                  entry)
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Pred. No. 7.9e-43;
5; Mismatches 11;
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RESULT 15
AAG63382
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Matches 102; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                    Parathyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG63382;
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                        Kato A,
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                        Suzuki M,
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83 6%;
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Pred. No. 7.9e-43;
5; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                               The specification describes a treatment for dental diseases. The treatment comprises a substance that inhibits binding between parathyroid hormone-associated peptide and its receptor. The present sequence represents a murine protein, which is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-465459/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parathyroid hormone-associated peptide binding inhibitors useful for treating dental disease \,\,
                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 102-103; 140pp; Japanese.
                                                                121 SA 122
||
117 SA 118
                                                                                                                               61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMFYCARQ----TTMTYFAYWGQGTLVTV 116
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Result
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4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
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sequence 49, App1	. <sub>I</sub>	,	A	Φ. U	Ĺ		w	4	en ω	· u	Sequence 59, Appl	U	Sequence 56, Appl	4	0	Sequence 56, Appl	ŭ	, U	Ó	u	44	Ν	é		60	6		. 4	. 7

## ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 60
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
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Matches 99
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APPLICANT: Marks, James D
APPLICANT: Marks, James D
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
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                                                                                                                                                                                                         Score 529.5; DB 10;
Pred. No. 4.6e-42;
                                                                                                                                                                                           Mismatches
                                                                                                                                                                                           13;
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US-10-006-773-4
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                                                                                                                                                                               FILE REFERENCE: 21085.0029U6
CURRENT APPLICATION NUMBER: US/10/281,479A
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: 60/991,478
PRIOR FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 60/46,402
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
                                    NUMBER
SOFTWARE: Pace
SOFTWARE: Pace
SOFTWARE: 119
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Publication No. US20020132983A1
GENERAL INFORMATION:
APPLICANT: Junghans, Richard P.
TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti-
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Best Local Similarity
Matches 103; Conserv
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SEQ ID NO 4
LENGTH: 140
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CURRENT APPLICATION NUMBER: US/10/006,773
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: 60/250,089
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LOBUGIO, Albert S.
APPLICANT: Buchsbaum, Donald J.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THEN
TITLE OF INVENTION: AGENTS.
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                                                                                                                                     PRIOR APPLICATION NUMBER: 60/201,344 PRIOR FILING DATE: 2000-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                  NUMBER OF SEQ ID NOS: 102
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ORGANISM: artificial sequence
                        TYPE: PRT
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                                                                                            PatentIn version 3.0
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Kimberly, Robert P.
Koopman, William J.
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Pred. No. 8.1e-42
5; Mismatches 1
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APPLICANT: Zhou, Tong
APPLICANT: Ichikawa, Kimihisa
APPLICANT: Ichikawa, Kimihisa
APPLICANT: Kimberly, Robert P.
APPLICANT: Kimberly, Robert P.
APPLICANT: Kimberly, Right J.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A T
TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND
FILE REFERENCE: 21085.0029U5
CURRENT APPLICATION NUMBER: US/10/275,180A
CURRENT FILING DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.0
SEQ ID NO 61
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-10-286-132A-61
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US-10-275-180A-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 61, Application US/10275180A
Publication No. US20030190687A1
GENERAL INFORMATION:
APPLICANT: The UAB Research Foundation
APPLICANT: Zhou, Tong
APPLICANT: Ichikawa, Kimihisa
                                Sequence 61, Application US/10286132A publication No. US20030198637A1 GENERAL INFORMATION:
APPLICANT: Zhou, Tong APPLICANT: Kimberly, Robert P. APPLICANT: Koopman, William J.
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Best Local Similarity
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Best Local (
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OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687Ale =
OTHER INFORMATION: Synthetic Construct
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Local Similarity 83.6%;
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                                                                                                                                                                                                                                                                                                                                 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
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Kimberly, Robert P.
Koopman, William J.
LoBuglio, Albert S.
Buchsbaum, Donald J.
                                                                                                                                                                                                                                                                                                         PDSVKGRETISRDNAKNTLYLOMSSLRSEDTAMYYCARRGDSMITT---DYWGQGTTLTV 117
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Pred. No. 3.8e-41;
2; Mismatches 15
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Pred. No. 3.8e-41
2; Mismatches 1
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                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/391,478
PRIOR FILING DATE: 2002-06-24
PRIOR FILING DATE: 2001-01-01
PRIOR APPLICATION NUMBER: 60/346,402
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,344
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
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                                                                                                                      SOFTWARE: PatentIn version 3.0 SEQ ID NO 23
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Best Local Similarity
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PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR PILING DATE: 2001-05-02
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 102
                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 21085.0029U6
CURRENT APPLICATION NUMBER: US/10/281,479A
CURRENT FILING DATE: 2003-01-28
CURRENT FILING DATE: 2003-01-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LOBUGLIO, Albert S.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THER
TITLE OF INVENTION: AGENTS
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CURRENT FILING DATE: 2003-01-22
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TYPE: PRT
ORGANISM: artificial sequence
PEATURE:
                                               ORGANISM: artificial sequence
OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932Ale = Synthe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION: Description of Artificial Sequence:/No. US20030198637Ale = Synthe
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Kimberly, Robert P.
Koopman, William J.
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Pred. No. 3.8
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US-10-286-132A-23
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                                                                                            RESULT 8
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
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              Sequence 23, Application US/10275180A Publication No. US20030190687A1 GENERAL INFORMATION:
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Best Local Similarity
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Best Local
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TITLE OF INVENTION: AN ANTISODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
FILE REFERENCE: 21085.0029U7
CURRENT APPLICATION NUMBER: US/10/286,132A
CURRENT FILLING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US 60/346,402
PRIOR PILING DATE: 2001-11-01
PRIOR PILING DATE: 2001-11-01
PRIOR PILING DATE: 2001-05-02
PRIOR PILING DATE: 2001-05-02
PRIOR PILING DATE: 2000-05-02
APPLICANT: The UAB Research Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
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102; Conserv
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Koopman, William J.
LoBuglio, Albert S.
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83.6%;
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Pred. No. 1.6
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US-10-275-180A-23
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APPLICANT: Ichikawa, Kimihisa
APPLICANT: Kimberly, Robert p.
APPLICANT: Kimberly, Robert p.
APPLICANT: Kimberly, Robert p.
APPLICANT: Kimberly, Robert p.
APPLICANT: Kimberly, Robert p.
APPLICANT: Kimberly, Robert p.
APPLICANT: Kimberly, Robert p.
APPLICATION INDUCTING LIGAND RECEPTOR AND USES THEREOF
FILE REFERENCE: 21085,0029US
FILE REFERENCE: 21085,0029US
FILE REPERENCE: 21085,0029US
CURRENT APPLICATION NUMBER: US/10/275,180A
CURRENT FILING DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
SEQ ID NO 23
LENGTH: 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 46, Application US/09423800 Patent No. US20020165363A1 GENERAL INFORMATION:
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SEQ ID NO 46
                                                                                                                                   Matches 102;
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/423,800
CURRENT FILING DATE: 199-11-12
PRIOR APPLICATION NUMBER: PCT/JP98/02116
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1997-05-15
PRIOR FILING DATE: 1997-05-15
                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: JP PRIOR FILING DATE: 1997-07-18
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APPLICANT: TSUNEN
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                                     Local Similarity
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61 PDSVKGRFTISRDNAKWTLYLQMSSLRSBDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
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                                                                                             1 BYOLQESGGGLYKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY
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ISHII, KIM
                                                                                                                                   Conservative
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                                                                                                                               Score 519; DB 10;
Pred. No. 4.1e-41;
5; Mismatches 11;
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Pred. No. 1.6e-40
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; TYPE: PRT; ORGANISM: Homo sapiens US-10-337-981-46
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US-10-182-018-46
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US-10-337-981-46
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US-10-182-018-46
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CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: PCT/JP98/02116
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: JP 12505/1997
PRIOR APPLICATION NUMBER: JP 12505/1997
PRIOR APPLICATION NUMBER: JP 194445/1997
PRIOR FILING DATE: 1997-05-18
PRIOR FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 87
                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                       Sequence 46, Application US/10182018
Publication No. US20030049211A1
GENERAL INFORMATION:
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Best Local Similarity
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Query Match 80.6%;
Best Local Similarity 83.6%;
Matches 102; Conservative
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                                                                                                                                                                                                     APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
TITLE OF INVENTION: THERAPEUTIC AND PREVENTIVE AGENTS FOR DENTAL DISEASES
FILE REFERENCE: PH-1092-PCT
CURRENT APPLICATION NUMBER: US/10/182,018
CURRENT FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: JF 2000-83034
PRIOR PILING DATE: 2000-01-25
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                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 75
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TITLE OF INVENTION: CACHEXIA REMEDY
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                                                                                                                   TYPE:
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                                                                                                                                 ENGTH: 118
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••
Score 519; DB 15;
Pred. No. 4.1e-41;
5; Mismatches 11,
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Pred. No. 4.1e-41;
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                                   Length 118;
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Length 137;

Indels

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Gaps

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                                          TITLE OF INVENTION: CACHEXIA REMEDY
FILE REFERENCE: 04853-0036
CURRENT ABPLICATION NUMBER; US/09/423,800
CURRENT FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: PCT/JF98/02116
PRIOR TILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: JP 125505/1997
PRIOR APPLICATION NUMBER: JP 125505/1997
PRIOR FILING DATE: 1997-05-15
PRIOR FILING DATE: 1997-07-18
PRIOR FILING DATE: 1997-07-18
PRIOR FILING DATE: 1997-07-18
PRIOR FILING DATE: 1997-07-18
PRIOR FILING DATE: 1997-07-18
PRIOR FILING DATE: 1997-07-18
PRIOR FILING DATE: 1997-07-18
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US-10-169-003-46
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GENERAL INFORMATION:

APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA

TITLE OF INVENTION: Stabilized Antibody Composition and Pharmaceutical Preparation

TITLE OF INVENTION: Injection

PILE REFERENCE: PH-1093-PCT

CURRENT APPLICATION NUMBER: US/10/169,003

CURRENT FILING DATE: 2002-06-26

PRIOR FILING DATE: 2002-06-26

PRIOR APPLICATION NUMBER: JF 11-375203

PRIOR FILING DATE: 1999-12-28
                                                                                                                                                                                                                                                                                                              Patent No. Usavv.
Patent No. Usavv.
Patent INFORMATION:
Caro, K
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Best Local Similarity
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Publication No.
            SOFTWARE:
SEO ID NO 76
                                                                                                                                                                                                                                                                          APPLICANT:
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TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                  PELICANT: TSUNENARI, TOSHIAKI
PELICANT: ISHII, KIMIE
ITLE OF INVENTION: CACHEXIA R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117
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                               PatentIn Ver. 2.1
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1997-07-18
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Pred. No. 4.1e-41;
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-337-981-76
                                                                                                                    RESULT 15
US-09-881-823-12
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APPLICANT: ISHII, KIMIE
TITIE OF INVENTION: CACHEXIA REMEDY
FILE REFERENCE: 04853-0036
CURRENT APPLICATION NUMBER: US/10/337,981
CURRENT FILLING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: DF112505/1997
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: DF 125505/1997
PRIOR APPLICATION NUMBER: JP 194445/1997
PRIOR APPLICATION NUMBER: JP 194445/1997
PRIOR FILING DATE: 1997-07-18
PRIOR FILING DATE: 1997-07-18
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US-09-423-800-76
                                                           Sequence 12, Application US/09881823
Patent No. US20020068066A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Best Local Similarity
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APPLICANT: SHI, WENYUAN APPLICANT: ANDERSON, MAXWEL APPLICANT: MORRISON, SHERIE
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APPLICANT: TSUNI
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                              102;
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                       MAXWELI
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Pred. No. 4.9e-41;
5; Mismatches 11;
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Pred. No. 4.9e-41;
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Indels

4.

Gaps

135

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APPLICANT: WIMS, LETITIA
APPLICANT: WIMS, LETITIA
APPLICANT: WHIS, R: US/09/881,823
CURRENT APPLICATION WHERE: US/09/881,823
CURRENT APPLICATION WHERE: US 07/378,577
FRIOR FILING DATE: 1999-08-20
AUMBER OF SEG ID NOS: 32
SOFTMARE: Patentin version 3.0
SEG ID NO 12
SOFTMARE: Patentin version 3.0
SEG ID NO 12
CORGANISM: Murine
US-09-881-823-12
QUEST MATCH
BEST LOCAL Similarity 80.5%; Pred. No. 7.1e-41;
CORGANISM: Matches 99; Conservative 11; Mismatches 12; Indels 1; Gaps 1;
BEST LOCAL Similarity 80.5%; Pred. No. 7.1e-41;
Matches 99; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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644
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                                                                                                    Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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### SUMMARIES

Result No.	Score	Query Match	Length	₽B	ID	Description	
<b>1</b>	511.5	79.4	247	5	PCT-US94-07659-2	Sequence 2,	Appli
N	505.5	•	119	4	8-875-674A-	o i	Appli
ω	502	78.0	135	ω	US-08-579-378A-16		
4.	501.5		119	4.	US-08-875-674A-3	(D)	Appli
ហ	500.5	77.7	119	N	-08-475	Seguence 16	•
o	500.5	77.7	119	N	US-08-483-199-16		•
7	500.5	77.7	119	N	US-08-484-508-16		٠.
œ	494	76.7	118	μ	<u>6</u>		Appli
Q	490	76.1	135	w	US-08-579-378A-20		
10	490	•	443	ហ	PCT-US96-13152-4		Appli
11	489.5		239	Ŋ	US-08-553-497A-18		
12	488	•	123	بر	US-08-356-272-3		Appli
13	486	75.5	120	N	US-07-934-373C-4		Appli
14	486	•	120	ω	US-08-437-642B-4	Sequence 4,	Appli
15	486		120	4.	US-08-146-206C-4	Sequence 4,	Appli
16	485.5	75.4	121	۲	US-08-339-582-2	Sequence 2,	Appli
17	485.5	75.4	123	4	US-09-344-587-13		Appl
18	485	75.3	109	N	US-08-793-490-6		
19	483.5	75.1	117	ω	US-08-752-693A-3		
20	483.5	75.1	136	4.	US-08-976-183A-31		
21	483.5	75.1	136	4,	US-08-976-183A-32	Sequence 32,	
22	483.5	75.1	136	4.	US-08-976-183A-33		Appl
23	483.5	75.1	136	4	US-08-976-183A-34		
24	483	75.0	116	ພ	US-08-888-366-10		
25	482.5	74.9	125	<b>j</b>	ě		
26	482.5	74.9	125	N	US-08-331-397B-65	Sequence 65	•
27	482.5	74.9	125	N	US-08-759-804A-64		•

Query Match

79.4%;

Score 511.5;

DB 5;

Length 247;

29 481 74.7 122 2 US-07-934-373C-21 30 481 74.7 122 3 US-08-437-6428-21 31 481 74.7 122 4 US-08-145-206C-21 32 481 74.7 122 5 PCT-US93-07832-21 33 479.5 74.5 117 4 US-09-339-922A-6 34 479.5 74.5 237 2 US-08-224-991-16 35 479.5 74.5 237 2 US-08-926-789-18 36 479.5 74.5 241 2 US-08-926-789-18 37 479.5 74.5 241 2 US-08-926-789-18 38 479.5 74.5 241 2 US-08-926-789-18 38 479.5 74.5 241 2 US-08-926-789-18 38 479.5 74.5 245 4 US-09-08-821-5 39 479.5 74.5 245 4 US-09-08-821-5 40 478.5 74.3 136 2 US-08-253-877C-57 41 478.5 74.3 136 2 US-08-253-877C-57 42 478.5 74.3 136 2 US-08-253-897C-57 43 479 74.1 140 3 US-08-883-607-32 45 477 74.1 140 3 US-08-883-607-32 45 476 73.9 120 4 US-09-025-769B-38																		
744.7 744.7 744.7 744.7 744.7 744.7 744.7 744.7 744.7 744.7 744.3 745.3	45	4.4	43	42	4.	40	ω φ	38	37	36	ω U	4	w	32	31	30	29	
111211222222 1112222222 111233655117722222 12006551177722222	476	477	478	478.5	478.5	478.5	479.5	479.5	479.5	479.5	479.5	479.5	479.5	481	481	481	481	
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2 US-07-934-931-21 3 US-08-437-6428-21 4 US-08-146-206C-21 5 PCT-US93-07832-21 6 US-08-926-789-16 7 US-08-926-789-16 7 US-08-926-789-18 7 US-08-926-789-18 7 US-08-926-789-18 7 US-08-926-789-18 7 US-08-926-789-18 7 US-08-926-789-18 7 US-08-926-789-18 7 US-08-926-789-18 7 US-08-926-789-18 7 US-08-926-789-18 7 US-08-926-789-18 7 US-08-926-789-18 7 US-08-926-789-18 7 US-08-928-928-57 7 US-08-928-368-368-38	120	140	116	239	136	136	265	245	241	241	237	237	117	122	122	122	122	1
US-07-94-373C-11 US-08-437-642B-21 US-08-147-206C-21 PCT-US93-07832-21 US-09-339-922A-6 US-08-224-591-16 US-08-224-591-18 US-08-224-591-18 US-08-224-591-18 US-08-224-591-18 US-08-224-591-18 US-08-224-591-18 US-08-224-591-18 US-08-224-591-18 US-08-224-591-18 US-08-224-591-18 US-08-224-591-18 US-08-224-591-18 US-08-224-591-18 US-08-224-591-18 US-09-68-821-5 US-09-68-821-5 US-09-68-399-4 US-08-883-366-12 US-08-983-366-12 US-08-983-360-38	4.	w	N	N	N	_	441	4	N	Ŋ	N	Ŋ	*	ທ	4	W	N	,
	US-09-025-769B-38	US-08-983-607-32	US-08-888-366-12	US-07-956-399-4	US-08-452-164A-57	US-08-253-877C-57	US-09-420-592A-5	US-09-069-821-5	US-08-926-789-18	US-08-224-591-18	US-08-926-789-16	US-08-224-591-16	US-09-339-922A-6	PCT-US93-07832-21	US-08-146-206C-21	US-08-437-642B-21	US-07-934-373C-21	OF-CA-COLUMNIE
	38, Appl	32, Appl	12, Appl	1, Appli	57, Appl	57, Appl	5, Appli	5, Appli	18, Appl	l8, Appl	le, Appl	le, Appl	6, Appli	21, Appl	•	-	•	100

### ALIGNMENTS

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FILLING LATE:
CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/090,534
FILING DATE: 09-UUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: SULTON, JEffrey A.
REGISTRATION NUMBER: 34/028
REFERENCE/DOCKET NUMBER: P50171-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5094
FILEPHONE: (610) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
FCT-US94-07659-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
PCT-US94-07659-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Recurring Ant.
TITLE OF INVENTION: DARL
TITLE OF INVENTION: DARL
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19406-2799
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gross, Mitchell
APPLICANT: Jonak, Zdenka L.
APPLICANT: Theisen, Timothy
APPLICANT: Hurle, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSES: SmithKline Beecham Corporation - Corp.
ADDRESSES: Intellectual Property
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application PC/TUS9407659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Young, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant and Humanized Il-1 beta
Antibodies for Treatment of Il-1 Mediated Inflammatory
Disorders in Man
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US-08-875-674A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/CU96/(
APPLICATION NUMBER: 18-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: HENRY A. MARZULLO, JR.
REGISTRATION NUMBER: 20,910
REFERENCE/DOCKET NUMBER: 910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 723-4300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: MONTER
                                                                                                                                                                                                                                                                                         TELEFAX: (914)-723-4301
(NFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                              HYPOTHETICAL: NO
ANTI-SENSE: NO
ANTI-SENSE: NO
TYPE: -N Terminal fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 3.5' (1.4 MB).
COMPUTER: Compatible PC IBM (80486, 8 M Ram).
OPERATING SYSTEM: Windows 95.
SOPTWARE: Word Perfect 5.0 for Windows 95.
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LOMBARDERO VALLADARES, J.
APPLICANT: PREZ RODR GUEZ, R.
APPLICANT: SIERRA BL ZQUEZ, P.
APPLICANT: TORMO BRAVO, B. R.
                                                                          IMMEDIATE SOURCE:
                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Anti-CD6 monoclonal antibodies and their uses
IDENTIFICATION METHOD: Experimental, OTHER INFORMATION: Sequence corresponding to the variable region
                                                                                       ORGANISM: Mice Balb/C INDIVIDUAL ISOLATE: io TISSUE TYPE: Murine h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Scarsdale
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                           COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                            COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 SS 138
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                                                       Sub-clone ior tlA
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                                                                                                                                                                                                                                                                           119 Amino acid residues.
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                                                                                                                                                                                                                            Unknown
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                                                                                       Murine hibridoma
                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                           Unknown.
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US-08-579-378A-16
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-875-674A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/08579378A Patent No. 6210671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 07/983,946
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95114696.8
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
RESTERENCE/DOCKET NUMBER: 11823-00222
                                                                                            TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Co, Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One MarketPlaza, Steuart Tower, Suite 2000
MOLECULE TYPE:
                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION UMBER: US 08/160,074
PILING DATE: 30-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Humanized I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0. FILING DATE: 27-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
                    TOPOLOGY:
                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                  amino acid
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                  linear
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82.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/579,378A
                                                                                              16:
                                                                                                                                                                          11823-002220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
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Pred. No. 1.4e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSEDTAMYYCARRDYDLD---YFDSWGQGTTLTV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 119;
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Sequence corresponding to the humanized

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RESULT 4
US-08-875-674A-3
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MEDIUM TYPE: Floppy disk 3.5" (1.4 MB).

COMPUTER: Compatible PC IBM (80486, 8 M Ram).

COMPUTER: Compatible PC IBM (80486, 8 M Ram).

OPERATING SYSTEM: Windows 95.

SOFTWARE: Word Perfect 5.0 for Windows 95.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/875,674A

FILING DATE: 17-July-1997

CLASSIFICATION: 530

PRIOR APPLICATION NUMBER: PCT/CU96/00004

APPLICATION NUMBER: PCT/CU96/00004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Applic
Patent No. 6572857
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Best Local
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                                                                                                                                                                                                                                                                                                                        FILING DATE: 18-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: HENRY A. WARZULLO, JR.
REGISTRATION NUMBER: 20,910
REFERENCE/DOCKET NUMBER: P-12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 723-3300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: MONTER
APPLICANT: LOMBAR
                                                                             HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: -N TO
ORIGINAL SOURCE:
TISSUE TYPE: Anim:
CELL LINE: NSO " (
                                                                                                                                                                                                                                                                        TELEFAX: (914)-723-430
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
FEATURE: IDENTIFICATION METHOD: By similarity with known sequence.
                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                         ENGTH:
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                                              Sub-clone ior tlA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08875674A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       One Chase Road
                                                                                                                                                                                                                                                                                         (914)-723-4301
OR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIERRA BL ZQULZ, ...
TORMO BRAYO, B. R.
WENTION: Anti-CD6 monoclonal antibodies and their uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOMBARDERO
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                                                                                                                                                                                                       Unknown.
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                                                                                                                                 -N Terminal fragment
                                                                               Animal cells.
SO " SP 2/0 " CHO
                                                                                                                                                                                     Protein
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80.3%;
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US-08-475-000-16
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                                                                                                                             Query Match
Best Local Similarity
Matches 97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATENT NO. 5811267
GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
Patent No. 6572857
OTHER INFORMATION:
OTHER INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                       TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 08
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                   LENGTH: 119 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Emeryville
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61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYYEDVWGAGTLVTV
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5. 5811267
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                                                                                 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSSTYY 60
                                                       EVKVVESGGVLVRPGGSLKLSCAASGFTFSRYTMSWVRQTPEKRLEWVATISSGGGNTYY 60
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SS 119
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                                                                                                                                 77.7%; Score 500.5; ilarity 79.5%; Pred. No. 4.7¢ Conservative 10; Mismatches
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82.0%;
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Pred. No. 3.7e-46;
1; Mismatches 18;
                                                                                                                               4.7e-46;
ches 12;
                                                                                                                                                                   DB 2;
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; Sequence 16, Application US/084
; Patent No. 5948647
; GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
ITILE OF INVENTION: ANTIGEN
; TITLE OF INVENTION: MOLECUI
                                                                                                                                                                                                                                                                                    S
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Watches 97; Conserve
                                                                                                               US-08-484-508-16
                                                                                                                                  RESULT 7
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US-08-483-199-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: SAVEREIDE, PAUL
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 08:
TELECOMMUNICATION INFORMATION:
TELECHONE: (510) 601-2585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
COPERATES. Datasetts Datasetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SAVERBIDE, PAUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,199
FILLING DATE: 07-UIN-1995
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: RING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: INITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                    118
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                                                                                                                                                                                                                                                                                61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVWGAGTLVTV 120
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    119 amino acids
amino acid
    XY: linear

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                                                                                                                                                                                    SA 119
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                                                                                             Application US/08484508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08483199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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         ANTIGEN-BINDING SITES OF ANTIBODY MOLECULES SPECIFIC FOR CANCER ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                    77.7%; Score 500.5; DB 2; 79.5%; Pred. No. 4.7e-46; tive 10; Mismatches 12;
18
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US-08-326-362-2
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COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPETMARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-484-508-16
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Ap
Patent No. 573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                          APPLICANT: Bosslet, Klaus
APPLICANT: Bosslet, Klaus
APPLICANT: Seeman, Gerhard
APPLICANT: Dippold, Wolfgang
TITLE OF INVENTION: Monoclonal Anti-Ganglioside Antibody,
TITLE OF INVENTION: Its Preparation and Use as a Tumortherapeutic Agent
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL
REGISTRATION NUMBER: 36,:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: UV-08/484,508
FILING DATE: 07-0UN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
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ADDRESSEE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (510) 601-585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: INTERPORTED TO THE CTTY: Emeryville
                                                                                                                                                                       Local Similarity es 97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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)GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08326362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVKVVESGGVLVRPGGSLKLSCAASGFTFSRYTMSWVRQTPEKRLEWVATISSGGGNTYY 60
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                                                                                                                                                                                                                                          Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.7%;
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Pred. No. 4.7e-46;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/08579378A Patent No. 6210671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/032
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: DE P 42 0
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 0248
TELECOMMUNICATION INFORMATION:
TREFERENCE/DOCKET NUMBER: 0248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO: 2:
                                                                 FILING DALL.
CLASSIFICATION: 42a
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/160,074
APPLICATION NUMBER: 30-NOV-1993
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: ISC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                 FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
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LENGTH: 118 amino acid
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ADDRESSEE: Townsend and Townsend and Crew
STREET: One MarketPlaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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TITLE OF INVENTION: Humanized a
TITLE OF INVENTION: L-Selectin
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CITY: San Francisco
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TYPE: amino acid
TOPOLOGY: linear
APPLICATION NUMBER:
                                                                                                                                                                                                   APPLICATION NUMBER:
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79.5%;
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EP 95112895.8
                                                                                                                                                                                                   US/08/579,378A
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GENERAL INFORMATION:
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APPLICATION NUMBER: EP 95 112 895.8

FILING DATE: 17-Aug-95

APPLICATION NUMBER: EP 95 114 969.9

FILING DATE: 19-Sep-95

ATTORNEY/AGENT INFORMATION:
NAME: Norman D. Hanson

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: BOER 1059-PCT

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
NOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95114696.8
FILING DATE: 19-SEP-19-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Martin, Ulrich, et al.
TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fa
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acid
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TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 11823-002220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 805 Th
CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 76.1%; Score 490; DB 3; Local Similarity 78.7%; Pred. No. 7.2e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 17-AUG-1995
                                                                                                                                                                                                APPLICATION NUMBER: 08
FILING DATE: 27-Dec-95
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
ZIP: 10022
                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Felfe & Lynch
ADDRESSEE: Attn: Norman D. Hanson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 SS 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVASISTGG-STYX 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                805 Third Avenue
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                                                                                                                                                                                                                     08/578,953
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                         BOER 1059-PCT-PFF/NDH
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PCT-US96-13152-4
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Best Local 9
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ROSELL, EI
APPLICANT: BLASCO, FE
APPLICANT: PIULATS,
TITLE OF INVENTION: F
TITLE OF INVENTION: F
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 443
                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/53,497A FILING DATE: 17-NOV-1995 CLASSIFICATION: 530
                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PRIOR DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
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STRANDEDNESS: double
TOPOLOGY: linear
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VENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
VENTION: ANTIBODIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JAUME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.1%; Score 490; DB 5; Length 443; 78.7%; Pred. No. 3.3e-44;
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       MERCK 1726
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                                                                                                       Patent No. 576694
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Best Local Similarity
            TELEX: 240867
INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
                                      REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 503-8177
TELEFAX: (201) 503-8807
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: FLOPPY disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                     APPLICATION NUMBER:
FILING DATE: 15-DBC:
CLASSIFICATION: 435
CLASSIFICATION: C121
CLASSIFICATION: G011
CLASSIFICATION: A611
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LENGTH: 239 amino acid
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                                                                                                   NAME: Battle, Carl we REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: East Hanover STATE: N. J.
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15-DEC-1994
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G01N33/574
G01N33/577
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80.5%;
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                                                                                                                                                              WO PCT/EP93/01533
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                                                                                    118-8040
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Pred. No. 1.7e-44;
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US-07-934-373C-4
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                               Matches
                                                               Query Match
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                                                                                                                                            TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
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APPLICANT: Paul J
APPLICANT: Leonar
                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-UN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Immunoglobulin Variants NUMBER OF SEQUENCES: 48
                                               Local Similarity
                                                                                                                                                                                                                                                                   NAME: Lee, Wendy M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 21-Aug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
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                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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                            94;
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 1 EVQLQESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKKLEWVATISSGGSSTYY 60
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Amino Acid
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Gy: linear
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                               Conservative
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                                              75.5%;
77.0%;
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                               9; Mismatches
                                              Score 486; DB 2; Length 120; pred. No. 1.7e-44;
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                               Indels
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Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
                                                                                                                          Matches
                                                                                                                                                           Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PCT/US92/05126
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PRIOR APPLICATION DATA:
07/934373
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                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
07/715272
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COMPUTER: Widelie PC-DOS/MS-DOS
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TITLE OF INVENTION: Immunoal
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                                                                                                                                                                                                                              LENGTH: 120 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 15-JUN-1992
                                                                                                                                                                                                               TOPOLOGY:
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61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTREGGGFTVNWYFDVNGAGTLVTV 120
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                                                                                                                          94; Conservative
                                                                                                                                          Similarity
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                                                                                                                                                                                                               Linear
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                                                                                                                                         75.5%;
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                                                                                                                        Score 486; DB 3; Length 120;
Pred. No. 1.7e-44;
9; Mismatches 17; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Windatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-No. 6407213-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LÉNGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
Search completed: November Job time : 17.9172 secs
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US-08-146-206C-4
US-08-146-206C-4
; Sequence 4, Application US/08146206C
; Patent No. 6407213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: South San Francisco
STATE: California
COUNTRY: USA
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ALIGNMENT	KVMS10 KVMS80 KVMS80 KVMS80 KVMS50 PL0081 S09963 S25177 PH0093 S25177 PH0093 S25176 PN0446 PN0446 PN0446 S09966 PN0446 PN
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### RESULT 2 S26343 S26343 Ig kappa chain V region - mouse CJSpecies: Mus musculus (house mouse) CJSpecies: Mus musculus (house mouse) CJAccession: S26343 RJStark, S.E.; Caton, A.J. J. Exp. Med. 174, 613-624, 1991 A,Title: Antibodies that are specific for a single amino acid interchange in a protein A,Reference number: S26309; MUID:91341421; PMID:1908510 S C;Keywords: heterotetramer F;16-94/Domain; immunoglobulin homology <IMM> F;23-92/Disulfide bonds: #status predicted 문 밁 5 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin V region; immunoglobulin homology A;Accession: A93822 A;Molecule type: protein A;Residues: 1-111 <MCK> A;Molecule type; protein A;Residues: 1-111 <MEL; A;Residues: 1-111 <MEL; R;McKean, D.J.; Bell, M.; Potter, M. R;McKean, D.J.; Bell, M.; Potter, M. Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978 A;Title: Mechanisms of antibody diversity: multiple genes encode structurally related A;Reference number: A93822; MUID:79012520; PMID:99744 A;Contents: Till Ig kappa chain V regions (PC3741, T111) - mouse C;Species: Mus musculus (house mouse) C;Date: O2-Apr-1982 #sequence revision O2-Apr-1982 #text\_change 21-Jan-2000 C;Accession: A93204; A93822; A01934 A; Title: Rearrangement of genetic information may produce immunoglobulin diversity. A; Reference number: A93204; MUID:79073152; PMID:103003 R; Weigert, M.; Gatmaitan, Nature 276, 785-790, 1978 A;Accession: A93204 A; Contents: PC3741 Matches Query Match Local 103; S 53 3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQDPKLLIYRASNLESGI w Similarity VLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYRASNLESGI PARFSGSGSRTDFTLTINEVEADDVATYYCOOSNEDPYTEGGGTKLEIK 111 PARESGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLBIK 111 Conservative 91.18; ₽. Score 532; DB 1; Pred. No. 1.6e-41; 핂.; Mismatches Schilling, J.; Hood, ٨ Length 111; Indels 0; Gaps 62 62

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R/Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in A;Reference number: 826309; MUID:91341421; PMID:1908510
A;Accession: $26344
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S26344
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A. Title: Induced pocket to accommodate the cell attachment Arg-Gly-Asp motif in A;Reference number: $63596; MUID:96174482; PMID:8594203

A. Accession: $63596
                                              A;Cross-references: EMBL:X59209; NID:g52336; PIDN:CAA41919.1; PID:g1334074
C;Superfaxily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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C;Species: Mus musculus (house mouse)
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A; Residues: 1-107 <ST
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A;Status: preliminary
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       Query Match
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Keywords: heterotetramer; immunoglobulin
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   Score 513;
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Pred. No. 7e-40;
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Pred. No. 3.5e-40;
5; Mismatches 3
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A;Residues: 21-122 <TII>
A;Experimental source: B cell, strain [NZB x NZW]F1, clone 17p.73
C;Comment: The M63 precursor sequence is shown.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgW, the subunits associate int C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                    A; Accession.
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 21-11; 'L',121-123,'A',125-129,'L',131 <WE2>
A; R; Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A; Title: Both 19M and 19G anti-DNA antibodies are the products of clonally selective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 21-119,'Y',121-131 <MC3>
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
A;Accession: C93204
A;Accession: C93204
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Biochemistry 17, 2392-2400, 1978
A;Title: Primary structures of N-terminal extra peptide segments link expression of immunoglobulin genes.
                                                                                                                                                                                                                                            A; Molecule type: mRNA
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Biochemistry 12, 760-771, 1973
A;Title: Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains
A;Reference number: A90374; MUID:73140225; PMID:4691517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 1-53;69-107 «
A; Accession: C93822
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A;Title: Mechanisms of antibody diversity: multiple genes encode structurally related
A;Reference number: A93822; MUID:79012520; PMID:99744
A;Contents: M63; AB22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 21-46, '0', 48-53, 'B', 55-57, 'Z', 59-86, 'F', 88-131 < MCK>
A; Roete: this sequence his since been revised in reference A93822
R; McKean, D.J.; Bell, M.; Potter, M.
R; McKean, D.J.; Bell, M.; Potter, M.
R; McKean, D.J.; Bell, M.; Potter, M.
R; McKean, D.J.; Bell, M.; Potter, M.
R; McKean, D.J.; Bell, M.; Potter, M.
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A, Residues: 21-119,'Y', 121-131 <WEI>
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A; Residues: 1-35 <BUR>
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Matches 98; Conserv
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4; Mismatches
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1078; A01935
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A;Title: Variable region sequences of pathogenic anti-mouse
A;Reference number: S09955; MUID:90269328; PMID:2347362
                                                                                                                                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C;Accession: S09965
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu J. Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu A;Reference number: A45722; MUID:93100833; PMID:7677958
A;Accession: D45722
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A; Residues: 1-111 < REI>
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F;36-114/Domain:
F;43-112/Disulfid
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                                                                                                                                                               Cross-references: EMBL:X51853; NID:g55394; PIDN:CAA36146.1; PID:g930230; Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARFSGSGSRTDFTLITINPVEADDVATYYCQQSNEDPLTFGTGTRLEIK 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYLASNLESGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
                                                                                                                                                    immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin homology <IMM>
                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig kappa chain precursor V region #status immunoglobulin homology <IMM>
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                                                                                         84.6%;
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Pred. No. 1e-38;
5; Mismatches
                                                                 Score 494; DB 2; I
Pred. No. 4.4e-38;
6; Mismatches 7;
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Pred. No. 1.5e-39;
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                                                                                                          Length 111;
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          Ig kappa chain V and J regions, monoclonal antibody OHP 4B2.2.1 - mouse (fragment) C;Species: Mus musculus (house mouse)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C;Accession: E53285
R;Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.
Mol. Immunol. 28, 1063-1072, 1991
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A; Title: Molecular characterization of
                                                                                                                                                               RESULT 9
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A;Accession: A90374
A;Molecule type: protein
A;Rosidues: 21-131 <MC2>
A;Rote: the sequence is compatible with that of MOPC 321 except in having 47-Glx, 51-2
C;Comment: The MOPC 321 sequence is shown.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light ()
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Date: 31-May-1979 #sequence revision 31-May-1979 #text_change 31-Mar-2000
C;Accession: A90412; A90373; A90374; A01933
R;Burstein, Y; Schechter, I.
Biochemistry 17, 2392-2400, 1978
A;Fitle: Primary structures of N-terminal extra peptide segments linked to expression of immunoglobulin genes.
A;Reference number: A90412; MUID:78235887; PMID:98179
A;Contents: MOPC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: A90373; MUID:73140224; PMID:4120629 A;Contents: MOPC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Mouse immunoglobulin chains. Pattern of sequence variation A;Reference number: A90374; MUID:73140225; PMID:4691517 A;Contents: TEPC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;MoLecule type: protein
A;Residues: 21-132 <MCK>
A;Rosidues: 21-132 <MCK>
A;Note: the partial sequence of the C
R;McKean, D.; Potter, M.; Hood, L.
Biochemistry 12, 760-771, 1973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R,McKean, D.; Potter, M.; Hood, Biochemistry 12, 749-759, 1973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: this precursor was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein A; Residues: 1-37 < BUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A90373
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                                                                                                                                                                                                                                                                                               ;1-20/Domain: signal sequence #status predicted;21-132/Product: Ig kappa chain V regions (MOPC;36-114/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                          ;43-112/Disulfide bonds: #status predicted
                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                      Keywords: heterotetramer
                                                                                                                                                                                                              Local
         83
                                          63 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR
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                                                                                                                             VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
PARESGSGSRTBETLTIBPVZABDVATYFCZZSBZBPWTFGSGTKLBIKR
                                                                                       VLTQSPASLAVŠLOQRATISCRASKŠVNTYGNSFMZWYZZKPGZPPKLLIYRASNLZSGI
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                                                                                                                                                                                      Conservative
                                                                                                                                                                               83.9%; Score 490; DB 1;
78.2%; Pred. No. 1.2e-37;
tive 20; Mismatches 4
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                                                                                                                                                                                                                                                                                                                    <SIG>
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                                                                                                                                                                                                                            Length 132;
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    mouse (tentative sequence)

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monoclonal anti-steroid

antibodies:

primary

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, qd
                                                                                      Ig kappa chain V region (PC7043) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 01-Sep-1981 #sequence revision 01-Sep-1981 #text change 21-Jan-2000
C;Accession: A01937; S42187; S42194; S42190; S42189; S42188; S42191; S42192
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin div
A;Reference number: A93204; MUID:79073152; PMID:103003
A;Accession: A01937
A;Molecule type: protein
A;Residues: 1-111 <WEI>
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
                                                                                                                                                                                                                                                                                                                             RESULT 11
KVMS43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C;Accession: B01937, A01937
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
A;Accession: B01937
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A;Residues: 1-111 <WEI>
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>
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A;Molecule type: DNA; protein
A;Residues: 1-111 <SAW>
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C;Species: Mus musculus (house mouse)
C;Bate: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
C;Accession: B01937; A01937
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A;Reference number: A53285; MUID:92017897; PMID:1922102
A;Accession: E53285
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Best Local S
Matches 90
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Best Local 9
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84.4%; Pred. No. 1.3e-37;
tive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Mismatches
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Pred. No. 1e-35;
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A;Cross-references: EMBL:225454; NID:9407842; PIDN:CAA80941.1; PID:9407843
A,Note: V-kappa-21E; anti-collagen
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
F;16-94/Domain: immunoglobulin homology F;23-92/Disulfide bonds: #status predicted
Ig kappa chain V region (PC6308) - mouse C;Species: Mus musculius (house mouse) C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change C;Accession: C01937; A01937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 12-99 <MOZ>
A;Residues: 12-99 <MOZ>
A;Residues: 12-99 <MOZ>
A;Roser terences: EMBL:225446; NID:g407834; PIDN:CAA80933.1; PID:g407835
A;Note: V-kappa-21E; anti-collagen
A;Accession: S42191
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A;Residues: 15-9 <MOA>
A;Residues: 15-9 <MOA>
A;Residues: 15-9 <MOA>
A;Rosidues: PIDN:CAA80935.1; PID:g407837
A;Note: V-kappa-21E; anti-collagen
A;Accession: S42188
                                                                                                             KVMS08
                                                                                                                                   RESULT 12
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A; Residues: 10-99 < MOO>
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A;Note: V-kappa-21E ; anti-collagen
A;Accession: S42192
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A; Residues: 10-99 < MOY>
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A;Residues: 13-99 <MOF>
A;Residues: 13-99 <MOF>
A;Cross-references: EMBL:Z25450; NID:g407838; PIDN:CAA80937.1;
A;Note: V-Kappa-21E; anti-collagen
A;Accession: S42189
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A; Residues: 12-99 < MOW>
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A; Residues: 10-99 < MOJ >
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A;Accession: $42187
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                                                                                                                                                                                                                                                                                                             vltospaslavsigoratisckasosvdydgdsymmydokpgoppklliyaasnlesgi
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Pred. No. 1.2e-35;
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R; Weigert, M.; Gatmaitan, L.; Loh, Nature 276, 785-790, 1978 A; Title: Rearrangement of genetic: E.; Schilling, J.; Hood,

A;Reference number: A93204; A;Accession: C01937 genetic information may produce 4; MUID:79073152; PMID:103003 immunoglobulin diversity.

A; Nolecule type: protein
A; Residues: 1-111 <WEI>
C; Complex: An immunoglobulin heterotetramer subunit consists of two
hain disulfide bonds. In some cases, such as IgA and IgM, the subunit
hain disulfide bonds in some cases, such as IgA and IgM, the subunit consists of two
hain disulfide bonds. In some cases, such as IgA and IgM, the subunit hain disulfide bonds in some cases. subunits identical light associate

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Ig kappa chain V region (M-T321) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Abte: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: $19972
R;Meissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A;Bescription: Structural characterization of CD4 mAb.
A;Reference number: $1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 1-111 <MEI>
A;Residues: 1-111 <MEI>
G;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;L6-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted
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S19972
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(;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 31-Mar-2000
C;Accession: B01938; A01938
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Mature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
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KVMS75
                                                                                               A;Cross-references: EMBL;X65094; NID:g52290; PIDN:CAA46222.1; PID:g52291
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Kupwords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-112 <WEI>
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78.8%;
l Similarity 80.9%;
89; Conservative
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Similarity 80.7%;
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82.6%;
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          8
                                Score 460; DB 2;
Pred. No. 5.4e-35;
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Pred. No. 3.5e-35;
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Pred. No. 1.9e-35;
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A, Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A, Reference number: A93204; MUID:79073152; PMID:103003
A, Accession: E01937
A, Molecule type: protein
A, Residues: 1-11 (MEI)
C, Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: heterotetramer; immunoglobulin
C, Keywords: heterotetramer; immunoglobulin
C, Keywords: immunoglobulin homology < IMM>
F, 16-94/Domain: immunoglobulin homology < IMM>
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Search completed: November Job time: 14.6047 secs
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                                                                                               63 PARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPWTFGSGTKLEIK 111
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MEDLINE=79012520; PubMed=99744;

McKean D.J., Bell M., Potter M.;

"Mechanisms of antibody diversity: multiple
related mouse kappa variable regions.";
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 517;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAMEWORK-4
BY SIMILARI
                                                                                                                                         Craniata; Vertebrata; |
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                        PRT;
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se immunoglobulin
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                                                                                                                                                            Euteleostomi;
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RESULT 4

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Best Local :
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                                                                                                                                                                                                                                                                                                                     the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes."; Biochemistry 17:2392-2400(1978).
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21-JUL-1986
15-JUL-1999
                                                                                                            MEDLINE=73140225; PubMed=4691517;
MCKean D.J., Potter M., Hood L.E.;
"Mouse immunoglobulin chains. Pattern of sequence variation
kappa chains with limited sequence differences.";
kappa chains with limited sequence differences.";
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P01661;
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MEDLINE=78235887; PubMed=98179;
Burstein Y., Schechter I.;
"Primary structures of N-terminal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; )
MEDLINE=79012520;
McKean D.J., Bell
                                                              REVISIONS.
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                                                                                                                                                                                                                                                                                    SEQUENCE OF 21-131.
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21-UUL-1986 (Rel. 01, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
15 kappa chain V-III region MOPC 63 precursor
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MEDLINE=79073152; PubMed=103003;
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PubMed=99744;
M., Potter M.
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Pred. No. 2.
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Best Local :
RESIDUES.
PIR; A90412; KVMS32.
HSSP; P01679; 2FBJ.
InterPro; IPR007110; I
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PIR; B90412; KVMSM6.

HSSP; P01679; 22BJ.

InterPro; IPR007110; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; Ig; 1.

SMART; SM00406; IGv; 1.
                                                                                                                                                                         Burstein Y., Schechter I.; "Primary structures of N-terminal extra peptide segments linked the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes."; Biochemistry 17:2392-2400(1978).
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21-JUL-1986
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DOMAIN
                                                              Biochemistry 12:749-759(1973).
-1- MISCELLANEOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM TH
                                                                                                                                                                                                                                                SEQUENCE OF 1-37.
MEDLINE=78235887; PubMed=98179;
                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                       MEDLINE=73140224; PubMed=4120629;
                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986
15-JUL-1999
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related mouse
                                                                                                                            McKean
                                                                                                                                                    SEQUENCE OF 21-132.
                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mmunoglobulin
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-JUL-1999 (Rel. 38, Last annotation update)
kappa chain V-III region MOPC 321 precurso
                                                  REPORTED FOR MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
                                                                                                               D.J., Potter M., Hood | immunoglobulin chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARTSGSGSRTDFTLTIDFVEADDAATYYCQQNNEDFWTFGGGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYLASNLESGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS50835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131
131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of antibody diversity: multiple genes encode structurally se kappa variable regions."; Acad. Sci. U.S.A. 75:3913-3917(1978).
                                                                                                                                                                                                                                                                                                                                                                         (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; IGv; 1.
35; IG LIKE; 1.
V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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43
58
73
73
112
121
131
                                                                                                                                                                                                                                                                                                   Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.5%;
89.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14291 MW;
  Ig-like
                                                   N WAS
                                                                                                            Hood f.E.;
nains. Partial amino acid sequence of a kappa
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                                                  ALSO DETERMINED. IT DIFFERS FROM THAT 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
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5; Mismatches
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Pred. No. 3
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BY SIMILARI
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COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG KAPPA CHAIN V-III REGION MOPC 63. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPLEMENTARITY-DETERMINING-3
                                                                                                                                                                                                                                                                                                   Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAMEWORK-
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                                                                                                                                                                                                                                                                                                                                      precursor.
                                                                                                                                                                                                                                                                                                                                                                                                     132 AA
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thi; Muridae; Murinae; Mus.
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RESULT 6
KV3G MOUS
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Query Match
Best Local S
Matches 86
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Best Local
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P01659;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 JUL-1990 (Rel. 38) Last annotation update)
15 kappa chain V-III region TEPC 124.
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NON TER
SEQUENCE
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DISULFID
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PROSITE;
                                                                                                                                                                     DOMAIN
DOMAIN
                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                        kappa chains with limited seques belochemistry 12:760-771(1973). HSSP; PO1679; 2EBJ. InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                              McKean D.J., Potter M., Hood L.E.;
"Mouse immunoglobulin chains. Pattern of sequence
"Mouse immunoglobulin chains. Pattern of sequence
kappa chains with limited sequence differences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Butheria; Rodentia;
                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                           Immunoglobulin
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
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SMART; SM00406; IC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003006;
InterPro; IPR003596;
                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=73140225; PubMed=4691517;
                                                                                                                                                                                                                                                                                                                                            nterPro;
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                                                                                                                                                                                                                                                                                                  Pro; IPR003596;
PF00047; ig; 1.
SM00406; IGV;
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                                                                                                  "E; PS50835; IG LIK.
Lobulin V region.
1 23
24 38 53 Cc.
54 60 FRA.
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123
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PS50835; IG_LIK
obulin V region;
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112 AA;
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59
113
122
Conservative
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112
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Ig_MHC.
Ig_v.
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                                                                        12339 MW;
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                                    82.7%;
                78.2%;
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18;
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Pred. No. 5
                Score 483;
Pred. No. 2.
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
                                                                                                                              COMPLEMENTARITY-DETERMINING-3 FRAMEWORK-4.
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                                                                                                                                                                                     COMPLEMENTARITY-DETERMINING-2.
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                                                                        7CFD328DBE8E9D71 CRC64;
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                                                                                                            SIMILARITY.
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Mismatches
                                    DB 1;
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6.
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                                  Length 112;
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DARFFEE 8000
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KV3M_MOUSE
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Best Local S
Matches 90
P016/5;
p016/5;
p016/5;
p016/5;
21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
21-UUL-1986 (Rel. 03, Last annoration update)
15-UUL-1999 (Rel. 38, Last annoration update)
19 kappa chain V-III region PC 7043.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostor Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; /
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NON TER
SEQUENCE
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region PC 7183.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfem, PR00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=79073152; PubMed=103003; Weigert M., Gatmaitan L., Loh B.,
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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HSSP; P01679; 2FBJ.
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Mammalia; Eutheria; Rodentia;
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21-JUL-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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Pred. No. 9
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BY SIMILARI
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COMPLEMENTARITY-DETERMINING-3
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-1.
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Sciurognathi; Muridae;
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Mismatches 10
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                                                         Euteleostomi;
; Murinae; Mus
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Best Local S
Matches 90
   PROSITE; PS50835; 1
Immunoglobulin V re
DOMAIN 1
DOMAIN 24
DOMAIN 39
DOMAIN 54
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SEQUENCE.

Gatmaitan L., Loh E.,
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                                                                                                             Pfam; PF00047; ig; 1
SMART; SM00406; IGV;
                                                                                                                                                                                                     Nature 276:785-790(1978).
PIR; C01937; KVMS08.
HSSP; P80362; 1MTL.
                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 kappa chain V-III region PC 6308.
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DOMAIN
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DOMAIN
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                                                                                                                                                                                                                                                                 diversity."
                                                                                                                                                                                                                                                                                 Rearrangement of
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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The mait an L., Loh E.,
                                                                                                                                                      nterPro;
                                                                                                                                                                      InterPro; IPR003006;
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HSSP; P80362; 1WTL.
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PS50835; IG_LIKE; 1.
obulin V region.
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                                                                                                                                                    IPR003596;
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
                                                                                                                                                                                                                                                                               Gatmaitan L.,
ent of genetic
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Ig_MHC.
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82.6%;
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information
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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Pred. No. 1.2e-42;
9; Mismatches 10
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RESULT 10

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AC P01671

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DT 15-JUL-

DT 15-JUL-

DT 15-JUL-

DT 21-JUL-

DC Mammal

CX MCBI_T.

RN (1)

RA Weiger

RT "Rearr

RA Weiger

RT "Rearr

RI divers

RL HSSP;

DR Interp

DR Interp

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DR Interp

DR Interp

DR Interp

DR FINGURI

RA SMART;

DR SMART;

DR SMART;

DR SMART;

DR SMART;

DR JOMAIN

PT DOMAIN

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21.-UUL-1986 (Rel. 01, Created)
21.-UUL-1986 (Rel. 01, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
15 kappa chain V-III region PC 7175.
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SEQUENCE
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=79073152; PubMed=103003;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                  SEQUENCE
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HSSP; P01679; 2FBJ.
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Pred. No. 4.1e-42;
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
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                      MEDLINE=79012520; PubMed=99744;
McKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structural related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-!- MISCELLAUEOUS. THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
BOR. A01936; KYMSC1.
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Ig kappa chain V-III region PC 7769.
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MEDLINE=79073152; PubMed=103003;
MEDLINE=79073152; PubMed=103003;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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P80362; 1WTL.
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of genetic information may produce immunoglobulin
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Pred. No. 1.1e-41;
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FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
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Inter.
InterPro; Att.
InterPro; IPR003590,
InterPro; IPR003590,
IPfam; PP00047; ig; 1.
R SMART; SM00406; IGv; 1.
AR PROSITE; PS50835; IG LIKE; 1.
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21-JUL-1986
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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MEDLINE=79073152; PubMed=103003;

MEDLINE=79073152; PubMed=103003;
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Mammalia; Eutheria;
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Mus musculus (Mouse)
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Immunoglobulin V z
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HSSP; P80362; 1WTL.
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     88; Conser
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(Rel. 01, Last sequence update)
(Rel. 38, Last annotation update)
ain V-III region PC 6684.
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12039 MW;
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Rodentia;
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81.7%;
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information
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
 Score 456; DB
Pred. No. 1.8e
8; Mismatches
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BY SIMILARI
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Sciurognathi;
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thi; Muridae; Murinae; Mus.
                                         DB 1;
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RESULT 15

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ID KYJU MOUSE STANDARD; PR

AC P01673;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last seque)
DT 15-JUL-1999 (Rel. 38, Last annot. 19 kappa chain V-III region PC 2

OS Mus musculus (Mouse).

OC Bukaryota; Metazoa; Chordata; Cr

OC Mammalia; Eutheria; Rodentia; Sc
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Weigert M., Gatmai
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae;
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SMART; SM00406; IGv;
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InterPro;
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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Pred. No. 1.8e-41
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

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RN | 1.1

RP SEQUENCE.

RY MEDLINE=79073152; PubMed=103003;

RX MEDLINE=79073152; PubMed=103003;

RX MEDLINE=79073152; PubMed=103003;

RX MEDLINE=79073152; PubMed=103003;

RX MEDLINE=79073152; PubMed=103003;

RY "Rearrangement of genetic information may produce immunoglobulin

RT diversity.";

RI Mature 276:785-790(1978).

C1-!- MISCELLANEOUS: THE PC 4285 AND PC 4039 SEQUENCES ARE IDENTICAL.

PRI: A01939; KVMS85.

DR HSSP; P01679; 2FBJ.

InterPro; IPR003306; Ig_MHC.

DR InterPro; IPR00306; Ig_MHC.

DR InterPro; IPR003199; Ig_v.

Pfam; PP00047; ig; 1.

DR SMART; SM00406; IGv; 1.

DR SMART; SM00406; IGv; 1.

PR PROSITE; PS50835; IG_LIKE; 1.

RT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.

PT DOMAIN 39 53 FRAMEWORK-1.

FT DOMAIN 61 92 FRAMEWORK-2.

FT DOMAIN 61 92 FRAMEWORK-3.

FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 93 101 COMPLEMENTARITY.

PT DOMAIN 102 111 PRAMEWORK-4.

FT DOMAIN 102 111 PRAMEWORK-4.

FT DOMAIN 102 111 PRAMEWORK-4.

FT DOMAIN 102 111 PRAMEWORK-4.

FT DOMAIN 102 111 PRAMEWORK-6.

FT DOMAIN 102 111 PRAMEWORK-1.

FT DOMAIN 103 PRAMEWORK-1.

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11986 MW; BF38C59AA7858467 CRC64;
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78.9%;
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584
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

343	343.5	344.5	345	345.5	347.5	349.5	350.5	352.5	356	357	357.5	358	358.5	412	457	Score
58.7	58.8	59.0	59.1	59.2	59.5	59.8	60.0	60.4	61.0	61.1	61.2	61.3	61.4	70.5	78.3	Query Match
108	239	114	108	112	238	107	112	238	234	108	107	108	109	103	111	Length
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# ALIGNMENTS

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Q9UL78;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_IKE; 1.
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; Van der Merwe P.L.,
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SEQUENCE
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01-MAR-2003
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Mammalia; Eutheria;
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Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"T-cell-dependent antibody response to the dominant
streptococcal polysaccharide, N-acetyl-glucosamine,
with cardiac myosin.";
Tefort T
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
15, Last myosin immunoglobulin light chain variable region
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Immunol. Immunopathol. 87:184-192(1998) AF035036; AAD56272.1; -.
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F206026; AAF69324.1; -.
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103 AA;
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Primates;
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Rodentia;
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Catarrhini;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; P800047; ig; 1.
SMART; SM00406; IGv; 1.
PROSTIB; P850835; IG_LIKE; 1.
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Q9UL70;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable
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SMART; SM00406; IGV; 1.
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HSSP; P01607; 1REI
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EMBL; AF035044; AAD56280.1; -.
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Young D.C.;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Wu X., Liu B., Van der Merwe P.L.,
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                                                                                                    SRFSGSGSGTDFTLTTSSLQPEDVATYYCQKYNSAPRTFGPGTKLEIKR
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108 AA;
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                                                                                                                                                                                                                                                                                     Score 358; DB 4;
Pred. No. 3.5e-33;
19; Mismatches 19
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Best Local (
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Q9UL77;
Q9UL77;
01-MAY-2000
01-MAY-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50835; IG LIKE; 1.

NON TER 1 1 17

NON TER 107 107

SEQUENCE 107 AA: 11600 ....
PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98277139; PubMed=9614934;
WEDLINE=98277139; PubMed=9614934;
Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q96SA9;

01-DEC-2001 (TrEMBLrel. 19, Created)

01-DEC-2001 (TrEMBLrel. 21, Last sequence update)

01-DEC-2003 (TrEMBLrel. 23, Last annotation update)

01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

Anti-streptococcal/anti-myosin immunoglobulin kappa light chain variable region (Fragment).
                                                                                                                                                                                                                                                                              EMBL; AF035037; AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable
                                                                                                                                                                InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                           fetus.
                                                                                                                                                                                                                                                                                                                                                                                                                     "Myosin-reactive autoantibodies in rheumatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
EMBL; U96396; AAB68785.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.; molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=98375893; PubMed=9712075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                         PF00047; ig; 1; sm00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U
                                                                                                                                                                                                                                                                                                              Immunol. Immunopathol. 8
AF035037; AAD56273.1; -.
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                                                                     PS50835; IG_LIKE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTQSPASIAVSIGQRATISCRASESVDSYGYNFMHWYQQIPQQPPKILIYRASNIESGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRFSGSGSGTDFTLTISSLQPEDFATYYCQQS-YSTLTFGGGTKVBIKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                              . ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11520 MW; 4BB43E9C5B577F16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.2%;
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                                                                                                                                                                                                                                                                                                                                            87:184-192(1998)
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Pred. No. 3.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kalis N.N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                 carditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berney S.M
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                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-2002) to the EMB Submitted (JUN-2002) to the EMB EMBL; BC030813, AH30813.1; -. InterPro; IPR007110; Ig-1ike. InterPro; IPR003597; Ig-C1. InterPro; IPR003006; Ig-MHC. InterPro; IPR00396; Ig-v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8NEK1;
Q8NEK1;
01-OCT-2002
01-OCT-2002
01-MAR-2003
                                                                                                        Q8VCI6;
                                                                 01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2003 (TrEMBLrel. 23,
Hypothetical 26.2 kDa prote
SEQUENCE FROM N.A.
TISSUE=Colon;
                           NCBI_TaxID=10090;
                                     Bukaryota; Metazoa;
Mammalia; Butheria;
                                                        Hypothetical 26.2 kDa protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 2. T
SWART; SM00407; IGc1; 1.
SWART; SM00406; IGv; 1.
SWART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 2
PROSITE; PS50835; IG MHC; 1.
                                                                                                                                                                                                                                                                                   Hypothetical SEQUENCE 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUB=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                   77
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                                                                                                                                                                                                                                             70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 LTOSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPXLLIYRASNLESGIP
                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                             GIPARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR
                                                                                                                                                                                                   ENVLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MTQSPSSLSASVGDRVTITCRASQSISSY----LNWYQQKPGKAPNLLIYAASSLQSGVP
                                                                                                                                                                                                                                                                                  al protein.
234 AA; 2
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(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              801
                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                            Conservative
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                                     Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                  25530 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
Primates;
                                                                                                                                                                                                                                                   61.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.1%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                             20;
                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 357; DB
Pred. No. 4.5e
20; Mismatches
                                                                                                                                                                                                                                           Score 356; DB
Pred. No. 1.6e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
                                  Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                  6316E8DEF8D132F8 CRC64;
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                                    Muridae;
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                                                                                                                                                                                                                                                              Length 234;
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                                                                                                                                                                                                                                            Indels
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                                              Euteleostomi;
                                    Murinae:
                                                                                                                                                                                                                                           4
                                                                                                                                                                128
                                                                                                                                                                                  112
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Q8K1F2
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Best Local
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InterPro; IPR003596; Ig_v.
Pfam; PP00047; Ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS002590; IG MHC; 1.
Hypothetical protein.
SEQUENCE 238 AA; 26224 MW; ;
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
Q9UL81;
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SEQUENCE
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STRAIN-BALB/C; TISSUE=Hyperimmunized spleen;
Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul
"Innate proteolytic antibodies: Failed D-VIPase response to the
entantiomer of VIP and identification of L-VIPase VI domains.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AF516283; AAM64201.1; -.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-VIPase light chain variable region (Fragment).
Ans musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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Submitted (DEC-2001) to the
EMBL; BC019760; AAH19760.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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01-OCT-2002
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                                                                                                                                      PARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPLTFGAGTKLELKR
                                                                                                                                                                                     PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                          112 AA;
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                       PRELIMINARY;
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Pred. No. 2.6e-
17; Mismatches
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Pred. No. 4.1e
15; Mismatches
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                       PRT;
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                       107
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                                                                                                                                                                                                                                                                                                                                                                                    DB 11; Length 112;
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RESULT 11
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Best Local S
Matches 66
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01-JUN-2001
01-JUN-2001
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EMBL; AF035033; 1
HSSP; P01607; 1R1
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Submitted (JAN-2001) to the
EMBL; BC002035; AAH02035.1;
HSSP; P01679; 2FBJ.
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01-MAY-2000
01-MAR-2003
                                                                                                                                                                                   Pfam; PF00047; ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
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SEQUENCE
                                                                                                                          Hypothetical protein.
SEQUENCE 238 AA; 26344 MW;
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(Fragment).
Homo sapiens (Human).
**"karyota; Metazoa; Chordata; '
**"karyota; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical 26.3 kDa protein. Mus musculus (Mouse).
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v.
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      Similarity 69; Conserv
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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107 AA;
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      Conservative
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
tive immunoglobulin light chain variable
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                             59.5%;
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      16;
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Last
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   Score 347.5; DB
Pred. No. 1.5e-31
6; Mismatches 2
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Sciurognathi; Muridae;
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                                                                                                                       FB2B06A0B801330A CRC64;
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annotation update)
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Best Local S
Matches 68
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01-MAY-2000 (
01-MAY-2000 (
01-MAR-2003 (
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NON TER
SEQUENCE
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-VIPase light chain variable region (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                            Q9UL83
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        Myosin-reactive
                                                                    MEDLINE=98277139;
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EMBL; AF516282; AAM64200.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAILBALB/c; TISSUE=Hyperimmunized spleen;
Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Pau
"Innate proteolytic antibodies: Failed D-VIPase response to the
entantiomer of VIP and identification of L-VIPase VI domains.";
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STRAIN=BALB/c; TIS
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a X., _ nq D.C.;
                                                                                                                                                                                                                             (Fragment)
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                         Liu B.,
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
tive immunoglobulin light chain variable
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                                       PubMed=9614934;
n der Merwe P.L.,
                                                                                                                                                           Chordata;
Primates;
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Pred. No. 9.
                                                                                                                                                           Craniata; Vertebrata;
Catarrhini; Hominidae
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01-OCT-2002 (TEMBLrel. 22, Last sequence of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of t
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01-OCT-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Pau "Innate proteolytic antibodies: Failed D-VIPase response to the entantiomer of VIP and identification of L-VIPase VL domains."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON TER
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8K1F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGV; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF516284; AAM64202.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-BALB/c; TISSUE=Hyperimmunized spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clin. Immunol. Immunopathol. 87:184-192(1998) EMBL; AF035031; AAD56267.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P80362; 1WTL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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67; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS50835;
PARFSGSGSGTSYSLTISSMEAEDAATYYCQQYHSYPRTFGGGTKLEIKR
                                  PARFSGSGSRTDFTLTINPVEADDVATXYCQQSNEDPLTFGTGTRLBIKR
                                                                                                                         VLTQSPAIMSASPGEKVTMTCRASSSVSS---SYLHWYQQKSGASPKLMIYSTSNLASGV
                                                                                                                                                                                            VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIPARFSGSGSGTEFTLTISSLQFEDFAVYYCQHYNNWPFTFGPGTKVDIKR
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                                                                                                                                                                                                                                                                                                                                                                                                      114 AA;
                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIKE
                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                 Score 344.5; DB 11; Length Pred: No. 1.3e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                               8BD9833DBF3EEFD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9F9C5A92EBA96EEA CRC64;
                                                                                                                                                                                                                                                                     Mismatches
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Murinae; Mus
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   109
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Search completed: November 7, 2003, 07:34:36 Job time: 38.0346 secs
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                                                                                                                                                                                                                                                                             RESULT 15
Q8NEKO
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

C TISSUB=Prostate;
C Strausberg R.;
C Strausberg R.;
L Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC030814; AAH30814.1; -.
InterPro; IPR003597; Ig-11ke.
InterPro; IPR003597; Ig-12.
R InterPro; IPR003596; Ig-MHC.
InterPro; IPR003596; Ig-MHC.
R InterPro; IPR003596; Ig-V.
R InterPro; IPR003006; Ig-MHC.
R InterPro; IPR00307; Ig-12.
R SMART; SM00407; IGC1; 1.
R SMART; SM00407; IGC1; 1.
R SMART; SM00406; IGV; 1.
R SMART; SM00406; IGV; 1.
R PROSITE; PS00835; IG-LIKE; 2.
R PROSITE; PS00835; IG-LIKE; 2.
R PROSITE; PS00835; IG-MIC; 1.
W Hypothetical protein.

M Hypothetical protein.
                                                                                                                                                                                                  Query Match 58.8%; Score 343.5; DB 4; Length 239; Best Local Similarity 61.3%; Pred. No. 4.4e-31; Matches 68; Conservative 16; Mismatches 26; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QRNEKO;
QRNEKO;
QRNEKO;
QRNEKO;
QROUT-2002 (TrEMBLrel. 22, Last sequence update)
QROUT-2003 (TrEMBLrel. 23, Last sequence update)
QROUT-2003 (TrEMBLrel. 23, Last annotation update)
QROUT-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Homo saptens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8NEK0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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Result
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Maximum DB seq length: 200000000
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Maximum Match 10
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                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                               Score
                                          573
573
573
543
542
531
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| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
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| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
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| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
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                                                                                                                                                                                                                                                                          Query
Match
                100.0
98.1
98.1
97.4
97.4
92.8
92.8
90.9
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584
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                             Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*
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AAB20442
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AAB20438
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AAR17332
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Anti-FIX/FIXa anti
Anti-FIX/FIXa anti
Anti-FIX/FIXA anti
Anti-FIX/FIXA anti
Murine 184 light ch
Muxine anti-CD18 A
MAD 1.4 light chai
                                                                                                                                                                                                                                                                          Description
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Antibody s Synthetic p64-k4 pro Light chai Chimeric A TSH recept Monoclonal MAD NM-01 Sequence o Sequence o Sequence o Sequence o Sequence o Sequence o Sequence o Sequence o Light chai Kappa ligh Anti-C5 MA Veneered 1 Light chai Monoclonal Human 1gs FvKC-II vKG FvKC-II KB Jouble-hea Light chai Mouse 4C10 SNV-env le Synthetic Synthetic	3 108	•	
AAU07516 AAU07516 AAU077497 BAR29008 AAR29008 AAR29008 AAR29008 AAR29008 AAR29008 AAR29078 AAR29078 AAR29079 AAR996770 AAR09259 AAR09259 AAR09259 AAR4865172 AAR4865172 AAR79158 AAR79159 AAR791		75	42
AAU07516 AAU07516 AAU07497 AAU07497 AAU07497 AAR29008 AAW30278 AAW30278 ABP96779 ABP96779 AAR4861572 AAR4865172 AAR4865172 AAR79158 AAR4865172 AAR79158 AAR486610 AAR486610 AAR79159 AAR79150 AAR79160 AAR79150 AA		82.	
AAU07516 AAU07516 AAU07497 AAU077497 AAU077497 BP64-k4 AAW30278 ABP967769 ABP967769 ABP96776 AAW09259 AAW09259 AAW09274 AAR165172 AAR79158 AAR79158 AAR79158 AAW19016 AAW02294	0 329	83.	٠.
AAU07516 AAU07516 AAU07497 BAU07497 AAW20008 AAW30278 AAW30278 AAW30278 AAW30278 AAW30278 AAW996769 AAW99259 AAW09259 AAW4865172 AAW65172 AAW65172 AAW79158 AAR79158 AAW00830 AAW19016 AAW00830 AAW19016 AAR10920 AAW27353 AAW27353 AAW02294 AAW02395 AAW37353		.5 83.	488
AAU07516 AAU07516 AAU07497 AAU07497 AAR29008 AAW30278 ABW30278 ABP96769 ABW996769 ABW99279 AAW09259 AAW09259 AAW09259 AAW165172 AAR65172 AAR79158 AAW02294	9 107	90 83.	
AAU07516 AAU07516 AAU07497 AAR29008 AAR29008 AAR29008 AAR29008 AAR29008 AAR19539 ABP96776 AAR10539 ABP96776 AAR10539 AAR4865172 AAR4865172 AAR79158 AAR486616 AAR486616 AAR486617 AAR486617 AAR486617 AAR486617 AAR486617 AAR486617 AAR486617 AAR486617 AAR486618 AAR486617 AAR686810 AAR4866810 AAR486810	84.	٠,	
AAU07516 AAU07516 AAU07497 AAAU07497 AAAU07497 AAAR29008 AAW30278 ABP96769 ABP96769 ABP96770 AAW09259 AAW09259 AAW09259 AAW09274 AAW09259 AAW09259 AAW09259 AAR65172 AAW09279 AAR79158 AAW00830 AAR79158 AAR10920 AAR79156 AAR64202 AAR79156 AAR64202 AAR79156 AAR64202 AAR702294 AAW002294 Yeast-		491 84.	
AAU07516 AAU07516 AAU07497 AAU07497 AAR29008 AAW30278 ABP96769 ABP96779 ABP96779 ABP96779 ABP96779 ARA48615 AAR486157 AAR486157 AAR486157 AAR486157 AAR48616 AAR48616 AAR48616 AAR48616 AAR48616 AAR48616 AAR48616 AAR48616 AAR48616 AAR48616 AAR48616 AAR48616 AAR48616 AAR48616 AAR48616 AAR48616 AAR69110		84.	
AAU07516 AAU07516 AAU07516 AAU077497 AAR29008 AAW30278 AAW30278 AAW30278 AAW30278 ABP96770 ABP96770 AAW09259 AWW09259 AWW09259 AWW092574 AAW09274 A	•	84.	
AAU07516 AAU07516 AAU077497 AAR077497 AAR0708 AAR0708 AAR0908 AAR090278 ABP96769 ABP96769 AAR09259 AAR09259 AAR09274 AAR09259 AAR09274 AAR09274 AAR09274 AAR09274 AAR09274 AAR09274 AAR09274 AAR79158 AAR79159 AAR79159 AAR79150 AAR		84.	
AAU07516 AAU07516 AAU07497 AAR29008 AAR29008 AAW30278 AAW30278 AAW30278 AAW996769 ABP967769 AAW09259 AAW09274 AAW09274 AAR48615 AAR65172 AAR731346 AAR79158 AAR79158 AAR48616 AAR79158 AAR48616 AAR79158 AAR48617 AAR79158 AAR48616 AAR79158 AAR69830 AAR79158 AAR60830 AAR77617 AAR60830 AAR77617 AAR60830 AAR77617 AAR60830 AAR77617 AAW00830 AAR77617 AAR60830 AAR77617 AAR760830 AAR760830 AAR760830 AAR760830 AAR760830 AAR760830 AAR760830 AAR760830 AAR760830 AAR77617 AAR760830 AAR760830 AAR760830 AAR760830 AAR760830 AAR760830 AAR760830 AAR760830 AAR760830 AAR760830	2 215	84.	
AAU07516 AAU07516 AAU07516 AAU077497 Synthe AAR29008 Light AAR19539 ABP96770 ABP96770 AAR09259 AAW09259 AAW09274 AAR165172 AAR748615 AAR748615 AAR791158 ABR79715 AAR791168 AAR48616 AAW19016 AA	4	84.	
AAU07516 AAU07516 AAU077516 AAU077497 Synthetic AAR29008 Light chai AAR30278 AAR10539 ABP10539 ABP10539 ABP10539 ABP10539 ABP10539 ABP10539 ABP10539 ABR10539 ABR10539 ABR10539 ABR10539 ABR10539 ABR10539 ABR10539 ABR10539 ABR10539 ABR10530 ABR1053	ð	84.	
AAU07516 AAU07516 AAU07497 Synthetic AAR29008 Light chai AAR10539 ABP96769 ABP96776 ABP96770 ABP96777 ABP96777 ABP96777 ABP96778 ABP96779 ABP96779 ABP96779 ABP96779 ABP96779 ABP96779 ABP96779 ABP96779 ABP96779 ABP96779 ABP96779 ABP9774 ABP9774 ABP9774 ABP9774 ABP9775 ABP9775 ABP9775 ABP9775 ABP7975 AB		•	
AAU07516 AAU07516 AAU07516 AAU077497 Synthetic AAR29008 Light chai AAR10539 ABP96770 ABP96770 ABP96770 ABW09259 ABW09274 ABW09274 ABW09274 ABW09274 ABW09276 ABR79158 AAR48616 ABR79158 ABR79158 AAR79158 AAR79158 AAR79158 AAR48616 AAW19016 AAW19016 AAW19011 AAW19016	<u>_</u>	84.	
AAU07516 AAU07516 AAU07497 AAU07497 AAU07497 AAW29008 Light chai. AAW30278 AAW30278 AAW30278 AAW30278 AAW30278 AAW30278 AAW30278 AAW996769 AAW99259 AAW09259 AAW09274 AAW09274 AAW48615 AAW65172 AAW48620 AAR65172 AAW48620 AAR65172 AAW48620 AAR79158 AAW79259 AAW79108 AAW19016	3 110	85.	
AAU07516 AAU07516 AAU07516 AAU077497 Synthetic AAR29008 Light chai AAR190278 Chimeric Might chai AAR10539 ABP96776 ABP96776 ABP96777 TSH recept ABP96777 TSH recept ABP96777 TSH recept ABP96778 ABP96779 ABP96779 ABP96779 ABP96779 ABP96779 ABP96779 ABP96779 ABP96779 ABP96779 ABP9774 ABP9775 ABP9775 ABP9775 ABP7975 ABP7975 ABP7975 ABP7975 ABP7975 ABP7975 ABP79775		85.	
AAU07516 AAU07516 AAU07797 Synthetic AAR29008 AAW30278 AAR10539 ABP96770 ABP96770 ABW09259 ABW09274 AAW09274 AAW09274 AAW09274 AAW09274 AAW09274 AAW09276 AAW09276 AAW09277 AAW0927		85.	
AAU07516 AAttibody s AAU07497 AAR29008 AAW30278: AAR10539 AAR10539 ABP967769 ABP96770 ABW09259 ABW09274 AAW09274 AAW09274 AAW68615 AAW68615 AAW68615 AAW68615 AAW68616 AAW686170 AAR486172 AAR65172 AAR65173 AAR65173 AAR65173 AAR66173 AAR66		85.	
AAU07516 AAU07516 AAU077497 AAR29008 AAW30278 AAR300278 AAR1639 ABP96769 ABP96779 ABP96779 ABW09279 AAW09279 AAW09279 AAW09279 AAR48615 AAW65172 AAR48620 AAR65172 AAR48620 AAR63346 AAR63346 ABB79725 AAR13346 AAR13346 AAR13346 AAR155 AAR13346 AAR155 AAR13346 AAR155 AAR13346 AAR155 AAR1346		85.	
AAU07516 AAU07516 AAU077497 AAR29008 AAW30278 AAR30278 AAR10539 ABP96769 ABP96770 ABP96770 ABW09259 AAW09274 AAR4865172 AAR4865172 AAR486630 AAR33346 Sequence of AAR33346 Sequence of	S	86.	
AAU07516 Antibody so Autory Structure AAU077497 AAR29008 AAW302789 AAR10539 ABP967769 ABP967769 ABP96770 AAW09259 AAW09274 AAW09274 AAR65175 AAR65175 AAR65170 AAW09274 AAR48660 AAW09274 AAR48670 AAW09274	Đ	86.	
AAU07516 AAU077497 AAR29008 AAW30278 AAR30278 AAR10539 ABP96779 ABP96779 ABP96779 ABW09274 AAW09274 AAW48615 AAR486172 AAR4865172 AAW465172 AAW465172 AAW465172 AAW465172 AAW465172 AAW4665172 AAW4665172 AAW409274 AAR48665	œ	86.	`
AAU07516 AAU07497 AAU077497 AAR29008 AAW30278 AAW30278 AAW10539 ABP96776 ABP96770 ABW09259 AAW09274 AAR48615 Sequence of	0 111	508 87.	
AAU07516 Antibody so AAU07497 AAR29008 AAR29008 AAR30278 AAR30278 AAR10539 AAR10539 ABP96769 ABP96769 ABP96770 ABP96770 ABP96770 ABP96770 ARM09259 Monoclonal AAW09274 MAB NM-01 1		87.	
AAU07516 Antibody so AAU07497 AAU07497 AAR29008 AAW30278 AAW30278 AAW30278 AAW10539 AAR10539 ABP96770 ABP96770 ABW09259 MOnoclonal		87.	
AAU07516 Antibody antibody AAU07497 Synthetic AAR29008 p64-44 pxc AAW30278 Light char AAR10539 Chimeric Chimeric AAR10539 TSH recept ABP96770 TSH recept		13 87.	
AAU07516 Antibody s AAU07497 Synthetic AAR29008 p64-k4 pxc AAR30278 Light chap AAR10539 Chimeric MAR10539 TSH recept	Ŋ	17 88.	
AAU07516 Antibody s AAU07497 Synthetic AAR29008 p64 k4 px AAR30278 Light chai AAR10539 Chimeric M	ហ	17 88.	
AAU07516 Antibody synthetic AAR29008 p64-44 pxc AAW30278 Light chal	7	18 88.	G
AAU07516 Antibody E AAU07497 Synthetic AAR29008 p64-k4 pro	2 131	21 89.	
AAU07516 Antibody a AAU07497 Synthetic	7	24 89.	
AAU07516 Antibody s	1 252	26 90.	
	1 112	26 90.	
AAU07480 Synthetic a	11	26 90.	
19 AAW44168 Monoclonal antibod	4 131	28	

# ALIGNMENTS

RESULT 1 AAB20435

AAB20435 standard; Protein; 249 AA

21-JUN-2001 (first entry)

AAB20435;

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22-MAR-2001.
                                                                           Peptide
                                           Region
                                                                                                                Key
Protein
                                                                                                                                          Chimeric -
                                                                                                                                                                Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.
                WO200119992-A2.
                                                            Protein
                                                                                               Region
                                                                                                                                                                                                       Anti-FIX/FIXa antibody 198/AB2 scFv
                                                                                                                                          Mus musculus.
Synthetic.
                                                                                              /label= VH
98..102
                                 230.,238
/label= CDR3
                                                                                                                        Location/Qualifiers
                                                                    23..136
label= Linker
                                                   label≃ VL
                                                             37..249
                                                                                      abel= CDR3
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RESULT 2
AAB20442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of a single chain FV (scFv) derivative CC of antibody 198/AB2, comprising the heavy (VH) and light (VI) chain CC variable regions of 198/AB2 joined by an artificial, flexible linker CC peptide. The scFv was obtained by PCR amplification of cDNAs for CC 198/AB2 VH and VL regions and cloning in vector DAP2. 198/AB2 is CC an example of anti-human Factor IX (FIX)/activated Factor IX (FIXA) and their derivatives, CC ancibodies of the invention. Anti-FIX/FIXA and their derivatives, CC activity or FIXA activating activity. Administration leads to an increase in the proceagulant activity. Administration leads to an increase in the proceagulant activity of FIXA, even in the presence CC in the absence of FVIII or FVIII, and in the case of FVIII or FVIII or FVIII and their case of FVIII or FVIII and their case of FVIII or FVIII and their case of FVIII or FVIII and the case of FVIII or The antibodies and derivatives are used in a CC claimed pharmaceutical composition for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                     Chimeric
Chimeric
                                                                                                                Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
Factor VIII cofactor; blood coagulation disorder; haemophilia A
haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse
 Protein
                      Peptide
                                                          Chimeric
                                                                                                     myc-tag
                                                                                                                                                              Anti-FIX/FIXa antibody 198/B1-myc-tag fusion.
                                                                                                                                                                                      21-JUN-2001
                                                                                                                                                                                                                                  AAB20442 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Fig 16; 138pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scheiflinger F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                             198
                                                                                                                                                                                                                                                                                                                                          138
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                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                        ENVLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF30725
                                                                                                                                                                                                                                                                                                         GIPARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLBIKR 112
                                                                                                                                                                                                                                                                                            GIPARPSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTPGTGTRLBIKR
                                                        Escherichia coli.
                                                                   Mus musculus.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                     249 AA;
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                     (first entry)
...2
/label= Signal_peptide
23..294
                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                   294
                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                      Score 584; DB 22;
Pred. No. 2.2e-42;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dorner
                                                                                                                therapy; mouse
                                                                                                                                                                                                                                                                                                                                                                                                             Length
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Query Match
Best Local Sim
Matches 110;
                                                                                                                                                                                                                                                                                            The present sequence is that of a fusion protein comprising: a PelB CC leader; a single chain Fv (scFv) derivative of antibody 198/B1 CC leader; a single chain Fv (scFv) derivative of antibody 198/B1 cc comprising the heavy (VH) and light (VL) chain variable regions of CC 198/B1 joined by an artificial, flexible linker peptide; a spacer; and a C-terminal 6His affinity tail.

CC 198/B1 is an example of anti-human Factor IX (FIX)/activated Factor IX (FIX) antibodies of the invention. Anti-FIX/FIXa antibodies and their derivatives, including scFv fragments, have FVIII a cofactor activity or FIXa activating activity. Administration leads to an increase in the procoagulant activity of FIXa, even in the presence of FVIII inhibitors. This allows for rapid blood coagulation even in the absence of FVIII or FVIIIa, and in the case of FVIII inhibitor patients. The antibodies and derivatives are used in a claimed patients. The activity especially haemophilia A and haemorrhagic coagulation disorders, especially haemophilia A and haemorrhagic athathed surrelives activity.
                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                 exhibited FVIII-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-290358/30.
N-PSDB; AAF30732.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 18; Fig 34; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scheiflinger F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
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222
                                                                               162
                                      63
                                                                                                                   w
                                                                                                                                                                                 Similarity
                                                                                                      VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
                                  PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
                                                                        VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
                                                                                                                                                                                                                                         294 AA;
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99AT-0001576
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23..144
/label=
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23...271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label=Myc_tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "encoded
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39..294
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100.0%;
                                                                                                                                                                                                                                                                                 activity.
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                                                                                                                                                       Score 573; DB 22;
; Pred. No. 2.3e-41
0; Mismatches 0
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                                                                                                                                                                                              Length 294;
                                                                                                                                                         Indels
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                                                                                                                                                         Gaps
                                                                                                                   62
                                                                          221
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RESULT 3
AAB20437
The present sequence is that of a fusion protein comprising: a PelB leader; a single chain Fv (scFv) derivative of antibody 198/B1 comprising the heavy (VH) and light (VL) chain variable regions of 198/B1 joined by an artificial, flexible linker peptide; a spacer; Escherichia coli alkaline phosphatese; and a C-terminal 6His affinity tail. 198/B1 is an example of anti-human Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the invention. Anti-FIX/FIXa antibodies and their derivatives, including scFv fragments, have FVIIIa confactor activity or FIXa activating activity. Administration leads to an increase in the procoagulant
                                                                                                                                                   New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
                                                                                                                                Example 16; Fig 26; 138pp; English.
                                                                                                                                                                                                                                        Scheiflinger F,
                                                                                                                                                                                                                                                                                                             13-SEP-2000; 2000WO-EP08936
                                                                                                                                                                                                                                                                                                                                       22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                             WO200119992-A2
                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric
                                                                                                                                                                                                                                                                 (BAXT ) BAXTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alkaline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-FIX/FIXa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB20437 standard; Protein; 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB20437;
                                                                                                                                                                                                                   2001-290358/30.
                                                                                                                                                                                                        AAB30727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibody 198/81-alkaline phosphatase
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                                                                                                                                                                                                                                                                                        99AT-0001576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label=
23..271
                                                                                                                                                                                                                                         Kerschbaumer
                                                                                                                                                                                                                                                                                                                                                                                                        276..725
/label= Alkaline_phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Signal_peptide
23..732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'label= VH
                                                                                                                                                                                                                                                                                                                                                                                  label= His_tag
                                                                                                                                                                                                                                                                                                                                                                                                                                 label= Spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label= Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= VL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..159
                                                                                                                                                                                                                                                                                                                                                                                                                                              .275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      = SCFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l= Mature_protein
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                                                                                                                                                                                                                                        Dorner F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     procoagulant;
haemophilia A;
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                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activity of FIXa, even in the presence of FVIIIa inhibitors. This allows for rapid blood coagulation even in the absence of FVIII or FVIIIa, and in the case of FVIII inhibitor patients. The antibodies and derivatives are used in a claimed pharmaceutical composition for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic diathesis. The scFv-alkaline phosphatase was expressed in E. coli. It exhibited FVIII-like activity.
                                                  Protein
                                                                                            Peptide
                                                                                                                                     Misc-difference
                                                                                                                                                          Region
                                                                                                                                                                               Peptide
                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                   Protein
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                                                                                                                                                                                                                                                                                                                                         Chimeric
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                                                                                                                                                                                                                                                                                                                                                                        Factor IX; FIX; Factor IXa; FIXa; miniantibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia haemorrhagic diathesis; haemostatic; amidolytic; therapy; moubivalent antibody; plasmid pZip-198AB2#102.
                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-FIX/FIXa antibody 198/B1 bivalent miniantibody.
                                                                                                                                                                                                                                                                                                 Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLTOSPASLAVSLGORATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARFSGSGSRTDFTLTINEVEADDVATYYCQQSNEDPLTFGTGTRLEIKR
                                                                                                                                                                                                                                                                                                                              Mus musculus.
Synthetic.
Escherichia coli.
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                                                                       275..284
           /1abel= His_tag
                                                  285..319
                                                                                                                                                                             /note= "encoded
145..159
                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                       'label= Helix
                                                          'label= Hinge
                                                                              'label= Spacer
                                                                                                                          'note= "encoded
                                                                                                                                              /label= VL
                                                                                                                                                                                                                                                                         /label= Signal_peptide
/note= "PelB leader"
                                                                                                                                                          label= Linker
60..271
                                                                                                                                                                                                             label= VH
                                                                                                                                                                                                                                                     label= Mature_protein
                                                                                                                                                                                                                                  label= scFv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                             274
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                                                                                                      "encoded
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Pred. No. 5.5e-41;
0; Mismatches 0;
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WO200119992-A2

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RESULT 5
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Best Local Simi
Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of a bivalent miniantibody comprising a PelB leader peptide, the single chain Fv (soFv) fragment of antibody 198/B1 (subclone AB2), an amphipathic helical structure and a C-terminal 6His tag. The protein was expressed in Becherichia coli from plasmid pEjp398AE#102 (see AAF30728). Antibody 198/B1 is an example of anti-human Factor IX (FIX)/Activated Factor IX (FIXa) antibodies of the invention. Anti-FIX/FIXa antibodies and their derivatives have FVIIIa cofactor activity or FIXa activating activity. Administration leads to an increase in the procoagulant activity of FIXa, even in the presence of FVIII inhibitors. This allows for rapid blood coagulation even in the absence of FVIII or FVIIIa, and in the case of FVIII inhibitors The antibodies and derivatives are used in a colaimed pharmaceutical composition for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic distributive. The bivalent miniantibody exhibited FVIII-11ke
                                                                 Chimeric
Chimeric
                      Protein
                                    Кeу
                                                                                                        Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; proceagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.
                                                                                                                                                                      Anti-FIX/FIXa antibody 198/A1 scFv.
                                                                                                                                                                                                    21-JUN-2001
                                                                                                                                                                                                                                                              AAB20436 standard; Protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as baemophilia A and haemorrhagic diathesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 16; Fig 28; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAF30728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-290358/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scheiflinger F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      162
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                                                                                                                                                                                                                                                                                                                                                                                                                    VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
                                                                                                                                                                                                                                                                                                                                                         PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
                                                                                                                                                                                                                                                                                                                                                                                                 VLTQXPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI 221
                                                                 Synthetic.
                                                                                Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99AT-0001576.
                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kerschbaumer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.4%;
99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 569; DB 22;
Pred. No. 5.5e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Falkner F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dorner F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 325;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                                                                                              62
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RESULT 6
AAR13089
ID AAR1
XX
AC AAR1
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DT 25-M
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25-MAR-2003

AAR13089

standard;

Protein; 112

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                                                                                                                                                                                           CC The present sequence is that of a single chain Fv (scFv) derivative CC of antibody 198/A1, comprising the heavy (VH) and light (VL) chain CC variable regions of 198/A1 joined by an artificial, flexible linker CC peptide. The scFv was obtained by PCR amplification of cDNAs for CC 198/A1 VH and VL regions and cloning in vector pDAP2. 198/A1 is CC an example of anti-human Factor IX (FIX) /activated Factor IX (FIX) (CC antibodies of the invention. Anti-FIX/FIXa and their derivatives, CC including scFv and CDR3 fragments, have Factor VIIIa (FVIIIa) cofactor CC activity or FIXa activating activity. Administration leads to an increase in the procoagulant activity of FIXa, even in the presence CC of FVIIIa inhibitors. This allows for rapid blood coagulation even in the absence of FVIII or FVIIIa, and in the case of FVIII composition for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic CC diathesis.
                                                                                                               Matches
                                                                                                                           Query Match
Best Local (
                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scheiflinger F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-2000; 2000WO-EP08936.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BAXT ) BAXTER AG.
                                                                                                                            Local Similarity
                                                        141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-290358/30.
DB; AAF30726.
  201
                                                                                                            105;
                 64 ARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
                                                                    4 LTQSPASLAVSLGQRATISCRASESVDSYGYNFWHWYQQIPGQPPKLLIYRASNLESGIP
                                                                                                                                                                      249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Fig 17; 138pp; English.
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99AT-0001576
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137..249
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                                                                                                                         93.0%;
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                                                                                                           Score 543; DB 2
Pred. No. 7e-39;
1; Mismatches
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                                                                                                                                       DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dorner
                                                                                                                                    Length 249;
                                                                                                            Indels
249
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                                                                                                           Gaps
                                                     200
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RESULT 7
ABB77332
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AC ABB7
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Best Local (
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EP440351-A.
                         Mouse 184 light chain variable
                                                                       17-JUN-2002
                                                                                                                                                               ABB77332 standard; Protein; 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human myeloma protein REI (EP-239400), See also AAQ12682-84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A recombinant human Ig comprises a human heavy chain framework and murine CDRs (with the heavy chain framework mutated at sites near the CDRs), a human light chain framework and murine CDRs. It has a mean IC50 nearly equal to that of the murine monoclonal antibody from which the CDRs were derived. It is designated mutated Gai/Rei. The human Ig is capable of binding to a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant immunoglobulin(s) reactive with leukocyte CI
antigen - comprise human heavy chain framework and murine
complementarity regions useful in treatment of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 25; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-216985/30.
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19-JAN-1990;
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01-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         murine CDRs are obtd. from murine hybridoma 1B4
CC HB 10164). The light chain framework is derived
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LAW M
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                                                                                                                                                                                                                                                                                    PARTSGSGSRTDFTLTINPVBADDVATYYCQQSNEDPLTFGAGTKLELKR
                                                                                                                                                                                                                                                                                                                  PARFSGSGSRTDFTLTINFVEADDVATYYCQQSNEDFLTFGTGTRLBIKR 112
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90US-0467692.
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to correct PA field.)
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Pred. No. 3.9e-39;
3; Mismatches 3
                      region
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RESULT 8
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to identifying differences (I) in mammalian specie specific surface amino acid residues on an immunoglobulin which converts the antigenicity of a first mammalian species to a second mammalian species. The new method is used for identifying and replacing immunoglobulin surface amino acid residues which converts the antigenicity of a first mammalian species to that of a second mammalian species. The method simultaneously reduces the immunogenicity and strictly preserves ligand binding properties. The replacement of exterio amino acid residues has no effect on the ligand binding properties but greatly alters immunogenicity. The present sequence is that of a PCR primer used in the construction of the "veneered" 194 heavy and light chain variable regions plus those necessary to fuse the human signal and that of the moves 194 light which these variable regions. The present sequence is
           Monoclonal antibody; MAb; heavy chain; light chain; constant region; variable region; amplification; primer; polymerase chain reaction; PCR, chimera; 1g; immunoglobulin; humanised antibody; leucocyte; integrin.
                                                                                                                           25-MAR-2003
06-JUL-1994
                                                                                                                                                                            AAR47494;
                                                                                             Murine anti-CD18 Ab 60.3 light chain
                                                                                                                                                                                                         AAR47494 standard; Protein; 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying and replacing immunoglobulin surface amino acid useful for converting the antigenicity of a first mammalian a second mammalian species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 12; 36pp; English.
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01-AUG-1997;
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                                                                                                                                                                                                                                                                                                                  PARFSGSGSRTDFTLTINEVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
                                                                                                                                                                                                                                                                                                                                                   VLTQSPASLAVSLGORATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYRASNLESGI
                                                                                                                                                                                                                                                                                        PARFSGSGSRTDFTLTINEVEADDVATYYCQQSNEDPLTFGAGTKLELKR
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96US-0609218.
97US-0905280.
91US-0702217.
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                                                                                                                           entry)
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Pred. No. 3.9e-39;
3; Mismatches 3;
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Best Local :
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Monoclonal antibody; phospholipase; myocardial infarction
                                 MAb 1.4 light chain, directed against type II phospholipase
                                                                      10-FEB-1997
                                                                                                        AAW01143;
                                                                                                                                      AAW01143 standard; Protein; 131 AA
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                        VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI
                                                                                                                                                                                                                                          PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIK 111
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                                                                                                                                                                                                                                                                                     VLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYRASNLESGI
                                                                                                                                                                                                                                                                                                                                                                                                                           111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 21;
                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                    entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hsiao K,
                                                                                                                                                                                                                                                                                                                                                      Score 531; DB 15;
Pred. No. 3.4e-38;
2; Mismatches 4;
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                         infarction, acute kidney failure, chronic rheumatism, cardiac shock, pancreatitis, adult respiratory distress syndrome and colitis. The antibodies were generated by immunising Balb/C mice with recombinant human type II phospholipase A2. Spleen cells from the mice were fused with mouse myeloma P3UI (P3x63Ag8.UI) and the hybridomas obtained were screened for phospholipase A2 inhibitory activity. Active clones were isolated including 12H5, 1.4 and 10.1. These were cultured and the antibody isolated from the culture supernatant by precipitation with ammonium sulphate and purification on a column of protein A-Sepharose C14B. Because the antibody acts on the primate and mouse forms of enzyme as well as human it is particularly suitable for preclinical testing.
                                                     AAW44168;
                                                                                                                                                                                                                                                                                                                                  Sequence
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chronic rheumatism; adult respiratory distress syndrome;
cardiac shock; treatment; preclinical testing; disease; hybridoma
                           16-JUN-1998
                                                                                    AAW44168 standard; Protein; 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibodies which inhibit type II phospholipase A2 useful in the treatment of myocardial infarction, cerebral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Figure 10; 69pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawauchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-DEC-1994;
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                                                                                                                                                                                                                                VLTQSPASLAVSLGQRATISCRASESVDSYGYNFWHWYQQIFGQPPKLLIYRASNLESGI
                                                                                                                                                       PARFSGSGSRTEFTLTINPVEADDVATYHCQQSNEDPFTFGSGTKLEIK 131
                                                                                                                                                                                                                VLTQSPASLAVSLGQRATISCRASESVDSYGISFMHWYQQKPGQPPKLLIYRASNLESGI
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                          (first entry)
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/label= CDR 2
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/label= CDR 1
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Pred. No. 7.2e-38;
5; Mismatches 3;
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Monoclonal antibody 1.4 light chain against type II phospholipase A2

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RESULT 11
AAU07480
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AC AAU07
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Best Local
           Synthetic antibody scFv(F8) light chain variable region, VL-F8.
                                                               24-OCT-2001
                                                                                                                                                   AAU07480 standard; Protein; 112
                                                                                                           AAU07480
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27-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 528; DB 19;
Pred. No. 7.2e-38;
5; Mismatches 3
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CC solubility to an antibody comprising these peptides. The peptides or L-FR4 cresent within a variable region of an antibody which makes the antibody cosluble and stable in cytoplasm. Peptides having the sequences of HFR1 to entibody. CC entibody, covalently linked to the H-CDR1, H-CDR2) - (H-FR2) - (H-CDR1) - (H-FR2) - (H-CDR2) - (H-FR3) - (H-CDR3) - (H-CDR3) and cc entibody, covalently linked to the H-CDR1, H-CDR2, H-CDR3 in the oxder cc (H-FR1) - (H-CDR1) - (H-FR2) - (H-CDR2) - (H-FR3) - (H-CDR3) - (H-CDR3) and cc entibody, covalently linked to the H-CDR3 in the oxder cc (H-FR2) - (L-CDR2) - (L-CDR2) - (L-CDR3) - (L-CDR3) - (H-FR3) - (L-CDR3) - (L-FR1) - (L-CDR2) - (L-CDR2) - (L-CDR3) - (L-CDR4) - (L-FR1) - (L-CDR3) - (L-CDR4) - (L-FR1) - (L-CDR3) - (L-CDR4) - (L-FR1) - (L-CDR3) - (L-CDR4) - (L-FR1) - (L-CDR3) - (L-CDR4) - (L-FR1) - (L-CDR3) - (L-CDR4) - (L-FR1) - (L-CDR3) - (L-CDR4) - (L-FR1) - (L-CDR3) - (L-CDR4) - (L-FR1) - (L-CDR3) - (L-CDR4) - (L-FR1) - (L-CDR3) - (L-CDR4) - (L-FR1) - (L-CDR3) - (L-CDR4) - (L-FR1) - (L-CDR3) - (L-CDR4) - (L-FR1) - (L-CDR3) - (L-CDR4) - (L-FR1) - (L-CDR1) - (L-CDR2) - (L-CDR2) - (L-CDR3) - (L-CDR4) - (L-FR1) - (L-CDR1) - (L-CDR2) - (L-CDR2) - (L-CDR3) - (L-CDR4) - (L-FR1) - (L-CDR1) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR3) - (L-CDR4) - (L-FR1) - (L-CDR1) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR3) - (L-CDR4) - (L-CDR1) - (L-CDR1) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) - (L-CDR2) 
  Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptides which are able to confer stability and solubility to an antibody comprising these peptides, useful for treating pathologies (e.g. tumour) associated with accumulation of a molecule inside or outside a human, or animal cell -
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Matches Best Local Query Match

Similarity

90.1%; 93.6%;

Score 526; DB Pred. No. 9.1e 2; Mismatches

DB 22; .1e-38; В

Length 112; Indels

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 4; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptides which are able to confer stability and solubility to an antibody comprising these peptides, useful for treating pathologies (e.g. tumour) associated with accumulation of a molecule inside or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    outside a human, or animal cell -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial; antiviral; cytostatic; immunomodulatory; antibody; gene therapy; HIV; human immunodeficiency virus; metabolic disorder; immune disorder; auto-immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-502555/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CONS-) SOC CONSORTILE METAPONTUM AGROBIOS SRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-DEC-2000; 2000WO-IT00554.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200149713-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody light chain variable region; scFv8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibody scFv8 light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-OCT-2001
                                                                                                                                                                                                                                                                                                       102;
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                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                    ARFSGSGSRTDFTLTINPVBADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
                                                                                                                                                                                                        LTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGIP
                                                                                                                      ARFSGSGSRTDFTLTINPVEADDVATYYCÓÓSNEDPWTFGGGTKLEIKR 112
                                                                                                                                                                                                                                                                                                                                                                                             112
                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Franconi R,
                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99IT-RM00803.
                                                                                                                                                                                                                                                                                                                       90.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Desiderio A,
                                                                                                                                                                                                                                                                                                Score 526; DB 22;
Pred. No. 9.1e-38;
2; Mismatches 5
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••
                                                                                                                                                                                                                                                                                                                                          Length 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumour;
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                    63
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AAU07497 standard; Protein; 252 AA

Query Match

90.1%;

Score 526;

DВ

22;

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Sequence

252

AA;

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peptides having the sequences of L-FR1 to L-FR2 are present within the variable region of the light chain of an antibody, covalently linked to the L-CDR1, L-CDR2, L-CDR3) in the order (L-FR1)-(L-CDR1)-(L-FR2)-(L-CDR2)-(L-CDR3)-(L-CDR3)-(L-CDR3)-(L-CDR4). The antibodies and polynucleotides (e.g. by gene therapy) are useful for the manufacture of a medicament for the treatment of pathologies associated with accumulation of a molecule inside or outside a human, animal cell or plant cell. The pathologies are infections (e.g. viral infections as HIV, human immunodeficiency virus, infections, tumour, metabolic a humune (especially auto-immune) pathologies. The present sequence represents the synthetic antibody scfv(FB) which is used as a basis for constructing synthetic antibodies incorporating the peptides of the nvent one
                                                                                                                                                                                                                                                      The invention relates to peptides which are able to confer stability and solubility to an antibody comprising these peptides. The peptides are especially H-FR1, H-FR2, H-FR3, H-R4, I-FR1, L-FR3 or I-FR4 present within a variable region of an antibody which makes the antibody soluble and stable in cytoplasm. Peptides having the sequences of HFR1 to H-FR4 are present within the variable region of the heavy chain of an antibody, covalently linked to the H-CDR1, H-CDR2, H-CDR3 in the order (H-FR1)-(H-CDR1)-(H-CDR2)-(H-CDR2)-(H-FR3)-(H-CDR3)-(H-CDR3) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptides which are able to confer stability and solubility to an antibody comprising these peptides, useful for treating pathologies (e.g. tumour) associated with accumulation of a molecule inside or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-502555/55.
N-PSDB; AAS11887.
                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 81; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                outside a human, or animal cell -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CONS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-DEC-2000; 2000WO-IT00554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200149713-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Benvenuto E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cucumber mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunomodulatory; antibody; gene therapy; HIV; light chain; human immunodeficiency virus; tumour; metabolic disorder; immune disorder; auto-immune disorder; scFv(F8);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic antibody scfv(F8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial; antiviral; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU07497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENEA ENTE NUOVE TECNOLOGIE ENERGIA.
SOC CONSORTILE METAPONTUM AGROBIOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONSORTILE METAPONTUM AGROBIOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Franconi R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= VH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "Light chain variable region!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label= Linker_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is specifically claimed in claim 17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tavladoraki
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RESULT 14
ARRSULT 14
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                                                                            Query Match
Best Local S
Matches 101
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                                                                                                                                                                                                               The sequences given in AAR29008-09 were encoded by plasmids which were used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (IL-5R). The antibody comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma AUK64-7 which contained the plasmids p64-k4 and p64-h2. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reconstituted human antibody to human interleukin-6 receptor has low antigenicity and contains mouse V-region complemental determining regions
                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 124-125; 207pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ30757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bendig
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19-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-APR-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasmid; p64-k4; p64-h2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p64-k4 protein product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
30-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR29008 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1992-398882/48.
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                                                                              101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ž,
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                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
VLTQSPASLAVSLGQRATISCRASESVDSYGYNFWHWYQQIPGQPPKLLIYRASNLESGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPWTFGGGTKLEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITQSPASIAVSLGQRATISCRASESVDSYGNSFMHWYQQKFGQFFKLLIYRALNLESGIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
                                                                                                                                                                       131
                                                                            89.7%;
ilarity 92.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jones ST,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ody; interleukin-6; receptor; IL-6R; light chain; variable region; mouse; monoclonal; hybridoma; Al
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(first entry)
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92JP-0032084.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131
                                                                       Score 524; DB 13;
Pred. No. 1.6e-37;
3; Mismatches 5;
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2; Mismatches
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                                                                                                                    Length 131;
                                                                            Indels
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RESULT 15
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Best Local Sim
Matches 101;
                                                                         This is the amino acid sequence for the light chain of muM4TS.11, a novel antibody which specifically binds to the platelet derived growth beta receptor (PDGF-R beta), but not within the fifth extracellular Ig-like domain, where the antibody inhibits PDGF BB-induced proliferation of a cell expressing the PDGF beta receptor. The antibody can be used in a method of inhibiting intimal hyperplass in the vasculature of a mammal. The antibodies can be used for the treatment of disorders related to PDGF activity such as disorders involving proliferation of smooth muscle cells, and including restenosis following angioplasty.
                                                       Sequence
                                                                                                                                                                                                                                                  Antibodies to platelet derived growth factor beta receptor - in PDGF BB-induced proliferation of cells expressing the receptor, particularly for inhibiting intimal hyperplasia
                                                                                                                                                                                                                            Claim 11; Fig 7B; 87pp; English.
                                                                                                                                                                                                                                                                                                           N-PSDB; AAT90985.
                                                                                                                                                                                                                                                                                                                        WPI; 1997-503114/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Binding-site
                                                                                                                                                                                                                                                                                                                                                                            (BOEF )
                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-OCT-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MuM4TS.11; antibody; platelet; beta receptor; PDGF-R beta; inhibition; intimal hyperplasia; vasculature; restenosis; angioplasty; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW30278 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
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                Similarity
                                                                                                                                                                                                                                                                                                                                                                          BOEHRINGER MANNHEIM PROTEIN DESIGN LABS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARFSGSGSRTDFTLTINFVEADDVATYYCQQSNEDFLTFGTGTRLEIK
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                                                       131 AA;
                                                                                                                                                                                                                                                                                                                                                 Landolfi NF,
  89.2%;
ilarity 92.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of MuM4TS.11
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20..131
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                                                                                                                                                                                                                                                                                                                                                 Martin U;
                                                                                                                                                                                                                                                                                                                                                                           I GMBH.
Score 521; DB 18;
Pred. No. 2.8e-37;
2; Mismatches 6;
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                          Length 131;
  Indels
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or, used
  Gaps
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VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI 62

Search completed: November 7, 2003, 07:27:03 Job time : 49.2991 secs

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Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                       494
487
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                                                                                                                                                                                                                                                                                                                                             Match
               90.1
89.9
89.2
89.2
87.8
87.8
87.2
87.2
85.4
85.5
82.6
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584
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195.799 Million cell updates/sec
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l: /cgn2_6/ptodata/2/pubpaa
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                                                                                                                                                                                                                                                                                                                                             Length DB
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gn2 6/ptcdata/2/pubpaa/BCT_NEW PUB.pep:*
gn2 6/ptcdata/2/pubpaa/US06_NEW PUB.pep:*
gn2 6/ptcdata/2/pubpaa/US06_PUBCOMB.pep:*
gn2 6/ptcdata/2/pubpaa/US07_NEW PUB.pep:*
gn2 6/ptcdata/2/pubpaa/US07_NEW_PUB.pep:*
gn2 6/ptcdata/2/pubpaa/US08_NEW_PUB.pep:*
gn2 6/ptcdata/2/pubpaa/US08_NEW_PUB.pep:*
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gn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/US090_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/US100_NEW_PUB.pep:*
gn2_6/ptodata/2/pubpaa/US100_NEW_PUB.pep:*
gn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
gn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
                                                                                    10 US-09-144-886-81

2 US-10-169-351-32

10 US-10-169-351-49

10 US-09-144-886-80

10 US-09-144-886-87

10 US-09-144-886-84

10 US-09-144-886-84

10 US-09-144-886-86

10 US-09-144-886-86

10 US-09-144-886-86

10 US-09-144-886-86
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US-09-810-502-36
2 US-10-160-506-81
2 US-10-169-351-48
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Sequence 84, Appl
Sequence 86, Appl
Sequence 85, Appl
Sequence 2, Appl
Sequence 24, Appl
Sequence 36, Appl
Sequence 81, Appl
Sequence 48, Appl
                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                              Sequence 37, Appl
Sequence 31, Appl
Sequence 32, Appl
Sequence 49, Appl
Sequence 80, Appl
Sequence 87, Appl
Sequence 103, App
                                                                                                                                                                                                                                                                                              Sequence 37,
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<b>4</b>	44	43	42	41	40	39	38	37	36	S	4	w	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
434	437	437	437	440.5	442	442	442	442	443	444	444	445	445	445	445	459	462	464	466	467	467	471	471	471.5	472	473	474	475	476
74.3	74.8	٠	74.8	75.4	75.7	•	75.7		•	76.0	76.0	76.2	76.2	76.2		78.6	79.1	•	•	80.0	80.0	80.7	80.7	80.7		81.0		•	81.5
112	271	271	131	151	269	106	106	106	269	131	112	238	238	129	129	112	108	238	132	238	238	108	108	112	108	108	108	108	111
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-886-	US-10-207-655-12	US-10-053-530-12	US-09-879-461-58	US-10-222-026A-33	US-10-027-770-5	US-09-925-179-6	US-09-802-096-6	US-09-802-077-6	US-10-027-770-2	US-09-286-240-2	4	1	US-10-384-933-54	US-10-153-271-2	US-09-839-447A-2	-10-194-975-	US-10-169-351-109	US-09-903-327A-4	US-09-879-461-2	1	-10-384-933-	-10-169-351-	US-10-169-351-36	-10-160-506	US-10-169-351-42	US-10-169-351-38		US-10-169-351-44	US-10-160-506-77
95,	2	Sequence 12, Appl	58		ۍ.	φ. Φ	σ,	Sequence 6, Appli	N.	Ν		b	υī	D D	2 Ap	115	100	4	Sequence 2, Appli	11	11	0		82	2		0	44	Sequence 77, Appl

## ALIGNMENTS

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US-09-810-502-37

| Sequence 37, Application US/09810502 |
| Sequence 37, Application US/09810502 |
| Patent NO. US20020034765A1 |
| GENERAL INFORMATION: A METHOD FOR REDUCING THE IMMUNOGENICITY |
| MARK, GEORGE L. |
| MARK, GEORGE L. |
| MARK, GEORGE S. |
| MARK, GEORGE L. |
| MARK GEORGE S. |
| MARK GEORGE S. |
| CORRESPONDENCE ADDRESS: |
| ADDRESSE: MARCK & CO., Inc. |
| STREET: P.O. BOX 2000, 126 E. Lincoln Ave. |
| CITY: Rahway |
| CITY: Rahway |
| COUNTRY: USA |
| COMPUTER READABLE FORM: |
| MEDIUM TYPE Diskette |
| COMPUTER: IBM COmpatible |
| OPERATING SYSTEM: Windows |
| OF WART APPLICATION DATA: |
| APPLICATION NUMBER: US/09/810,502 |
| FILING DATE: 16-Max-2001 |
| CASSIFICATION NUMBER: 08/905,280 |
| FILING DATE: 01-Aug-1997 |
| APPLICATION NUMBER: 08/905,218 |
| FILING DATE: 11-May-1991 |
| APPLICATION NUMBER: 08/109,187 |
| FILING DATE: 11-May-1991 |
| APPLICATION NUMBER: 08/109,187 |
| FILING DATE: 11-May-1991 |
| APTORNEY/AGENT INFORMATION: |
| NAME: Hand, J. Mark
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US-10-169-351-32
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                                                                                                                                RESULT 3
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US-09-144-886-81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.117USC
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 81
LENGTH: 112
                                                    Sequence 32, Application US/10169351
Publication No. US20030157090A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 81, Application US/09144886 Patent No. US20020155114A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
APPLICANT: BENVENUTO, EUGENIO
APPLICANT: FRANCONI, ROSELLA
APPLICANT: DESIDERIO, ANGIOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                   102;
                                                                                                                                                                                      64
                                                                                                                                                                                                                   64 ARFSGSGSRTDFTLTINEVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
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                                                                                                                                                                                  ARFSGSGSRTDFTLTINEVEADDVATYYCQQSNEDPYTFGGGTKLEIKR
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94.5%;
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Pred. No. 1.9e-42;
2; Mismatches 5;
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Pred. No. 7.2e-44;
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FILE REFERENCE: 4161-4

CURRENT APPLICATION NUMBER: US/10/169,351

CURRENT FILING DATE: 2002-10-29

PRIOR REPLICATION NUMBER: PCT/ITOO/00554

PRIOR REPLICATION NUMBER: IT RM99A000803

PRIOR FILING DATE: 1999-12-30

NUMBER OF SEQ ID NOS: 118

SOCTWARE: Patentin Ver. 2.1

SEQ ID NO 49

LENGTH: 252

TYPE: PRT

ORGANISM: Artificial Sequence
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; OTHER INFORMATION: acid sequecne
US-10-169-351-32
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US-10-169-351-49
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APPLICANT: BENVENUTO, EUGENIO
APPLICANT: FRANCONI, ROSELLA
                                                                                                                                                      Matches
                                                                                                                                                                                           Query Match
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Best Local Similarity
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SEQ ID NO 32
LENGTH: 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FRANCONI, ROSELLA
APPLICANT: DESIDERIO, ANGICIA
APPLICANT: TAVLADORAKI, PARASKEVI
TITLE OF INVENTION: STABILIZING PEPTIDES,
TITLE OF INVENTION: WHICH INCLUDE THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/169,351
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: PCT/IT00/00554
PRIOR FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: IT RM99A000803
PRIOR FILING DATE: 1999-12-30
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                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: scFv(F8) OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 118
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                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                    Local Similarity
les 102; Conserv
                                                            144 LTQSPASLAVSLGQRAFISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYRALNLESGIP 203
64 ARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
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                                                                                                     LTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGIP 63
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                                                                                                                                                  Score 526; DB 12;
Pred. No. 5.6e-42;
2; Mismatches 5
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Pred. No. 2.3e-42;
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204 ARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPWTFGGGTKLEIKR 252

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US-09-144-886-87
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; OTHER INFORMATION: 1B6 region VL epitope 1
US-09-144-886-80
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APPLICANT: Marks, James D
APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.117USO
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SCHEMBER OF SEQ ID NOS: 98
                                                                                                                                                                              Query Match
Best Local
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SEQ ID NO 87
LENGTH: 112
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Best Local Similarity
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                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone OTHER INFORMATION: C25 region VL epitope 2
-09-144-886-87
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APPLICANT: Amersdorfer, Peter
                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                              Similarity
ARFSGSGSGTDFTLTINPVEADDVATYYCQQSNEDPFTFGSGTKLEIKR 112
                       ARFSGSGSRTDFTLTINFVEADDVATYYCQQSNEDFLTFGTGTRLEIKR 112
                                                                         ltospaslavsleoratiscrasesvdsyghsfmowyoorpgoppkiliyrasnlepgip
                                                                                                                 LTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGIP 63
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                                                                                                                                                             Conservative
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                                                                                                                                                                            89.2%;
91.7%;
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92.7%;
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                                                                                                                                                                            Score 521; DB 10;
Pred. No. 6.9e-42;
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Pred. No. 2.9e-42;
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APPLICANT: Amersdorfer, Peter
APPLICANT: Amersdorfer, Peter
ITITLE OF INVENTION: Therapeutic Monoclonal An
ITITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.117USO
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 198-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
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US-09-144-886-84
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                                                                                                                                                                                                                                                                                   SEQ ID NO 84
LENGTH: 112
TYPE: PRT
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                                                                                                                      Query Match
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Publication No. US20
GENERAL INFORMATION
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LENGTH: 112
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Fatent No. US20020155114A1
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Best Local Similarity 92.7%;
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APPLICANT: TAVLADORAKI, PARASKEVI
TITLE OR INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES
TITLE OF INVENTION: WHICH INCLUDE THEM
TILE REFERENCE: 4161-4
CURRENT APPLICATION NUMBER: US/10/169,351
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: PCT/IT00/00554
PRIOR APPLICATION NUMBER: TRM99A000803
PRIOR PILING DATE: 2000-12-30
PRIOR PILING DATE: 1999-12-30
PRIOR PILING DATE: 1999-12-30
PRIOR PILING DATE: 1999-12-30
PRIOR SEPCITA US/10-12-30
PRIOR PILING DATE: 1999-12-30
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APPLICANT: FRANCONI, ROSELLA
APPLICANT: DESIDERIO, ANGIOLI
APPLICANT: TAVLADORAKI, PARAK
                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone OTHER INFORMATION: 1A1 region VL epitope 2
                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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                                                                                                   Similarity
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o. US20030157090A1
                                                                          Conservative
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                                                                      Score 513; DB 10;
Pred. No. 3.9e-41;
5; Mismatches 6;
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Pred. No. 3.1e-41;
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                                                                                                                 Length 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 85, Application US/09144886 Patent No. US20020155114A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 86
LENGTH: 112
                                                                                 Matches
                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                  SEQ ID NO 85
LENGTH: 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 2500.117USO
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTMARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Meurotoxins
FILE REFERENCE: 2500,1170SO
                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone OTHER INFORMATION: 1F1 region VL epitope 2
                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone OTHER INFORMATION: C39 region VL epitope 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 97; Conserv
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                           4 LTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGIP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGIP
                                                                                                Similarity
ARFSGSGSRTDFTLTINFVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARESGSGSRTDETLTIDPVEADDAATYYCQQNNEDPYTEGGGTKLEIKR 112
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                                                                               Conservative
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                                                                                            87.2%;
89.0%;
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                                                                           Score 509; DB 10;
Pred. No. 9.3e-41;
5; Mismatches 7;
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Pred. No. 3.9e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 112;
                                                                           Indels
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                                                                       Gaps
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; OTHER INFORMATION:
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US-09-144-886-94
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US-09-144-886-94
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US-09-881-823-2
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                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                            TITLE OF INVENTION: Thérapeutic Monoclonal Antibodies That Neutralize TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.117USO
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 94
LENGTH: 112
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries FILE REFERENCE: 22851-032
CURRENT APPLICATION NUMBER: US/09/881,823
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 07/378,577
PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 94, Application US/09144886 Patent No. US20020155114A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SHI, WENYUAN
APPLICANT: ANDERSON, MAXWELL
APPLICANT: MORRISON, SHERIE
APPLICANT: TRINH, RYAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: WIMS, LETITIA APPLICANT: CHEN, LI
                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 134
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 PARFSGSGSRIDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 VLTOSPVSLAVSIGORATISCRASESVOSYGNSFMNWYQQKPGQPPQLLIYRASNLEYGI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 ARPSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIKR
4 LTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARFSGSGSRTDFTLTINEVEADDVATYYCQQNNADPPTFGGGTKLEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARFSGSGSRTDFTLTIDFVEADDAATYYCQQNNEDFYTFGGGTKLEIKR 112
                                                                 85.4%;
ilarity 88.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                         Description of Artificial Sequence: BoNT/A clone 2B6 region VL epitope 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.5%;
                                                                 Score 499; DB 10;
Pred. No. 8.1e-40;
5; Mismatches 7;
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Pred. No. 2.7e-40;
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                                                                   Indels
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US-09-810-502-36
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                                                                                                                                                                   Matches
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Best Local (
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Patent No. US20020034765A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/810,502
FILING DATE: 16-Mar-2001
CLASSIFICATION: -(Inknown)
PRIOR APPLICATION UNMBER: 08/905,280
FILING DATE: 01-Aug-1997
APPLICATION NUMBER: 08/609,218
FILING DATE: 01-Mar-1996
APPLICATION NUMBER: 08/609,218
FILING DATE: 01-Mar-1996
APPLICATION NUMBER: 08/109,187
FILING DATE: 19-May-1993
APPLICATION NUMBER: 07/702,217
FILING DATE: 17-May-1991
FILING DATE: 17-May-1991
FILING DATE: 17-May-1991
FILING DATE: 17-May-1991
                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 1841OCC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: A METHOD FOR REDUCING THE IMMUNOGENICITY OF ANTIBODY VARIABLE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Padlan, Eduardo A.
        63
                             63 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNBDPLTFGTGTRLBIKR 112
                                                                                                                                                                 96;
                                                                                                          3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIFGQPDKLLIYRASNLESGI
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                                                                                                                                                                                      Similarity
PDRFSGSGSGTDFTLTISSVEAEDVATYYCQQSNEDPLTFGQGTKLEIKR 112
                                                                              vmīgssnslavsligeratīscrasesvdsygnsfmhwyqqxpgqppxlliyrasnlesgi
                                                                                                                                                                                                                                                                                                                                              LENGTH: 112 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 07065-0907
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                                                                                                                                                                   Conservative
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                                                                                                                                                                                    84.6%;
                                                                                                                                                                 6; Mismatches
                                                                                                                                                                                  Score 494; DB 9;
Pred. No. 2.4e-39;
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                                                                                                                                                                                                     Length 112;
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                                                                                                                                                             Gaps
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FILE REFERENCE: 4161-4

CURRENT APPLICATION NUMBER: US/10/169,351

CURRENT FILING DATE: 2002-10-29

PRIOR APPLICATION NUMBER: PCT/IT00/00554

PRIOR FILING DATE: 2000-12-29

PRIOR APPLICATION NUMBER: IT RM99A000803

PRIOR FILING DATE: 1999-12-30

NUMBER OF SEQ ID NOS: 118

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Mus musculus US-10-160-506-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-10-160-506-81
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LENGTH: 112
TYPE: PRT
                                                                      Matches
                                                                                          Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 81, Applicate Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 48, Application US/10169351
Publication No. US20030157090A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BENVENUTO, EUGENIO
APPLICANT: FRANCONI, ROSELLA
APPLICANT: DESIDERIO, ANGIOLA
APPLICANT: TAVLADORAKI, PARASKEVI
TITLE OF INVENTION: WHICH INCLUDE THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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PRIOR FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: 60/362,612
PRIOR FILING DATE: 2002-03-08
NUMBER OF SEQ ID NOS: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bander, Neil H.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING TITLE OF INVENTION: METHODS SCHOOL SING BINDING AGENTS SPECIFIC FOR TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN FILE REFERENCE: 10448-162001

CURRENT APPLICATION NUMBER: US/10/160,506

CURRENT FILING DATE: 2002-05-30

CURRENT FILING DATE: 2002-05-30
                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: VL-CMV/2G OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                              ENGTH: 108
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4 LTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGIP 63
                                                                      95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 VLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYAASNLESGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 VITOSPASIAVSIGORATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112
                                                                                    Similarity
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                                                            Score 479; DB 1
Pred. No. 6e-38;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 487.5; DB 12;
Pred. No. 9.9e-39;
""matches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLYPEPTIDES AND ANTIBODIES
                                                                                                DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12;
                                                                7;
                                                                                                Length 108;
                                                                Indels
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Post-processing: Minimum Match 0%
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Listing first 45 s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*

3: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*

4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/laa/FCTUS_COMB.pep:*

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Copyright (c) 1993 - 2003 Compugen Ltd.
                        US-08-137-117D-33
US-08-436-717-33
US-08-436-717-13-10
US-08-111-080-12
US-08-111-080-22
US-08-211-980-12
US-08-211-980-12
US-08-211-980-22
US-08-211-980-26
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<b>4</b>	4	43	4	41	40	39	38	37	36	ω S	ω 4	ω ω	ω N	31	30	29	28
<u>4</u> 3	438	440	440	440	440	440	440	440	440	440	440	440.5	442	442	442	444	445
75.0	75.0	75.3	75.3	75.3	75.3	75.3	75.3	75.3	75.3	75.3	75.3	75.4	75.7	75.7	75.7	76.0	76.2
120	120	131	131	131	131	131	111	111	111	111	111	151	113	106	106	113	129
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US-08-211-980-24	US-08-111-080-24	US-08-484-537-67	US-08-487-200-67	US-08-474-040-67	US-08-477-728-67	US-07-634-278-67	US-08-484-537-54	US-08-487-200-54	US-08-474-040-54	US-08-477-728-54	US-07-634-278-54	US-09-318-786-33	US-08-553-497A-10	US-08-466-163B-6	US-08-466-151-6	US-08-553-497A-6	US-09-556-605-2
Sequence 24, Appl	24	67	67	67.	67	67	54		54	Sequence 54, Appl	-	33,	j,	Sequence 6 Appli	•	Sequence 6. Appli	Sequence 2, Appli

## ALIGNMENTS

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Sequence 33, Application US/08137117D

Patent No. 5795965

GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: BENDIG, MATY
APPLICANT: SALDANHA, JOSE
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION:
APPLICANT: USA
COUNTRY: USA
STREET: 3000 K Street, N.W., Suite 500
CITY: Mashington
CITY: Washington
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIT: 20007-5109
ZIT: 20007-5109
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ZIT: 200
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; MOLECULE TYPE: US-08-436-717-33
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                                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 3-95476

FILING DATE: 25-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: WEGNER, Harold C.

REGISTRATION NUMBER: 25,258

REFERENCE/DOCKET NUMBER: 53466/1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
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                                                                                                           NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                        FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP9:
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: FROM DECOMPATING SYSTEM: PC-DOS/MS-DOS

COERNATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: JONES, Steven
APPLICANT: SALDANHA, JOSE
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TSUCH
APPLICANT: SATO,
APPLICANT: BENDIO
                                  : YEOTOGY:
                                                     LENGTH:
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STREET: 3(
                                                                                                                                            TELEFAX:
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CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 92.7
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                                                  amino acids
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5817790
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3000 K Street, N.W., Suite 500
                                                                                                                                            (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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JONES, Steven
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92.7%;
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Pred. No. 6.5e-51;
3; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                 NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943
REFERENCE/DOCKST NUMBER: 321152000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEPAX: (650) 813-5600
TELEPAX: (650) 494-0792
TELEEX: 706141 MRSN FOERS SFO
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
Types: amino acids
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US-08-621-751A-10
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Best Local Similarity
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Best Local Similarity 92.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/08621751A Patent No. 5882644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Martin, Ulrich
TITLE OF INVENTION: MONOCI
TITLE OF INVENTION: PLATE!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Chang, Chung N.
APPLICANT: Landolfi, Nicholas F.
APPLICANT: Martin, Ulrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER LLP
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 22-MAI CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: PALO ALTO
                         63 PARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGTGTRLEIK 111
                                                                                                                                                  101;
                                                                     23 VLTQSPESLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYRASNLESGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPQQPPKLLIYRASNLESGI 62
                                                                                                  VLTQSPASLAVSLGQRATISCRASBSVDSYGYNEMHWYQQIPGQPPXLLIYRASNLESGI 62
                                                                                                                                                                                                                                                                            t: 131 amino acids
amino acid
PARFSGGGSRTDFTLTINEVEADDVATYYCOOSNEDPPTFGGGTKLEIK 131
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                                                                                                                                            Score 521; DB 2;
Pred. No. 1.4e-50;
2; Mismatches 6
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Pred. No. 6.5e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.30
                                                                                                                                                                               Length 131;
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                                                                                                                                            Indels
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RESULT 4 US-08-111-080-18

Sequence 18, Application 08/111080

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                                                                                                                                       Sequence 22, Application 08/111080 Patent No. 5558865
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/039
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BOTUL, MICHAEL F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 3162
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                             TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 08/039,457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US92/07111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/748,562
FILING DATE: 22-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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STREET: 60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                        98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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Pred. No. 9.9e-50;
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                                                                                                                                                                                                                                                                                       Patent No. 565569
GENERAL INFORMATION:
APPLICANT: Obno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/08211980 Patent No. 5665569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
               MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                             ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
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FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, MICHAEL F.
REGISTRATION NUMBER: 25,447
                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
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                                                                                                                                                     STREET: 6300 Sear
CITY: Chicago
STATE: Illinois
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APPLICATION NUMBER:
                                                                                                                                           COUNTRY:
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US/08/211,980
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Pred. No. 9.9e-50;
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              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1392
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1393
ATTORNEY/AGENT INFORMATION:
HAME: BOTUN, MICHAEL F.
REGISTRATION UMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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NAME: BOTUN, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,980
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MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION: HIV Immunotherapeutics
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                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                   FILING DATE:
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amino acid
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89.1%;
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                                                                         PCT-US92-07111-17
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APPLICANT: Ohno,
       Matches
                                      Query Match
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                                                                                                                                                     TELEFAX: (312) 984-974
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,562
FILING DATE: 22-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: NOLand, Greta B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 17
CORRESONATEORY
                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patenth Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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STREET: Street
CITY: Chicago
                                                                                                       TOPOLOGY:
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TYPE: amino acid
TOPOLOGY: linear
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REGISTRATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60603
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                                                                                                                     LENGTH: 121 amino acids
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                    ocal Similarity
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     Conservative
                                                                                                                                                                                                          (312) 984-9740
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                  87.8%;
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     6; Mismatches
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Score 513; DB 5; Le
Pred. No. 9.9e-50;
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                                    Length 121;
     Indels
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3 VLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIPGQPPKLLIYRASNLESGI 62

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RBSULT 10
PCT-US93-07967-22
; Sequence 22, Application PC/TUS9307967
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
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PCT-US93-07967-18
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GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 18:
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COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07967
                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: HIV Immunotherapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Borun, Michael F. REGISTRATION NUMBER: 25,447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 22-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
                                                                                                                                 63
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Pred. No. 9.9e-50;
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
COUNTALL
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FLOREM: PC-DOS/MS-DOS
                                                                                                  STREET: 65.
CITY: Chicago
CITY: Illinois
                                                                                                                                                                                                                                     APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
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FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME.
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TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: PCT/I
FILING DATE: 24-AUG-1992
PRIOR APPLICATION NUMBER: US 01
APPLICATION NUMBER: US 01
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Chicago
                                                                                                                                                                             ADDRESSEE: Marsh
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US93/07967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bozun, Michael F. REGISTRATION NUMBER: 25,447
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                                                                                                                                                                                                                                                                                                                                                                                                                             63 PARFSGSGSRTDFTLTIDFVBADDAATYYCQQNNEDPLTFGAGTKLELKR 112
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89.1%;
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Pred. No. 9.9e-50;
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US-08-211-980-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
                PRIOR APPLICATION DATA:
'APPLICATION MUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
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PILING DATE: 22-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
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CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                               APPLICATION NUMBER: US/08/211,980 FILING DATE:
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                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                    COUNTRY:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                 Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                   Borun
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US 08/039,457
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HOLECULE TYPE: protein
US-08-211-980-26
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                   TELEFAX: (312,
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
(ENGTH: 120 amino acids
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GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/039
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BOYUN, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 3162
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
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LENGTH: 120 amino acids
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ATTORNEY/AGENT INFORMATION:
NAME: BOYUN, Michael F.
REGISTRATION NUMBER: 25,447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 24-AUG-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/039,457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07967
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MEDIUM TYPE: Floppy
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TELECOMMUNICATION INFORMATION:
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LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH: 120 LENGTH
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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89.1%;
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Pred. No. 2.1e-49;
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Sequence 13, Application US/09065059
PATENT NO. 6068841
GENERAL INCORNATION:
APPLICANT: SEINO, Ken-ichiro
APPLICANT: KAYAGAKI, NO. 6068841uhiko
APPLICANT: VAGITA, Hideo
APPLICANT: OKUMURA, Ko
APPLICANT: NAKATA, MOTOMI
FITULE OF INVENTION: THERAPEUTIC AGENT FO
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
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US-09-065-059-13
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US-08-275-053-11
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Best Local:
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APPLICATION NUMBER: POINT OF SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Reconstitute OF INVENTION: Viring NUMBER OF SEQUENCES: 16 COMPUTER REALABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/275,053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
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Match 87.0%; Local Similarity 89.0%; ses 97; Conservative
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                                                                          McDermott, Will & Emery
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                                                                                                                                   THERAPEUTIC AGENT FOR HEPATITIS
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Pred. No. 2.1e-49;
S; Mismatches 7; Indels
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TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-065-059-13
Search completed: November Job time: 17.4486 secs
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TELEPAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENCTH: 112 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                   Query Match
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ATTORNEY/AGENT INFORMATION:
NAME: Bucca Ph.D., Daniel
REGISTRATION NUMBER: 9-42,368
REFERENCE/DOCKET NUMBER: 50356-151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                               local Similarity
                                                                               63 PARFSGSGSRTDFTLTIDFVEADDAATYYCQQNNEDPWTFGGGTKLEIKR 112
                                                                                                                        63 PARFSGSGSRTDFTLTINPVBADDVATYYCQQSNBDPLTFGTGTRLEIKR 112
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                  7, 2003, 07:30:11
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IIAA SEQUENCE 1.0
ID AAB20444 standard; Peptide; 16 AA.
                                                                                 The present sequence is that of complementarity determining region 3 (CDR3) of an antibody having anti-Factor IX (FIX) or anti-activated Factor IX (FIXA) activity. Such antibodies anti-activatives (including those that comprise the present CDR3 peptide) have Factor VIIIa (FVIIIa) cofactor activity or FIXA activating activity. Administration of the antibodies or their derivatives leads to an increase in the processulant activity of FIXA, even in the presence of FVIIIa inhibitors. This allows for rapid blood cosgulation even in the absence of FVIII or FVIIIa, and the case of FVIII inhibitor patients. The antibodies or their derivatives are used in a claimed pharmaceutical composition for treating patients with blood cosgulation disorders, especially in aemophilia A and haemorrhagic diathesis.
                            AAB20444 Length: 16 November 7, 2003 08:14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "any amino acid"
Misc-difference 3
                                                                                                                                                                                                                                                                                                                                               New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-2000; 2000WO-EP08936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pactor IX; FIX; Factor IXa; FIXa; antibody; pxocoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse; complementarity determining region; CDR.
                                                         Sequence
                                                                                                                                                                                                                                                                                                                Claim 7; Page 74; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-290358/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Scheiflinger F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200119992-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB20444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BAXT ) BAXTER AG.
CXXYGNSPKG FAYXXC
                                                            16 AA;
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                            Type: P
                              Check: 623
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> 0 < o| {0 IntelliGenetics > 0 <

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1 match found in sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 match found in sequence:
US-09-661-992-105; Sequence 105, Application US/09661992
(from "/srch/paa/US096_COMB.pep")
Sequence 105, Application US/09661992
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Format Options:
Nucleic acid code matching
Find non-matching hits only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Selected scope is Sequence.
Selected sequence key from "new.key":
seq105 (AA) ID seq105 AA preliminary pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quest - Quick User-directed Expression Search Tool Release 5.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Selected search type is key against sequence data banks or files.
                                                                                                                                                                                                                                                APPLICANT: Scheiflinger, Friedrich
APPLICANT: Kerschbaumer, Randolf
APPLICANT: Falkner, Falko-Guenter
APPLICANT: Dorner, Friedrich
TITLE OF INVENTION: Factor IX/Factor IXA Activating Antibodies and Antibody Derivative
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/661,992
CURRENT FILING DATE: 2000-09-14
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 105
LENGTH: 16
TYPER. TEST
                                                                                                                                                 OTHER INFORMATION: Description of the artificial sequence:CDR3 region Found using 'seq105' (new.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run mode
Time to start comparison
Notify at end of run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Report key used
Note position of hit
Display full annotations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence context
                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Data bank : Pending_AA , all entries
                                                                                       CXXYGNSPKGFAYXXC
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Format Options:

Nucleic acid code matching E Find non-matching hits only W Report key used Y Note position of hit Display full annotations Y Sequence context
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Selected sequence key from "new.key":
seq105 (AA) ID seq105 AA preliminary pattern
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Number of sequence hits:
Number of separate matches:
Number of sequence hits saved:
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! FINDPATTERNS on pir: * allowing 0 mismatches
  1 CXXYGNSPKGFAYXXC
November 7, 2003 07:41 ..
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Databases searched: NBRF, Release 76.1, Released on 12May2003, Formatted on 10Jun2003

Total finds: Total length: Total sequences: CPU time: 0 96,168,682 283,308 54.01

! FINDPATTERNS on swp:\* allowing 0 mismatches

1 CXXYGNSPKGFAYXXC

November 7, 2003 07:42 ..

Databases searched: SWISS-PROT, Release 41.1, Released on 6Jun2003, Formatted on 9Jun2003 SPTREMBL, Release 23.0, Released on 4Mar2003, Formatted on 7Mar2003

Total finds:
Total length:
Total sequences:
CPU time:

0 305,079,309 958,388 03:26.62

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Result
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 number of hits satisfying chosen parameters:
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Copyright (c) 1993 - 2003 Compug
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T747208
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37	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38
46.2	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5
92	588	583	488	488	488	402	352	351	128	118	110	109	109	96	92
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
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īg kāppā chain V r	phosphoprotein pho	probable acyl-CoA	protein F21D18.20	probable bacteriop	conserved hypothet	hypothetical prote	developmental regu	O.	Ig kappa chain V r	Ig light chain - h	Ig kappa chain V r	chain	Ig kappa chain V-I	probable metalloca	Ig kappa chain V r

## ALIGNMENTS

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A;Cross-references: EMBL:X89969; NID:g1055677; PIDN:CAA62006.1; PID:g1051125 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July C;Superfamily: bovine polyA binding protean II; ribonucleoprotein repeat homo F;173-239/Domain: ribonucleoprotein repeat homology <RRM2>
                                                                                                                                                                                                R;Nemeth, A.; Krause, S.; Blank, D.; Jenny, A.; Jenoe, P.; Lustig, A.; Wahle, E. Nucleic Acids Res. 23, 4034-4041, 1995
A;Title: Isolation of genomic and cDNA clones encoding bovine poly(A) binding protein A;Reference number: S59863; MUID:96071160; PMID:7479061
A;Accession: S59863
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: mRNA
A;Residues: 1-306 <NEMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-205 < WIL>
A; Cross-references: EMBL: Z81037; PIDN: CAB02750.1; GSPDB: GN00019; CESP: C17E4.5
A; Experimental source: clone C17E4
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, October 1996
A;Reference number: Z19113
A;Accession: T19356
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                         polyA binding protein II - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Nov-1999
C;Accession: $59863
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A;Map position: 1
A;Introns: 22/3; 120/2
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c;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19356
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                                                     Query Match
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Similarity 53.7; Conservative
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                        53.88;
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Pred. No. 2.9;
1; Mismatches
                        Score 44; DB 1; Length 306;
Pred. No. 4.2;
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Matches

Mismatches

51

Indels

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Gaps

0

Local

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CPB-binding protein - African clawed frog
NyAlternate names: cytoplasmic polyadenylation element-binding protein
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: A55377
R;Hake, L. E.; Richter, J.D.
Cell 79, 617-627, 1994
A;Title: CPEB is a specificity factor that mediates cytoplasmic polyadenylation
A;Reference number: A55377; MUID:95042759; PMID:7954828
A;Accession: A55377
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A55377
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A;Molecule type: DNA
A;Residues: 1-166 <VOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: T39586
R;Volckaert, G.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, August 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rna binding protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Immunol. 142, 3168-3163, 1989
A;Tille: Structural and idiotypic characterization of the L chains of human IgM A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: F30607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain V-III region (Bor) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
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A;Accession: T39586
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A; Residues: 1-109 <GON>
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                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Introns: 12/3; 97/2; 126/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: SPDB: SPBC16E9.12c
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A;Experimental source: strain 972h-; cosmid c16E9
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Best Local
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1; Mismatches
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Pred. No. 3
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A;Cross-references: GB:
C;Genetics:
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: B70749
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go
C; Connor, R.; Davies, R.; Devlin, K.; Felrwell, T.; Gentles, S.; Hamlin, N.; Holr
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rature 393, 537-544, 1998
Mature 393, 537-544, 1998
Mature 393, 537-644, 1998
Mature 39
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-568 <HAK>
A;Cross-references: GB:U14169; NID:g987224; PIDN:AAA80483.1; PID:g624634
A;Cross-references: GB:U14169; NID:g987224; PIDN:AAA80483.1; PID:g624634
C;Superfamily: African clawed frog CPE-binding protein; ribonucleoprotein repeat homology <RRM1>
                                                                                                       A; Map position: 1
A; Genome: nucleomorph
C; Keywords: nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                                                        R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
A;Accession: H90083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polyadenylate-binding protein [imported] - Guillardia theta nucleomorph C;Species: nucleomorph Guillardia theta C;Species: nucleomorph Guillardia theta A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001 C;Accession: H9083
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C;Superfamily: 4-coumarate-CoA ligase;
F;103-610/Domain: acetate-CoA ligase hc
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A; Residues: 1-626 < COL>
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Pred. No. 19;
1; Mismatches
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Pred. No. 17;
       Score 41;
Pred. No.
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R.(Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gol, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holxx Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E., Taylor, K.; Mitchead, S.; Barrell, B.G. A;Itle: Decliphering the biology of Mycobacterium tuberculosis from the complete of A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70763
A;Accession: D70763
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-429 <COL>
A;Residues: 1-429 <COL>
A;Residues: GB:Z74020; GB:AL123456; NID:93261584; PIDN:CAA998332.1; PID:914
A;Experimental source: strain H37Rv
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A;Title: Sequence analysis of the орготр об ст.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 02-Feb-2001
C;Accession: S75579
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: ilvA
C;Superfamily: threonine dehydratase
C;Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase;
C;Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase;
F;66/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
                                                                                                                                                                                                    A;Cross-references: EMBL:D90911; GB:AB001339; NID:g1653083; PIDN:BAA18140.1; PID:g165322 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 C;Superfamily: hypothetical procesin sl10804; translation elongation factor Tu homology C;Keywords: GTP binding; nucleotide binding; P-loop P;62-176/Domain: translation elongation factor Tu homology <BTU> F;62-176/Domain: translation elongation factor Tu homology <BTU> F;63-75/Region: nucleotide-binding motif F (be 75/Region: GTP-binding MXXD motif
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A;Molecule type: DNA
A;Residues: 1-453 <KAN>
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C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jun-2002
                             S
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                                                                               Similarity 7; Conserv
                               YGNSPKG 10
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Pred. No.
                                                                                                       Score 41;
Pred. No.
                                                                            Pred. No. 21;
Mismatches
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A41519
hypothetical exported protein BMEI1982 [imported] - Brucella melitensis (strain G;Speciles: Brucella melitensis (c;Speciles: Brucella melitensis (c;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002 C;Accession: AH3499 **Rapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; I x;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; I ; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D. proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
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A,Note: the polyprotein is cleaved to give at least eight mature proteins; however, A;Note: the polyprotein is cleaved to give at least eight mature proteins; however, A;Note: the authors translated the codon AMI for residue 630 as Asp, GAG for 844 as C;Superfamily: cowpea aphid-borne mosaic virus genome polyprotein B;C;Keywords: cysteine proteinase; genome-linked protein; hydrolase; membrane protein; F;2-326/Product: 32K proteinase cofactor #status predicted <PCF>F;327-919/Product: 58K membrane-binding protein #status predicted <MBP>F;320-947/Product: 24K viral proteinase #status predicted <VPG>F;948-1155/Product: 24K viral proteinase #status predicted <VPG>F;948-1156/Product: RNA-directed RNA polymerase #status predicted <RRP>
                                                                                                                                                                                                     A/Gene: tud
A/Cross-references: FlyBase:FBgn0003891
C/Superfamily: posterior-group protein
                                                                                                                                                                                                                                                                                                                                                                                                                          R;Golumbeski, G.S.; Bardsley, A.; Tax, F.; Boswell, R.E. Genes Dev. 5, 2060-2070, 1991
A;Tille: tudor, a posterior-group gene of Drosophila melanogaster, A;Reference number: A41519; MUID:92038995; PMID:1936993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBO J. 2, 2253-2258, 1983
A;Title: The nucleotide sequence
A;Reference number: A04211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 31-Mar-2000 C;Accession: A04211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome polyprotein B - cowpea aphid-borne mosaic virus N;Contains: 24K viral proteinase (EC 3.4.22.-); 32K proteinase cofactor; 58K membrane-b C;Species: cowpea aphid-borne mosaic virus, CABMV
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                                                                                                                                                                                                                                                                                            A;Cross-references: GB:X62420; NID:g8753; PIDN:CAA44286.1; PID:g8754
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1999 C;Accession: A41519; S19019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     posterior-group protein tudor - fruit fly (Drosophila melanogaster)
C; Species: Drosophila melanogaster
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A; Residues: 1-1866 < LOM>
                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-2515 < GOL>
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Best Local S
Matches 7
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7; Conserv
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2178
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87.5%;
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58.3%;
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                                                                                                                                                       Score 41;
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Pred. No. 84;
                                                                                                     Score 41; DB 2;
Pred. No. 1.1e+02;
0; Mismatches 1
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. : Ivanova, D.; Leter

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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;16-91/Domain: immunoglobulin homology <IMM:> F;23-89/Disulfide bonds: #status predicted
                                                          A;Reference number: 224392
A;Reference number: T47208
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary
A;Residues: 1-359 <BAR>
A;Residues: 1-359 <BAR>
A;Cross-references: EMBL:U36761; PIDN:AAAB3756.1
                                                                                                                                                                                             R;Barra, J.L.; Mautino, M.R.; Rosa, A.L. submitted to the EMBL Data Library, September 1995
A;Description: Eth-1r, a mutant allele of Neurospora crassa S-adenosylmethionine synthe
                                                                                                                                                                                                                                                                                       methionine adenosyltransferase (EC 2.5.1.6) [imported] - Neurospora crassa (fragment) C;Species: Neurospora crassa C;Species: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
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Mol. Immunol. 23, 239-244, 1986
A;Title: Amino acid sequence of a light chain variable region of a human rheumatoid fact
A;Reference number: A01893; MUID:86230578; PMID:3086710
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A;Molecule type: DNA
A;Residues: 1-107 <KUR>
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                                                                                                                                                                                                                                                                         C; Accession: T47208
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A;Residues: 1-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig kappa chain V-III region (Gol) - human
N;Alternate names: rheumatoid factor
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Homo sapiens (man)
Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 21-Jan-2000
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Local Similarity 43.8%;
les 7; Conservative
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Intron positions not resolved (incomplete sequence)
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Pred. No. 7.7;
2; Mismatches
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Pred. No. 7.6;
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Search completed: November Job time: 3.1721 secs

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2003, 07:36:21

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A;Gene: SGD:SAM1; ETH10
A;Cross-references: SGD:S0004170; MIPS:YLR180v
A;Map position: 12R
C;Function:
A;Description: transferase
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             methionine adenosyltransferase (BC 2.5.1.6) 1 - yeast (Saccharomyces cerevisiae) N;Alternate names: protein 19470.9; protein YLR180w; S-adenosylmethionine synthe C;Species: Saccharomyces cerevisiae C;Species: Saccharomyces cerevisiae C;Date: 23-Feb-1995 #sequence_revision 11-Aug-1995 #text_change 05-May-2000
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SS1425
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J. Biol. Chem. 262, 16704-16709, 1987
A;Title: SAM1, the structural gene for one of the S-adenosylmethionine synthetases in SA;Reference number: A92621; MUID:88059059; PMID:3316224
A;Accession: A28480
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C;Genetics:
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A;Residues: 1-245,'T',247-356,'F',358-382 <THO>
A;Cross-references: EMBL:J03477; NID:g172533; PIDN:AAA66932.1; PID:g172534
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A; Description: The sequence of S. cerevisiae cosmid 9470.
A; Reference number: S51414
A; Recession: S51425
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and is derived by analysis of the total score distribution.
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G99NG1;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Solute carrier family 21 member 12 (Sodium-independent transporter E) (Organic anion transporting polypeptide SLC21A12 OR OATPE.

Rattus norvegicus (Rat).
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                                                                                        "Identification of thyroid hormone transporters in humans: difference molecules are involved in a tissue-specific manner.";
Endocrinology 142:2005-2012(2001).
-1- FUNCTION: Mediates the Ma(+)-independent transport of organic anions such as the thyroid hormone T3 (triiodo-L-thyronine) are
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EMBL; BC030720; AAH30720.1; -.
EMBL; BC033602; AAH3602.1; ALT_INIT.
MGD; MGI:1351866; $1c21a12.
                                                                                                                                                                                             MEDLINE=21216537; PubMed=11316767; Unno M., Fujiwara K., Adachi H., Nishio T., Unno M., Onogawa T., Suzuki T., Asano N., Tanemoto M. Suzuki M., Kondo Y., Nunoki K., Shimosegawa Matsuno S., Abe T.; "Identification of thyroid hormone transport"
                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
NCBI_TaxID=10116;
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PF03132; OATP_N; 2.
AMs; TIGR00805; oat;
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an email to
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                       Integral membrane
) THE SLC21 FAMILY
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N-LINKED (GLCNAC...) (F
SIFG -> TAWG (in isoform
/FTId=VSP 006157.
Missing (in isoform 2).
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W; 0856B45F02C4EBAC CRC64
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Pred. No.
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Sciurognathi;
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5.7;
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thi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                         Tokui T., Okabe M., Seki M., Shiiba K., T., Iinuma K., Ito S.
                         protein.
OF TRANSPORTERS
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FD26_MYCTU
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STRAIN=CDC 1
Fleischmann
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                                            MEDINE-98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Comnor R., Badcock K., Basham D., Brown D., Chillingworth T., Comnor R., Badcock K., Basham D., Brown D., Chillingworth T., Comnor R., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Muzhy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative fatty-acid--CoA ligase fadD26 (EC 6)
                                                                                                                                                                                                                                                                                                                                            FD26 MYCTU
Q10976;
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                                                                                                                                                                                                                                  Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Corynebacterineae; Mycobacteriaceae; Nycoba
                                                                                                                                                                                                                       NCBI_TaxID=1773;
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TRANSMEM 103 123
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                                                                                                                                                                                         STRAIN=H37Rv;
                                                                                                                                                                                                  SEQUENCE FROM N.A.
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  Oshkosh;
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Pred. No.
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-LINKED (GLCNAC. ..) (POTENTIAL)
DB857B514654497B CRC64;
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                                                                                                                                                                                                                                       Mycobacterium
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5.7;
 Carpenter L.,
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Best Local s
Matches 7
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A.,
Peterson J., DeBoy R., Dodson R., Gwinn
Kolonay J.F., Nelson W.C., Umayam L.A.,
                                                                                                                                                                                                                              Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Haider K., Gas S., Barry C.B. III, Tekaia F., Gardcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holronsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L. Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.

Bacteria; Actinobacteria; Actinobacteridae; Actinor
Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THD1_MY
                                                                                                                                                          "Deciphering the biology of Mycobacterium tuberculosis complete genome sequence.";
Nature 393:537-544(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last amotation update)
Probable threonine dehydratase biosynthetic (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laboratory strains.";
Submitted (APR-2001) to
-:- SIMILARITY: BELONGS
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SEQUENCE 583 AA;
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Pfam; PF00501; AMP-binding; 1.
PROSITE; PS00455; AMP BINDING;
Hypothetical protein; Ligase; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE007122; AAK47327.1;
TIGR; MT2999; -.
TubercuList; Rv2930; -.
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7; Conserv
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Gwinn !
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          Carpenter
M.L., Haft
Ermolaeva M
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21-JUL-1986 (Rel. 01, Created)
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28-FEB-2003 (Rel. 41, Last annotation update)
28-FCB-2003 (Rel. 41, Cast annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssRNA positive-strand viruses,
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BINDING 66
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PROSITE; P800165; DEHYDRATASE SER THR; 1.
Isoleucine biosynthesis; Lyase; Pyridoxal
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InterPro; IPR001926; Bd enzyme_beta.
InterPro; IPR001934; S/T dehydrtse.
InterPro; IPR001721; ThrDh_C.
Pfam; PF00291; PALP; 1.
Pfam; PF00585; Thr_dehydrat_C; 1.
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"Whole genome comparison
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=12264;
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SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
   SWISS-PROT entry
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P25823;
01-MAY-1992
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MEDINE-20038995; Bardsley A., Tax F., Boswell R.E.;
Golumbeski G.S., Bardsley A., Tax F., Boswell R.E.;
"Tudor, a posterior-group gene of Drosophila melanogaster, encodes
novel protein and an mRNA localized during mid-oogenesis.";
Genes Dev. 5:2060-2070(1991).
-1- FUNCTION: REQUIRED DURING COGENESIS FOR THE FORMATION OF
PRIMORDIAL GERM CELLS AND FOR NORMAL ABDOMINAL SEGMENTATION.
-1- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT THE LIFE CYCLE.
-1- MISCELLANEOUS: THE TUD MRNA ACCUMULATES WITHIN THE POSTERIOR
REGION OF THE DEVELOPING COCYTE DURING THE EARLY TO MIDDLE STAG
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ephydroidea; Drosophilidae; Drosophila
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maternal tudor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1992 (Rel. 22,
01-MAY-1992 (Rel. 22,
28-FEB-2003 (Rel. 41,
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Pfam; PF00910; RNA helicase; 1.
PRINTS; PR00918; CALICVIRUSNS.
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InterPro; IPR006005; RNA helicase.
InterPro; IPR007095; RNA pol DS PS.
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PIR; A04211; GNWE
MEROPS; C03.003;
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ween the Swiss Institute of Bioinform,
European Bioinformatics Institute. The py non-profit institutions as long
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RNA polymerase; ATP-binding.
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1 326
MEMBRANE-BINDING PROTEIN (POTENTIAL).
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PROTEASE (POTENTIAL).

RNA-DIRECTED RNA POLYMERASE
ATP (POTENTIAL).

THIOL PROTEASE (POTENTIAL).
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Best Local :
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20-MAR-1987
15-JUL-1999
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SEQUENCE
                                                                                  Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SPROSITE; P850835; IG LIKE; 1.
Immunoglobulin V region.
DISULPID 23 89
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Newkirk M., Chen P.P., Carson D.A., Posnett D
"Amino acid sequence of a light chain variabl.
rheumatoid factor of the Wa idiotypic group,
reactivity with antipeptide antibodies.";
mol. Immunol. 23.239-244(1986).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrbini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
15 kappa chain V-III region GOL (Rheumatoid f.
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GO; GO:0019090; P:mitochondrial rRNA, mitochondrial export; IMP.
GO; GO:0007315; P:pole plasm assembly; IMP.
InterPro; IPR001097; Maternal tudor.
InterPro; IPR002999; Tudor.
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                                                                                                                                                                                     InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                               GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS
GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                     HSSP; P80362; 1WTL.
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SMART; SM00333; TUDOR; 10.
PROSITE; PS50304; TUDOR; 9
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  DB 1;
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RA Wood V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gantles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Miblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Miblett D., Odell C.,
RA Moliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Wutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Wolfers I., Jammonds M., Squares R., Squares S., Stevens K.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Wolfjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Welfjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Welfjens I., Vanstreels E., Rieger M., Weshfardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Cadieu E., Dreano S., Sanchez M., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Doga R.R., Cruzado L., Jimenz J., Sanchez M., del Rey F., Benito J.,
RA Gerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G. V., Usery P., Benito J.,
RA Shpakovski G. V., Usery P., Benito J.,
RA Shpakovski G. V., Usery P., Benito J.,
RA Shpakovski G. V., Usery P., Benito J.,
RA Shpakovski G. V., Usery P., Benito J.,
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Ra Shaller P., Sanchez M., Sanchez M., Benito J.,
Ra Shaller P., Sanchez M., Cal
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                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
5-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine adenosyltransferase) (AdoMet synthetase).
SAM1 OR SPEC14F5.05C.
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Yeast 16:1-10(2000).
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MEDLINE=20089020; PubMed=10620770;
Hiltin., Graub R., Jorg M., Arnold P.,
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycete
Schizosaccharomycetales; Schizosaccharomycetaceae;
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                                                                                                        diphosphate + S-adenosyl-L-methionine.
COFACTOR: Binds 2 divalent ions, such as magnesium 1 potassium ion per subunit (By similarity).
PATHWAY: Activated methyl cycle.
                                                                                                                                                                                                 FUNCTION: Catalyzes the formation of S-adenosylmethionine from methionine and ATP.

CATALYTIC ACTIVITY: ATP + L-methionine + H(2)0 = phosphate +
  European
                                                                                          SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
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There are no
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  restrictions
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MBL outstation -
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EMBL; AL023780; CAA19
PIR; T39451; T39451.
HSSP; P04384; IMXB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-UUL-1989 (Rel. 11, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
5-adenosylmethionine synthetase 1 (EC 2.5.1.6) (Methionine adenosyltransferase 1) (AdoMet synthetase 1)
SAMI OR ETHIO OR YLK180W OR L9470.9
Saccharomyces cerevisiae (Baker's yeast)
Buckaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Baccharomycetales; Saccharomycetaceae; Saccharomyces.
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METK YEA
P10659;
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Johnston M., Hiller L., Riles L., Albermann K., Andre B., Ansorge Benes V. Brueckner M., Delius H., Dubois E., Duesterhoeft A., Entian K., D., Floeth M., Goffeau A., Hebling U., Heumann K., Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P., Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D., Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M. Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose I Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S., Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P., Vierndeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler I Medler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII
                                                                                                                                                                                                                                                                                       STRAIN=S288c / AB972;
MEDLINE=97313267; PubMed=9169871;
Johnston M., Hillier L., Riles L.
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDILINE=88059059; PubMed=3316224; Thomas D., Surdin-Kerjan Y.; Thomas D., Surdin-Kerjan Y.; "SAMI, the structural gene for one of the synthetases in Saccharomyces cerevisiae. S., Biol. Chem. 262:16704-16709(1987).
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
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Metal-binding.

NP BIND 118 123 ATP (POTENTIAL).

METAL 18 18 MAGNESTUM (BY SIMILA METAL 270 POTASSIUM (BY SIMILA METAL 278 ATP (POTENTIAL).

BINDING 146 146 ATP (POTENTIAL).

SEQUENCE 382 AA; 41831 MW; 9970A9D1195C5738 C
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Pfam; PF00438; S-AdoMet synt; 1.
Pfam; PF02772; S-AdoMet syntD2; 1.
Pfam; PF02773; S-AdoMet syntD3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00376; ADOMET_SYNTHETASE_1;
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CAA19323.1; -.
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Pred. No. 10;
1; Mismatches
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P19358;
01-NOV-1990
01-OCT-1994
28-FEB-2003
01-NOY-1990 (Rel. 16, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
S-adenosylmethionine synthetase 2 (EC 2.5.1.6)
adenosyltransferase 2) (AdoMet synthetase 2).
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CONFLICT
SEQUENCE
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METAL
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EMBL; U17246; AAB67461.1; -.
EMBL; U17246; AAB67461.1; -.
PIR; S51425; S51425.
HSSP; P043344; 1MXB.
SGD; S0004170; SAMI.
GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:000478; F:methionine adenosyltransferase activity; IGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for come entities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                BINDING
                                                                                                                                                                                                                                                                                                                               Magnesium; Potassium; Metal-binding.
NP_BIND 118 123 ATP (POTENTIAL)
METAL 18 18 MAGNESIUM (BY S
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Pfam; PF00438; S-AdoMet_synt; 1.
Pfam; PF02772; S-AdoMet_syntD2; 1.
Pfam; PF02773; S-AdoMet_syntD3; 1.
TIGRPAMS; TIGR01034; metK; 1.
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"Protein expression during exponential Saccharomyces cerevisiae.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 387:87-90(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COFACTOR: Binds 2 divalent ions, such as ma
1 potassium ion per subunit (By similarity)
PATHWAY: Activated methyl cycle.
SUBUNIT: Heterotetramer.
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PS00377; ADOMET SYNTHETASE 2; 1.
ase; One-carbon metabolism; Multigene
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Pred. No. 10;
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Pfam; PF02772; S-AdoMet_syntD2; 1.
Pfam; PF02773; S-AdoMet_syntD3; 1.
Pfam; PF02773; S-AdoMet_syntD3; 1.
TIGRRAMS; TIGRO1034; metK; 1.
PROSITE; PS00376; ADOMET_SYNTHETASE_2; 1.
PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
Transferase; One-carbon metabolism; Multigene
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EMBL; U33057; AAB64944.1; -.
PIR; A31398; A31398,
HSSP; P04384; 1MXB.
SGD; S0002910; SAM2.
InterPro; IPP002133; S-AdoMet_synt.
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                                                                                             METAL
METAL
                                            SEQUENCE
                                                                                                                                    METAL
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Volpe T., Warner J.R., McLaughlin C.S.;
Submitted (SEP-1994) to the SWISS-PROT data bank
-!- FUNCTION: CATALYZES THE FORMATION OF S-ADENO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SBQUENCE FROM N.A.

Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles Dietrich F.S., Mulligan J., Allen E., Cherry J.M., Chung E., Berno A., Carpanter J., Chen E., Cherry J.M., Chung E., Hunicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H. Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., P. Roberts D., Schramm S., Schroeder M., Shogren T., Shroff Winant A., Yelton M., Botstein D., Davis R.W.; Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METHIONINE AND ATP.
-I- CATALYTIC ACTIVITY: ATP + L-methionine +
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Thomas D., Rothstein R., Rosenberg N., Surdin-Kerjan Y.;
"SAM2 encodes the second methionine S-adenosyl transferase
Saccharomyces cerevisiae: physiology and regulation of both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=89218973;
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Saccharomyces cerevisiae (Baker's yeast).
Bukaryota, Fungi, Ascomycotta; Saccharomycottina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                    SYNTHETASE.
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D., Lew H.,
             Length 383;
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                                                                                                                                                                                                                                                                                                                                                   TICREAMS; TICRO1034; metK; 1.

PROSITE; PS00376; ADOMET SYNTHETASE 1; 1.

PROSITE; PS00377; ADOMET SYNTHETASE 2; 1.

Transferase; One-carbon metabolism; ATP-binding; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR002133; S-AdoMet synt.
Pfam; PF00438; S-AdoMet synt; 1.
Pfam; PF02772; S-AdoMet syntD2; 1.
Pfam; PF02773; S-AdoMet syntD3; 1.
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01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
S-adenosylmethionine synthetase (EC 2.5.1.6)
adenosyltransferase) (AdoMet synthetase).
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HSSP; P04384; 1MXB.
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STRAIN=RN42;
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"Cloning and sequence of the Ascobolus immersus S-adenosyl-L-methionine synthetase-encoding gene.";
Gene 170:155-156(1996).
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COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt,
1 potassium ion per subunit (By similarity).
PATHWAY: Activated methyl cycle.
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CATALYTIC ACTIVITY: ATP + L-methionine + H(2)0
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YDDSAKGFDYKTC 100
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Pred. No. 11;
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                                                                                                                                     Length 393;
                                                                                                                                                                                       CRC64;
                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                       ç,
                                                                                                                                                                                                                                                                                                                                                   Potassium;
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RESULT 12

HGNC: 6904;

MAT2A.

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METK HUMAN

ID METK HOMAN

AC P31153

AC P31153

AC P31153

AC P31153

AC P31153

DT 01-ULL

DT 01-ULL

DT 01-VULL

DT 01-VULL

DT 15-SEP

S-aden

GR MATCA

OS HOMO B

OC ENGATY

RN SEQUEN

RN FISSUE

RN HORIKE

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RA Klausper R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Schmutz J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHIONINE AND ATP.

-IT FORMALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate + diphosphate + S-adenosyl-L-methionine.

-IT COPACTOR: Binds 2 divalent ions, such as magnesium or cobalt, 1 potassium ion per subunit (By similarity).

-IT PATHRAY: Activated methyl cycle.

-IT SUBUNIT: Homodimer.

-IT TISSUE SPECIFICITY: IN MAMMALIAN TISSUES, THERE ARE THREE DIFORMS OF ADOMET SYNTH. DESIGNATED AS ALPHA, BETA, AND GAMMA. AND BETA ARE EXPRESSED ONLY IN ADULT LIVER, WHILE GAMMA IS WISTRIBUTED IN EXTRAHERATIC TISSUES.
                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a coperative of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as long and to modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                           EMBL; X68836; CAA48726.1;
EMBL; BC001686; AAH01886.1;
EMBL; BC001894; AAH01854.1;
PIR; S27257; S27257
HSSP; P04384; 1MXB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
5-adenosylmethionine synthetase gamma form (EC 2.5.1.6) (Methionine adenosyltransferase) (AdoMet synthetase) (MAT-II).
MATT2A OR MATT2_OR AMS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Horikawa S., Tsukada K.;
"Molecular cloning and developmental expression of a human kidney adenosylmethionine synthetase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METK_HUMAN
P31153;
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93050159; PubMed=1426236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISTRIBUTED IN EXTRAHEDATIC TISSUES.
SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312:37-41(1992).
                                                                                                                                                                                  CAA48726.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THERE ARE THREE DISTINCT
A, BETA, AND GAMMA. ALPHA
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                                                                                                                                                                                                                                                                                                                                                                                            restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                      collaboration
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RESULT 13
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Best Local S
Matches 7
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PROSITE; PS00377, ADOMET SYNTHETASE 2; 1.

Transferase; One-carbon metabolism; Magnesium; Po Metal-binding; Multigene family; ATP-binding.

NP BIND 131 136 ATP (POTENTIAL).

METAL 57 57 MAGNESIUM (BY SIMILA METAL 283 283 POTASSIUM (BY SIMILA METAL 291 291 MAGNESIUM (BY SIMILA METAL 291 2
                         EMBL; U21547; AAC49260
PIR; S65800; S65800.
HSSP; P04384; 1MXB.
InterPro; IPR002133; S
                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEUCR
                                                                                                                                                                                                                                                                                                                                                                                                                ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         overexpression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthetase:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mautino M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Fungi; F
Sordariomycetidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-PEB-1996 (Rel. 3), Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
S-adenosylmethionine synthetase (EC 2.5.1.6)
addanosyltransferase) (AdoMet synthetase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 33,
01-FEB-1996 (Rel. 33,
28-FEB-2003 (Rel. 41,
S-adenosylmethionine s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P48466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97002541; PubMed=8849888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Micelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=5141;
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Pfam; PF00438; S-AdoMet_synt; 1.
Pfam; PF027772; S-AdoMet_syntD3; 1.
Pfam; PF02773; S-AdoMet_syntD3; 1.
TIGRPAMs; TIGR01034; metK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neurospora crassa.
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                                                                                                                                                                                                                                                                                                                                                    METHIONINE AND ATP.

CAPTALYTIC ACTIVITY: ATP + L-methionine + H(2)0 = diphosphate + S-adenosyl-L-methionine.

COFACTOR: Binds 2 divalent ions, such as magnesiu 1 potassium ion per subunit (By similarity).

PATHWAY: Activated methyl cycle.
                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLICS 142:789-800(1996).
FUNCTION: CATALYZES THE FORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO:0004478; F:methionine adenosyltransferase activity; TAS
Pro; IPR002133; S-AdoMet_synt, PF00438; S-AdoMet_synt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            601468;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M.R., Barra J.L., Rosa A.L.;
the Neurospora crassa locus encoding S-adenosylmethionine
ase: molecular cloning, sequence analysis and in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 7; Conserv
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                                                                                               AAC49260.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ascomycota; Pezizomycotina; Sordariomycetes; Sordariales; Sordariaceae; Neurospora.
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Pred. No.
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Best Local S
Matches 7
                 This SWI
between
the Euro
                                                             -!- CATALUTIC ACTIVITY: ATP + 1-methionine + H(2)O = phosphate +
diphosphate + S-adenosyl-1-methionine.
-!- COPACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
l pocassium ion per subunit (By similarity).
-!- PATHWAY: Activated methyl cycle.
-!- SUBUNIT: Homodiner.
-!- PATHWAY: ACTIVITY: IN MAMWALIAN TISSUES, THERE ARE THREE DISTINCT FORMS OF ADOMST SYNTH. DESIGNATED AS ALPHA, BETA, AND GAMMA. ALPHA AND BETA ARE EXPRESSED ONLY IN ADULT LIVER, WHILE GAMMA IS WIDELY DISTRIBUTED IN EXTRAHEPATIC TISSUES. IN ADDITION THE GAMMA FORM PREDOMINANTLY EXISTS IN FETAL RAT LIVER AND IS PROGRESSIVELY REPLACED BY THE ALPHA AND BETA FORMS DURING DEVELOPMENT.
-!- SIMILARITY: BELONGS TO THE ADOMST SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METK RAT
P18298;
01-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metal-binding.
NP BIND 130
METAL 30
METAL 56
METAL 282
METAL 290
BINDING 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
5-adenosylmethionine synthetase gamma form (EC 2.5.1.6) (Methionine adenosyltransferase) (AdoMet synthetase) (MAT-II).
                                                                                                                                                                                                                                                                                Bur.
                                                                                                                                                                                                                                                                                                                                                                          Horikawa S., Sasuga J., Shimizu K., Ozasa F
"Molecular cloning and nucleotide sequence
kidney S-adenosylmethionine synthetase.",
J. Biol. Chem. 265:13683-13686(1990).
                                                                                                                                                                                                             ÷
                                                                                                                                                                                                                                                                                             promoter.
                                                                                                                                                                                                                                                                                                 Hiroki T., Horikawa S., Tsukada K.; "Structure of the rat methionine adenosyltransferase
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=98121185; PubMed=9461287;
                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Wistar; TISSUE=Kidney;
MEDLINE=90337979; PubMed=1696256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02772; S-AdoMet_syntD2; 1.
Pfam; PF02773; S-AdoMet_syntD3; 1.
TIGRFAMs; TIGR01034; meTK; 1.
PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
Transferase; One-carbon metabolism; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                    FUNCTION: CATALYZES METHIONINE AND ATP.
                        SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                J. Blochem. 250:653-660(1997)
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7; Conserv
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158
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                                                                                                                                                                                                                                                             THE FORMATION OF S-ADENOSYLMETHIONINE
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of Bioinformatics and the Institute. There are no restions as long as its content
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Pred. No. 11;
1; Mismatches
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MAGNESIUM (BY SI
POTASSIUM (BY SI
POTASSIUM (BY SI
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ATP (POTENTIAL)
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                  Tsukada K.;
cDNA encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 395
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; Murinae; Rattus.
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RESULT 15
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Matches 7
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PROSITE; PS00377; ADOMET_SYNTHETASE 2; 1.

Transferase; One-carbon metabolism; Magnesium; Po Metal-binding; Multigene family; ATP-binding.

NP BIND 131 136 ATP (POTENTIAL).

METAL 31 31 MAGNESIUM (BY SIMILA)

METAL 57 57 POTASSIUM (BY SIMILA)

METAL 283 283 POTASSIUM (BY SIMILA)

METAL 291 291 MAGNESIUM (BY SIMILA)

BINDING 159 159 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METK CAEEL
P50305;
01-OCT-1996
EMBL; U41009; AAA82280.1; PIR; T34085; T34085.
                                                                        use by non-profit institutions as long modified and this statement is not removed, entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Probable S-adenosylmethionine synthetase C0627.1 (EC 2.5.1.6)
(Methionine adenosyltransferase) (AdoMet synthetase)
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EMBL; AB000717; BAA19170.1; JOINED.
EMBL; AB000716; BAA19170.1; JOINED.
EIR; A37118; A37118.
HSSP; P04384; IMXB.
InterPro; IPR002133; S-AdoMet_synt.
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STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Pfam; PF02772; S-AdoMet_syntD2; 1.
Pfam; PF02773; S-AdoMet_syntD3; 1.
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                                                                                                                                                                                                                                                                                                                                     mitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.

FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM METHIONINE AND ATP (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate + diphosphate + S-adenosyl-L-methionine.

COPACTOR: Binds 2 divalent ions, such as magnesium or cobalt, copperated in the persubunit (By similarity).

PATHMAY: Activated methyl cycle.
                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
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7; Conserv
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Pred. No. 11;
1; Mismatches
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Best Local S
Matches 7
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InterPro; IPR002133; S-AdoMet_synt.
Pfam; PF00438; S-AdoMet_syntp1; 1.
Pfam; PF02772; S-AdoMet_syntD2; 1.
Pfam; PF02773; S-AdoMet_syntD3; 1.
TIGRPAMS; TIGR01034; metK; 1.
PROSITE; P800376; ADOMET_SYNTHETASE 1; 1.
PROSITE; P800377; ADOMET_SYNTHETASE 2; 1.
PROSITE; P800377; ADOMET_SYNTHETASE 2; 1.
PROSITE; P800377; ADOMET_SYNTHETASE 2; 1.
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SEQUENCE
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METAL
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                                           80
                                                                                   Similarity 7; Conserv
                                           YDDSSKGFDYKTC
                                                              YGNSPKGFAYXXC 16
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119 124
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404 AA;
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45
271
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271 P
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147 A
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            2003, 07:28:09
                                                                                                                                                                                          Multigene family; ATP-binding. ATP (POTENTIAL).
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Pred. No. 11
                                                                                                                                                                               MAGNESIUM
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SPTREMBL 23:*

1: sp_archea:*
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4: sp_human:*
5: sp_invertebrate
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

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4 YGNSPKGFAY 13             101 YGNSPAWFAY 110	Query Match 55.0%; Score 44; DB 11; Length 120; Best Local Similarity 80.0%; Pred. No. 2.6; Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	SECUENCE 120 AA; 13204 MW; DC4834AB1DE56F3C CRC64;	120 120	NON TER 1 1	; PS50835; I	SMART; SM00406; IGv; 1.	0047; ig; 1.	•	IPR003006;	InterPro; IPR007110; Ig-like.	9420.1;	Submitted (SEP-2000) to the EMBL/GenBank/DDBU databases.	in Mammalian Cells.";	iotope of Pterin-Mimicking &	Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.:	SEQUENCE FROM N.A.	[1]	4	Sciurognathi; Muridae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mus musculus (Mouse).		cking anti-idiotope h	(TrEMBLrel. 23, Last annotation	19,	01-DEC-2001 (TrEMBLrel. 19, Created)	••	Q920E8 PRELIMINARY; PRT; 120 AA.	图8	ET 1

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Q1-MAR-2003
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                                                                                                                                                           the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based o 60,770 full-length cDNAs.";
Nature 420.563-573 (2002).
EMBL; AK032172; BAC27741.1; -.
SEQUENCE 292 AA; 31044 MW; 0874042BA4A60
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STRAIN=C57BL/6J; TISSUE=Olfactory brain;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
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Eukaryota; Metazoa; (
Mammalia; Eutheria; F
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PROSITE; PS00030; RRM RNP 1; 1.
SEQUENCE 205 AA; 22603 MW;
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SMART; SM00360; RRM; 1.
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MEDLINE=99069613; PubMed=9851916;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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01-B4.5 protein.
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O43484; PRELIMINARY; PRT; JUB AM.
O143841; PST (TEMBLE) 06, Created)
O1-JUN-1998 (TEEMBLE) 06, Last sequence update)
O1-CT-2002 (TEEMBLE) 22, Last annotation update)
Poly(A) binding protein II (Similar to poly(A)-binding protein, nuclear 1).
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MEDLINE=98094238; I
Lee Y.J., Lee J., 1
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Codere F., Fardeau M.,
"Short GCG expansions
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE=98122579; PubMed=9462747;

Brais B., Bouchard J.-P., Xie Y.-G., Rochefo
Tome F.M.S., Lafreniere R.G., Kommens J.M.,
Blumen S., Korcyn A.D., Heutink P., Mathieu
                                             EMBL;
                                                                                              Strausberg R.;
Submitted (JUL-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 035935
035935;
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                                                                                                                                                                                                                                                                                                     dystrophy.
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PROSITE; PS00030; RRM RNP 1; 1.
SEQUENCE 302 AA; 32296 MW;
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EMBL; U93050; AAC00210.1; -.

MGD; MGI:1859158; Pabpn1.

Interpro; IRR000504; RNA_rec_mot.

Pfam; PF00076; rrm; 1.

SMART; SM00350; RRM; 1.
                                                                                                                                                                                                                                                                         Nac. Genet.
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                                                                                                                                                                                                   EQUENCE FROM N.A.
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Lee Y.J., Lee J., Yang I.C., Hahn
"Genomic structure and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                           tted (JUL-2001) to the EMBL/GenBank/DDBJ databases AP026029; AAC39596.1; -. AP02601939; AAH10939.1; -.
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   HGNC:8565; PABPN1
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in the PA
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Pred. No. 6.9;
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2F0F6F7CC19C1986 CRC64;
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                                                                                                                                                                                                                                                                                                                                 gene
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Q8XN61;
01-MAR-2002
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MEDLINE=96071160; PubM
Nemeth A., Krause S., 1
Wahle E.;
SEQUENCE FROM N.A. STRAIN=13 / Type A; PubMed=11792842;
                                                                                                                                                       Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales;
Clostridium.
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Q28165; CTEMBLES. 01,
01-NOV-1996 (TEMBLES. 01,
01-NOV-1996 (TEMBLES. 01,
01-MAR-2003 (TEMBLES. 23,
                                                                                                                   NCBI_TaxID=1502;
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                                                                                                                                                                                                                                                                       Probable beta-glycosyltransferase.
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PROSITE; P550102; RRM; 1.
PROSITE; P500030; RRM_RNP_1; 1.
PROSITE; P500030; RRM_RNP_1; 1.
SEQUENCE 306 AA; 32766 MW;
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Pfam; PF00076; rrm; 1.
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EMBL; X89969; CAA62006.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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PROSITE; PS50102; RRM;
PROSITE; PS00030; RRM R
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SEQUENCE FROM N.A. STRAIN=968 h90;
MEDLINE=20223868; P
Ding D.Q., Tomita Y
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Hypothetical 18:1 kDa protein (Fragment).
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Nature 420:563-573 (2002).
EMBL; AK033598; BAC28379.1; -.
SEQUENCE 723 AA; 77737 MW; 66F7507B8C653
                                                                                                                                                                                     NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                  Eukaryota; Fungi;
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STRAIN=C57BL/6J; TISSUE=Cecum;
MEDLINE=22354683; PubMed=12466851;
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Bukaryota, Metazoa, Chorda
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Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

EMBL; APO03166; BAB80183.1; -.

InterPro; IPR001173; Glycoc trans 2.

Pfam; PF00535; Glycos transf 2; 1.

Transferase; Complete proteome.

SEQUENCE 294 AA; 34356 MW; 390BF593B712CA35 CRC64;
                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast)
Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090
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tes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 YGNSPKGFAY 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gremblrel 23, Tremblrel 23, Tremblrel 23, Tremblrel 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                          PubMed=10759889;
Y., Yamamoto A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
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70 0%;
                          Yamamoto A.,
                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation updat
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Last annotation updat
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Pred. No.
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                       Chikashige Y.,
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                          Haraguchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Best Local S
Matches 7
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Best Local S
Matches 7
                                                                                                                     01-MAR-2001
01-MAR-2001
01-MAR-2003
                                                                                                                                                                               Q9DDY9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00076; xrm; 1.

SMART; SM00360; RRM; 1.

PROSITE; P850102; RRM; 1.

PROSITE; P8500030; RRM RNP 1; 1.

SBQUENCE 166 AA; 18461 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-972h-;

VOICKAERT G., Wood V., Rajandream M.A., Barrell B.G.;

Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; 299759; CAB16904.1; -.

GeneDB SPombe; SPBC1689.12c; -.

InterPro; IPR000504; RNA_rec_mot.
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InterPro; IRR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS50102; RRM; 1.
                   Eukaryota; Metazoa; Chordat;
Amphibia; Batrachia; Anura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             014327;
Xenopodinae; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Schizosaccharomycete
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Putative poly(a) binding protein. SPBC16E9.12C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Large-scale screening of intracellular protein localization in living fission yeast cells by the use of a GFP-fusion genomic DNA library."; Genes Cells 5.169-190(2000).
                                      Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Cranian
                                                                                 PABPII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1999
01-MAR-2003
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                                                                                                  Poly(A) binding
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Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
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                                                                                                                                                                                                                                                                                                                                                                                  Similarity 7; Conserv
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160 AA;
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18116 MW;
                                                                                                                                                                                                                                                                                                                                                                                                         52.5%;
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87.5%;
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50,
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60,
                     Mesobatrachia;
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Pred. No.
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Pred. No. 8.1;
                   Craniata; Vertebrata;
esobatrachia; Pipoidea;
                                                                                                                                                                                                      PRT;
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                 Euteleostomi; ; Pipidae;
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RESULT 12
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Q9BZB7;
01-JUN-2001
01-JUN-2001
01-MAR-2003
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Q9YGX5;
01-MAY-1999
01-MAY-1999
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MEDLINE-2112522; PubMed-11223249;
MEDLINE-2112522; PubMed-11223249;
Welk J.F., Charlesworth A., Smith G.D., MacNicol A.M.;
"Identification and characterization of the gene encoding "Identification and characterization binding protein.";
Actinopterygii; Neopterygii; Cyprinidae; Danio. NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF329403; AAK01240.1; -.
Interpro; IPR000504; RNA, rec_mot.
PROSTIE; PES50102; RRM; 25
SEQUENCE 491 AA; 54162 MW; 56
                                                                 Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
                                                                                                              ZORBA OR ZOR-1.
                                                                                                                                    ZOR-1.
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Mammalia; Eutheria; Primates;
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PROSITE; PS00030; RRM; RNP_1; 1.
SEQUENCE 296 AA; 32449 MW; 319E1235DF4B33E3 CRC64;
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Pfam; PF00076; rrm; 1.
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Kim J., Choi S., H
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
polyadenylation element-binding protein
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                                      ) (Danio rerio).
; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
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Pred. No.
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Pred. No. 16;
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RESULT 14
QPDED
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OC ACTAN
OC CYPTI
OX NCBI
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01-FEB-1997
01-FEB-1997
01-MAR-2003
                                                                                                                          CPEB.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI TaxID=10090; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Katsu Y., Yamashita M., Ogawa K., Nagahama Y.;

"Goldfish cytoplasmic polyadenylation element binding protein
(CPEB):its interaction with CPE of
by cdk and Eg2 protein kinases.";

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB044534; BAB19051.1; ...
InterPro, IPR000504; RNA_rec_mot.

SMART; SM00360; RRM; 1.

PROSITE; PS50102; RRM; 1.
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01-MAR-2001
01-MAR-2003
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Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cyprinidae; Carassius.
NCBI TaxID=7957;
                                                                                                Mus musculus (Mouse)
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EMBL; AB011680; BAA75637.1; -.
ZFIN; ZDB-GENE-990927-1; ZOTBA.
InterPro; IPR000504; RNA_rec_mot.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
SEQUENCE 559 AA; 62255 MW; 36CF42B1AC70A377 CRC64;
                                                                                                                                                     Cytoplasmic
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SEQUENCE FROM N.A.
SUZUKİ H., Maegawa S., Murakawa M., Hoshijima K.,
Yasuda K., Inoue K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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7 (TrEMBLrel. 02,
8 (TrEMBLrel. 23,
2 polyadenylation
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I (TrEMBLrel. 16, )
I (TrEMBLrel. 23, )
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ilarity 53.8%;
Conservative
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element-binding protein
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element binding protein.
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Pred. No. 31;
1; Mismatches
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Pred. No.
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Ostariophysi; Cypriniform
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Best Local S
Matches 7
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InterPro; IPR000504; RNA_rec_mot.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gebauer F., Richter J.D.;

"Mouse cytoplasmic polyadenylation element binding protein: An evolutionarily conserved protein that interacts with the cytoply polyadenylation elements of c-mos mRNA,";

Proc. Natl. Acad. Sci. U.S.A. 93:14602-14607(1996).

EMBL; Y08260; CAA69588.1; -.
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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SEQUENCE 561 AA; 61917 MW;
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         350
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CPPKGNMPKGYVY 362
                                                                                        CXXYGNSPKGFAY 13
                                                                                                                                                                                     Conservative
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Pred. No.
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Job time : Search completed: November 6.37637 Becs 7 2003, 07:34:37

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Maximum Match 10
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A_Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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1 CXXYGNSPKGFAYXXC
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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40	41	42	42	44	44	58	99	72	Score
50.0	51.2	52.5	52.5	55.0	55.0	72.5	82.5	0	Query Match
107	2515	626	132	365	365	10	242	16	Query Match Length DB
23	22	22	23	23	19	22	22	22	: B
ABG76564	ABB64427	AAB66460	ABP62216	ABG95556	AAW59884	AAB20388	AAB20433	AAB20444	ĬD
HCV El antigen mon	Drosophila melanog	Protein encoded by	Human immunopeptid	Human novel secret	Amino acid sequenc	Anti-FIX/FIXa anti	Anti-FIX/FIXa anti	Anti-FIX/FIXa anti	Description

13-SEP-2000; 2000WO-EP08936.

<u>4</u> .	4 4 4 G	42	41	40	39	88	37	36	S	34	<u></u>	32	31	30	29	28	27	26	25	24	23	22	21	20	19	<u>1</u> 8	17	16	15	14	13	12	1	10
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24	2 4, 4	24	24	22	22	21	21	21	21	20	19	24	22	22	21	16	16	16	16	16	16	22	24	22	18	23	23	22	23	22	21	22	23	23
ABU61105	ABU65941	ABU65608	ABU71151	AAM38889	AAU29063	AAY57273	AAY57272	AAY57270	AAB44275	AAY41719	AAW86276	ABP71366	ABB58914	AAE09692	AAY43866	AAR82982	AAR82981	AAR82986	AAR82980	AAR82979	AAR82977	AAB62753	ABP71368	AAB62780	AAW31724	AAO18433	ABG77145	ABG03182	ABP08836	ABG22854	AAY95075	ABB63366	ABP43671	ABP62206
Human PRO864 polyp		secrete		Human polypeptide	Human PRO polypept	and	and	Wnt-4AF and Wnt-5c	PRO864	Human PRO864 prote	Signal transductio		Ħ	gene	y chain			humanised	humanised		O		PGL-1	HIV-1	ഥ	GD2 and	Anti-IGF-IR antibo		Human ORFX protein	Novel human diagno	Candida albicans p	Drosophila melanog	Methionine adenosy	Human immunopeptid

## ALIGNMENTS

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RESULT 1
AABSO444
ID AABSO444
ID AABSO444
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XX Comp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-FIX/FIXa antibody CDR3.
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                                                                                            22-MAR-2001.
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                                                                                                                                                                                                                                                                          /note= "any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "any amino acid"
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RESULT 2
AAB20433
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Best Local :
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                                                                                                                                                                                                                                                       Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.
                                                                                                                                                                                                                                                                                                                                                                                          AAB20433 standard; Protein; 242 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
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                                                                         Region
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                                                                                                                                                      Region
                                                                                                                                                                                                                     Chimeric
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                                                                                                   Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CXXYGNSPKGFAYXXC 16
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                                                                                                                                                                                                                     Synthetic.
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                                                                                                             /label= CDR3
120..134
/label= Linker
                                                                                     135..242
/label= VL
                                                            223..231
/label= CDR3
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100.0%; Pred. No.
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RESULT 3
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis
                                                                                                                                                                                                                                 Factor IX; FIX; Factor IXa; FIXa; antibody; procoagulant; Factor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Fig 14; 138pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-290358/30.
N-PSDB; AAF30723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scheiflinger F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-SEP-2000; 2000WO-EP08936.
                                                            14-SEP-1999;
                                                                                                                                                       W0200119992-A2
                                                                                                                                                                                     Mus musculus.
                                                                                                                                                                                                                                                                                               Anti-FIX/FIXa antibody 193/AD3 CDR3.
                                                                                                                                                                                                                                                                                                                              21-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diathesis.
                                                                                         13-SEP-2000; 2000WO-EP08936.
                                                                                                                         22-MAR-2001.
                                                                                                                                                                                                                complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                          AAB20388 standard; Peptide; 10 AA
                              (BAXT ) BAXTER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BAXT ) BAXTER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CXXYGNSPKGFAY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CALYGNSPKGFAY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99AT-0001576.
                                                          99AT-0001576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kerschbaumer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 66; DB 22;
Pred. No. 0.0051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Falkner F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22; Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dorner F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ņ
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Scheiflinger F, Kerschbaumer R,

Falkner F,

Dorner F;

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RESULT 4
AAW59884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 (CDR3) of the heavy chain of an antibody expressed by mouse anti-ractivated Factor IX (FIXA) activity. It is an example of anti-FIX/FIXA antibodies of the invention. Such antibodies and their derivatives (including those that comprise the present CDR3 peptide) have Factor VIIIa (FVIIIa) cofactor activity or FIXA activating activity. Administration of the antibodies or their derivating activity. Administration of the antibodies or their derivating activity. Administration of the antibodies or their derivatives leads to an increase in the procoagulant activity of FIXA, even in the presence of FVIII inhibitors. This allows for rapid blood coagulation even in the absence of FVIII or FVIIIA, and in the case of FVIII inhibitor patients. The antibodies or their derivatives are used in a claimed pharmaceutical composition for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic diathesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                       Feng P,
        New isolated polynucleotides and encoded polypeptides - used to develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergences.
                                                                       WPI; 1998-414099/35.
N-PSDB; AAV41925.
                                                                                                                                                                                                                                                                                                                                                                                   Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction; immunological disorder; autoimmune disease; anti-infectious agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of the cDNA clone Bcl-like (HAICH29).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW59884 standard; Protein; 365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood
                                                                                                                                                                                                                 21-JAN-1997;
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                                                                                                                                                                                                                                                                                           23-JUL-1998.
                                                                                                                                                                                                                                                                                                                           WO9831800-A2
                                                                                                                                                                                                                                                                                                                                                         Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 74; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coagulation disorders such as haemophilia A and haemorrhagic diathesis
                                                                                                                                                                      (HUMA-)
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tumours
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                                                                                                                                                                      HUMAN
                                                                                                                                                                                   AUCKLAND UNISERVICES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                    Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YGNSPKGFAY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                      GENOME
                                                                                                                                                                                                               97US-0034205.
97US-0034204.
                                                                                                                                                                                                                                                               98WO-US00960
                                                                                                                                      Krissansen GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.5%
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                                                                                                                                    Ni ď,
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0.0038;
hes 0;
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Best Local
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07-MAR-1997
07-MAR-1997
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07-MAR-1997
07-MAR-1997
07-MAR-1997
11-APR-1997
11-APR-1997
                                                                                                 11-APR-1997;
11-APR-1997;
11-APR-1997;
                                                                                                                                       11-APR-1997;
11-APR-1997;
11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; autoimmune disease; chemotaxis; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; liver neoplasm cardiovascular disorder; cardiac arrest; skin aging; cerebrovascular disorder; cerebral isohaemia; angiogenesis; sunburn; nervous system disorders; Alzheimer's disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the amino acid sequence of the cDNA clone Bcl-like (HAICH29), used in the method of the invention. The products of the clone can be used for treating conditions associated with abnormal expression of the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory diseases, the largies, and as anti-infectious agents. The products can also be used for detection and diagnosis.
                          11-APR-1997;
11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                               ocular disorder; corneal infection; wound healing; tissue regeneration; epithelial cell proliferation; organ transplantation; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG95556 standard; Protein; 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                   08-SEP-1998;
                                                                                                                                                                                                                                                                                                                                            16-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                    US6420526-B1
                                                                                                                                                                                                                                                                                                                                                                                                                      preservative; nutritional.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human novel secreted protein gene 120 polypeptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG95556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 12A-12D; 12Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264 CDKFSGHPKGFAY 276
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7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXXYGNSPKGFAY 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
9703-043312p

9703-043313p

9703-043314p

9703-043568p

9703-043568p

9703-043576p

9703-043576p

9703-043570p

9703-04369p

9703-043672p

9703-043672p

9703-043672p

9703-043674p

9703-043674p
                                                                                                                                                                                          97US:
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                                                                                                                                                                                          -043311P
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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9708-9708-9708-9708-9708-9708-9708-9708-9708-9708-9708-9708-9708-9708-9708-9708-

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97US-056877P
97US-056879P
97US-056880P
97US-056881P
97US-056881P
97US-056881P
97US-056884P
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97US-056889P
97US-056892P
97US-05693P
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97US-05274P
97US-055724P
97US-05631P
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97US-05632P
97US-05663P
97US-05664P
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97US-056875P
97US-056875P
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9710S-047592P
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9710S-047595P
9710S-047597P
9710S-047598P
9710S-047598P
9710S-04761P
9710S-047612P
9710S-047613P
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Best Local S
Matches 7
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12-SEP-1997;
02-OCT-1997;
06-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotraxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents one of the novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated protein that is one of 186 human secreted proteins, given in the specification, encoded by one of 309 cDNA sequences also given in the specification. The protein is used in a pharmaceutical composition used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Dismans, mice, rabbits, goats, horses cats, dogs, chickens or sheep. Dismans which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
                                                                                                                          Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein; nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein; NS3 protein; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endress GA,
Duan R, Ku
25-JAN-2002; 2002WO-US02303.
                                01-AUG-2002.
                                                                                                                                                                                         Human immunopeptide to HCV E2 glycoprotein Fab variable region #63.
                                                                                                                                                                                                                                                          ABP62216;
                                                                                                                                                                                                                                                                                        ABP62216 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Column 103; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human secreted protein for diagnosing, preventing, treating or amelioxating medical conditions and used as a food additive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-634796/68.
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                                                               WO200259340-A1.
                                                                                           Homo sapiens.
                                                                                                                                                                                                                        10-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preservative -
                                                                                                                                                                                                                                                                                                                                                                       264 CDKFSGHPKGFAY 276
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7; Conserv
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, Yu G, Ni J, F
hu J, Florence KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen CA, Pischer CL, Soppet DP,
, Yu G, Ni J, Feng P, Young
u J, Florence KA, Olsen HS, Ebner
Shi Y, Lafleur DW, Li Y, Zeng Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   365
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97US-058785P.
97US-061060P.
98WO-US04493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB:
Pred. No. 35;
l; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23; Length 365;
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Greene JM, Fer
r R, Brewer LA;
, Kyaw H;
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Ferrie AM;
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23 MAY 1997
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29 -MA

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RESULT 7
AAB66460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XSXCXGXBXXQXGXGXGXGXGXXGXXGX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to human immunopolypeptides, produced by a phage transfected cell library. The present sequence is one such immunopolypeptide. The immunopolypeptides have binding specificty for envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C virus (HCV). E2 glycoprotein is believed to be responsible for target cell binding and contains neutralising epitopes, while NS3 is thought to be involved in the replication of HCV. The immunopolypeptides are useful for diagnosing and treating a patient having or suspected to be having
                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis; attenuated microorganism; fad26; Rv2930; signature tagged transposon mutant; mutant library; mycobacterial infection; actinomycetales; antibacterial; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human immunopolypeptide with binding specificity for certain envelope glycoproteins and nonstructural proteins of hepatitis C (HCV), for diagnosing or treating patients having or suspected of
   Screening a mutant library for conditions and for identifying
                                        WPI; 2001-091804/10.
N-PSDB; AAF31627.
                                                                                                                                           06-JUL-1999;
08-JUL-1999;
                                                                                                                                                                                                                                           WO200102555-A1
                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                       Protein encoded by Mycobacterium tuberculosis fad26 (Rv2930)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Fig 12; 308pp; English.
                                                                                    Gicquel B,
                                                                                                                                                                                     06-JUL-2000; 2000WO-IB00950.
                                                                                                                                                                                                                  11-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                    09-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB66460 standard; Protein; 626 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              having HCV infection
                                                                                                                (INSP ) INST PASTEUR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXXYGNSPKGF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CQQYGDSPVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 AA;
                                                                                    Guilhot C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones IM,
                                                                                                                                           99US-0142982
99US-0142833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.5%;
63.6%;
                                                                                      Camacho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42;
Pred. No.
mutants unable to grow under specific loci involved in pathogenicity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DR.
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                                                                                                                                                                                                                                                                                                                                                                       gene.
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        identifying and isolating mutants of actinomycetales and for identifying compounds that have antibiotic activity. The method is used to identify mutants of microorganisms, preferably an actinomycetales, such as M. tuberculosis, M. bovis, M. leprae, M. avium, M. intracellulaire and M. paratuberculosis, that is unable to grow under specific conditions. It is especially useful for identifying loci involved in pathogenicity. It is useful in constructing vaccines. The method can be used to screen multiple libraries concurrently. It can screen libraries of different organisms or different strains of the same organism. The present protein is encoded by a gene which is disrupted by the insertion of the IS 1096 transposon to produce an attenuated mutant of Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   library with insertions in genes and/or regulatory regions of the organisms of interest, where the insertion contains a tag and/or a transposon associated with a tag. The mutants are identified by hybridisation of the tags to known sequences. The method is useful treating an individual suffering from a mycobacterial infection, suspected of being infected with a Mycobacterium, or having been exposed to an infectious Mycobacterium. It is also useful for
                                             New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB64427;
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                                                                                                                                                Venter JC, Adams M,
                                                                                                                                                                                                                    23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                      23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                         27-SEP-2001
                                                                                                                                                                                                                                                                                                                                          WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                             pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 20073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB64427 standard; Protein; 2515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is given in a specification relating to a method for screening a library of mutants. The method comprises constructing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 8; Fig 5A; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprises using signature tagged transposon mutagenesis
                                                                                                   N-PSDB; ABL08530
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                                                                                                                 2001-656860/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            626 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                    2000US-191637P.
2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.5%;
77.8%;
                                                                                                                                                  Li PWD,
                                            detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 42; DB;
; Pred. No. 1.3e
1; Mismatches
                                                                                                                                                Myers EW;
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                                               cell-cell
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Disclosure; SEQ ID NO 20073; 21pp + Sequence Listing; English

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RESULT 9
Query Match
Best Local :
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                                                                                                                          The invention relates to a human monoclomal antibody or its antigen binding fragments, which exhibit immunological binding affinity for a hepatitis C virus (HCV) El antigen, comprising an amino acid sequence homologous to the binding portion of a human antibody Fab molecule from a combinatorial antibody library. The vaccine composition comprising the antibodies or antigen binding fragments against HCV El or E2 antigen or its hypervariable region is useful in treating or preventing HCV infection in a subject. Sequences ABG76513-ABG76568 represent human monoclonal antibodies against HCV El antigen.
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                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccine comprising a human monoclonal antibody against hepatitis C virus (HCV) E1 or E2 antigen, useful for treating or preventing HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; HCV; hepatitis C virus; El antigen; monoclonal antibody; vaccine; hepatotropic; Fab; hypervariable region; E2 antigen; antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 56; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drakenberg K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JAN-2002; 2002WO-SE00044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KARO-) KAROLINSKA INNOVATIONS AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JAN-2001; 2001US-260889P
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Local Similarity
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7; Conserv
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87.5%;
50.0%;
63.6%;
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Pred. No. 8.4e+02;
Score
Pred.
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No.
45;
                       23;
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RESULT 11
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AC ABP43
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AC ABP43
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                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                        The present invention relates to human immunopolypeptides, produced by a phage transfected cell library. The present sequence is one such immunopolypeptide. The immunopolypeptides have binding specificty for envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C virus (HCV). E2 glycoprotein is believed to be responsible for target cell binding and contains neutralising epicopes, while NS3 is thought to be involved in the replication of HCV. The immunopolypeptides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                  New human immunopolypeptide with binding specificity for certain envelope glycoproteins and nonstructural proteins of hepatitis C (HCV), for diagnosism or treating patients having or suspected of having HCV infection -
 26-FEB-2003
                         ABP43671;
                                                     ABP43671 standard; Protein; 261 AA
                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABQ92705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JAN-2001; 2001US-264451P
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NS3 protein; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; Fig 12; 308pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maruyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-2002; 2002WO-US02303.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunopeptide to HCV E2 glycoprotein Fab variable region #53.
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                                                                                                                                                                                                                                                                           diagnosing and treating a patient having or suspected to be having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002-599801/64.
                                                                                                                        89 CQQYGPSPPGYTF 10J
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                                                                                                                                                  1 CXXYGNSPKGFAY 13
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                                                                                                                                                                              Similarity 6; Conserv
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                                                                                                                                                                                                                                      136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones IM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                Conservative
(first entry)
                                                                                                                                                                                            46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hepatitis C virus; HCV; E2 glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burton DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                            Score 40;
Pred. No.
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                                                                                                                                                                                                         Length 136;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to 446 newly isolated polynucleotide sequences. The activity of polynucleotides of the invention may be described as, vulnerary, neuroprotective, immunomodulator, cytostatic and anti-inflammatory. Compositions comprising nucleic acids of the invention are useful for treating a mammalian subject, or as mutritional sources or supplements. These are useful in gene therapy, particularly for treating wounds, burns or ulcers, Alzheimer's disease, Huntington's disease, wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang
pharmaceutical.
          Drosophila; developmental biology; cell signalling; insecticide;
                                                                    26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptides and their encoded proteins, useful as nutritional sources or supplements, or in gene therapy, particularly for treating wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
                                                                                                                        ABB63366 standard; Protein; 291 AA.
                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic; anti-inflammatory; gene therapy; nutritional supplement; wound; burn; ulcer; Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
                                      Drosophila melanogaster polypeptide SEQ ID NO 16890.
                                                                                                                                                                                                                                                                                                                                                                                         amyotrophic lateral sclerosis, autoimmune disorders, cancer or inflammation. The nucleic acids and polypeptides are also useful in diagnostic and research methods. The sequences given in records ABP43544-ABP43989 represent polypeptides encoded by polynucleotides of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID # 574; 357pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-OCT-2000; 2000US-0687527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-OCT-2001; 2001WO-US27760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                  specification,
                                                                                                                                                                                                                                                                                                                                                                              the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-426278/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neuroprotective; immunomodulator; cancer; chromosome 2p11.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methionine adenosyltransferase II alpha clone MGC:2907
                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.
                                                                                                                                                                                             92
                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed it cation, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                             YDDSSKGFDYKTC 104
                                                                                                                                                                                                                        YGNSPKGFAYXXC 16
                                                                                                                                                                                                                                                                                                           261 AA;
                                                                                                                                                                                                                                                   Conservative
                                                                    (first entry)
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                                                                                                                                                                                                                                                              Score 40; DB 23;
Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                             Length 261;
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Best Local :
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                            14-AUG-1998;
                                                                                                                                                                                                                               Candida albicans polypeptide sequence # 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
(JANC ) JANSSEN PHARM NV
                                                          23-DEC-1998;
                                                                                           01-MAR-2000.
                                                                                                                        EP982401-A2.
                                                                                                                                                      Candida albicans
                                                                                                                                                                                      vulvovaginitis;
                                                                                                                                                                                                   Candida albicans infection; growth; survival; medicament; AIDS;
                                                                                                                                                                                                                                                                   23-JUN-2000
                                                                                                                                                                                                                                                                                                 AAY95075;
                                                                                                                                                                                                                                                                                                                               AAY95075 standard; Protein; 385 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 16890; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                            119 GKRPKGFAY 127
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 AA;
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                              98GB-0017796.
                                                            98EP-0310694.
                                                                                                                                                                                    immunocompromised patient; treat.
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Pred. No.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and growth of Candida albicans. The C. albicans nucleic acid molecules encoding the polypeptides of the invention may be used as probes and primers for detecting homologous nucleic acid molecule sequences. The polypeptides and nucleic acid molecules and compounds identified as selectively modulating the expression of the polypeptides, may be used as medicaments or for the preparation of a medicament to treat C.albicans associated diseases, especially in AIDS patients and to treat vulvovaginitis in otherwise healthy females. The use of the polypeptides and polynucleotide sequences to treat C.albicans associated diseases has fewer side effects and less toxicity than previously used methods such as the use of amphotericin. This method is therefore especially suitable for
                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess responsible for genetic disorders or other traits.
Claim 20; SEQ ID No 53213; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Essential polypeptides isolated from Candida albicans, treatment of diseases caused by C.albicans, especially
                                  biodiversity
                                                                                                                                                                                              (HYSE-)
                                                                                                                                                                                                                           31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                        30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                          W0200175067-A2
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #22845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG22854 standard; Protein; 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunocompromised patients, such as AIDS patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a polypeptide that is critical for the survival and growth of Candida albicans. The C. albicans nucleic acid molecules
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                                                                                                                2001-639362/73.
B; AAS87041.
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                                                                                                                                                               RT,
                                                                                                                                                                                            HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385 AA;
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                                                                                                                                                               Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                      forensic;
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CC diagnostic amino acid sequences of the invention.

CC diagnostic amino acid sequences of the invention.

CC diagnostic amino acid sequences of the invention.
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Novel human polypeptides and polynuclectides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative,
                                                                        N-PSDB;
                                                                                                                                         Shimkets RA,
                                                                                                                                                                                                                                   30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
                                                                                                                                                                                                                                                                                                    29-MAY-2001; 2001WO-US10836.
                                                                                                                                                                                                                                                                                                                                                      06-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertenaton; hyperthyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ORFX protein sequence SEQ ID NO:17654.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                               WPI; 2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                                                                      WO200192523-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis.
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                                                                                                                                                                                         (CURA-) CURAGEN CORP
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                                                                           ABN24588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              503 AA;
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                                                                                                                                         Leach MD
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Pred. No.
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2.3e+02;
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Search completed: November 7, 2003, 07:27:04 Job time: 7.89987 secs 용 Ş The present invention describes substantially purified human proteins CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 CC (referred to as open reading from the manufacture of a medicament for treating a pathology associated with an ORFX-associated CC (reating or preventing a pathology associated with an ORFX-associated Syndrome associated with ORFX-associated disorder. ORFX polynucleotide contractive of a medicament for treating a contractive disorder or can be used in the CC treatment of cancer, hyperproliferative disorder. ORFX polynucleotide contractive, hyperproliferative disorders, carhosis of liver, consciously income and disorders, hammorrhage, osteoarthritie, neurodegenerative disorders, disorders related to organ contractive disorders, hammorrhage, consciously income deficiencies and disorders related to organ contractive disorders, hiperthouse the contractive disorders, hiperthouse the contractive disorders, hiperthouse contractive disorders, patients and disorders, infectious contractive disorders, and disorders, hiperthouse disease, autoimmune thyroiditis, myasthenia gravis, graft-versus-host contractive, autoimmune thyroiditis, myasthenia gravis, graft-versus-host contractive, autoimmune thyroiditis, myasthenia gravis, graft-versus-host contractive disorders, incisions, ulcers, for treating osteoporosis, contractive disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, creperfusion hipury in various tissues and conditions resulting from the sequence data for this patent did not form part of the printed contraction, but was obtained not sequences. Matches Query Match Best Local Sequence at ftp.wipo.int/pub/published\_pct\_sequences. Disclosure; SEQ ID 17654; 1037pp; English. hyperproliferative disorders and autoimmune disorders -65 YSNSPDGFA 73 4 YGNSPKGFA 12 7; Similarity 116 AA; Conservative 48.8%; 0 Score 39; DB 23; Length 116; Pred. No. 71; Mismatches 2; Indels 0; Gaps <u>.</u>

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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| Ggn2_6/ptodata/2/pubpaa/US07
| Ggn2_6/ptodata/2/pubpaa/PCT
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Copyright (c) 1993 - 2003 Compugen Ltd.
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15
        15 US-10-153-668-118

15 US-10-153-668-120

11 US-09-809-391-696

12 US-09-882-171-696

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10 US-09-828-708-3

10 US-09-828-708-3

10 US-09-828-708-3

10 US-10-269-805-36

10 US-10-269-805-36

10 US-09-978-978-226

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195.799 Million cell updates/sec
Sequence 118, App
Sequence 696, App
Sequence 696, App
Sequence 3, Appli
Sequence 10, Appli
Sequence 32, Appl
Sequence 36, Appl
Sequence 39, Appl
Sequence 226, App
Sequence 226, App
Sequence 226, App
Sequence 226, App
Sequence 226, App
Sequence 226, App
Sequence 226, App
Sequence 226, App
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## ALIGNMENTS

RESULT 1 US-10-153-668-118

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; SOFTMARE: PatentIn Ver. 2.0
; SEQ ID NO 118
; SEQ ID NO 118
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
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PRIOR APPLICATION NUMBER: US 60/293,172
PRIOR APPLICATION NUMBER: US 60/293,172
PRIOR APPLICATION NUMBER: US 60/293,172
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/316,031
PRIOR APPLICATION NUMBER: US 60/328,403
PRIOR FILING DATE: 2001-08-31
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: JP 2001-260681
PRIOR APPLICATION NUMBER: JP 2001-260681
PRIOR APPLICATION NUMBER: JP 2001-313175
PRIOR APPLICATION NUMBER: JP 2001-313175
PRIOR APPLICATION NUMBER: JP 2001-313175
PRIOR APPLICATION NUMBER: JP 2001-313175
PRIOR APPLICATION NUMBER: JP 2001-313175
PRIOR FILING DATE: 2001-10-10
                                               Query Match
Best Local Similarity
Matches 7; Conserv
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APPLICANT: MATSUDA, Akio
APPLICANT: MURAMATSU, Shuji
APPLICANT: ISHIZAWA, Kenya
TITLE OF INVENTION: STAT6 Activating Gene
FILE REFERENCE: 1254-0207P
1 CXXYGNSPKGFAY 13
                                               Conservative
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Pred. No. 9
                                               Mismatches
                                                                                            DB 15;
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                                                                                       Length 249;
                                             Indels
                                             0,
                                             Gaps
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; LENGTH: 306
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-668-120
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US-10-153-668-120
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                                                                                                                                          ; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-391-696
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US-09-809-391-696
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PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: UP 2001-157043
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: JP 2001-260681
PRIOR APPLICATION NUMBER: JP 2001-260681
PRIOR PILING DATE: 2001-08-30
PRIOR PILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 488
SOFTWALE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 1.86 Human Secreted proteins
FILE REFERENCE: PZ002P2
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LENGTH: 306
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                                                                                                                                                                                                               SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
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APPLICANT: MATSUD
APPLICANT: MURAMA
APPLICANT: ISHIZA
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                                                                       Matches
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CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 60/293,172
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/316,031
PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WATSUDA, Akio
APPLICANT: MURAWATSU, Shuji
APPLICANT: ISHIZAWA, Kenya
TITLE OF INVENTION: STAT6 Activating Gene
FILE REFERENCE: 1254-0207P
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148 CDKFSGHPKGFAY 160
264 CDKFSGHPKGFAY 276
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Similarity 53.8%;
7; Conservation
                                                                   Similarity
7; Conserv
                                 CXXYGNSPKGFAY 13
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                                                                     Conservative
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                                                                   gcore 44; DB; Pred. NO. 14; Mismatches

    Mismatches

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Pred. No. 12;
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US-09-882-171-696
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PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: PCT/US98/04493
PRIOR FILING DATE: 1998-03-06
PRIOR APPLICATION NUMBER: 60/040,162
PRIOR APPLICATION NUMBER: 60/040,333
PRIOR APPLICATION NUMBER: 60/040,333
PRIOR APPLICATION NUMBER: 60/040,333
PRIOR FILING DATE: 1997-03-07
PRIOR FILING DATE: 1997-03-07
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CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 09/809,391
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
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PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,633
                                         DR FILING DATE: 1997-05-23

RE ADPLICATION NUMBER: 60/047,582

RE FILING DATE: 1997-05-23

OR APPLICATION NUMBER: 60/047,596

RE FILING DATE: 1997-05-23

RE FILING DATE: 1997-05-23

RE FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1997-05-43

& APPLICATION NUMBER: 60/047,503

- DATE: 1997-05-23

- CO1047,592
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/038,621
PILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,626
FILING DATE: 1997-03-07
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APPLICATION NUMBER: 60/047,597
FILING DATE: 1997-05-23
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FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,336
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APPLICATION NUMBER: 60/040,163
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APPLICATION NUMBER: 60/047,584
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,592
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,581
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APPLICATION NUMBER: 60/047,492
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,583
FILING DATE: 1997-05-23
                                                                                                                                                                                                              APPLICATION NUMBER: 60/047,613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LING DATE: 1997-05-23
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. US20030175858A1
                       60/047,632
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PRIOR PILLING DATE: 1997-05-23
PRIOR FILLING DATE: 1997-06-41
PRIOR PILLING DATE: 1997-04-41
PRIOR PILLING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043, 56
PRIOR FILLING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043, 311
PRIOR PILLING DATE: 1997-04-11
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PRIOR APPLICATION NUMBER: 60/043, 67
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PRIOR APPLICATION NUMBER: 60/043, 67
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PRIOR APPLICATION NUMBER: 60/043, 313
PRIOR PILLING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043, 315
PRIOR PILLING DATE: 1997-04-11
PRIOR PILLING DATE: 1997-04-12
PRIOR PILLING DATE: 1997-08-22
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PRIOR APPLICATION NUMBER: 60/056, 89
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OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,908
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/048,964
OR RILING DATE: 1997-06-06
OR APPLICATION NUMBER: 60/057,650
OR FILING DATE: 1997-09-05
OR APPLICATION NUMBER: 60/056,884
OR APPLICATION NUMBER: 60/056,884
OR APPLICATION NUMBER: 60/057,669
OR APPLICATION NUMBER: 60/057,669
OR FILING DATE: 1997-09-05
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OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,881
OR PPLICATION NUMBER: 60/056,909
OR APPLICATION NUMBER: 60/056,909
OR FILING DATE: 1997-08-22
OR FILING DATE: 1997-08-22
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OR APPLICATION NUMBER: 60/056,875
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OR APPLICATION NUMBER: 60/047,586
OR FILING DATE: 1997-05-23
OR APPLICATION NUMBER: 60/047,590
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OR APPLICATION NUMBER: 60/047,594
OR FILING DATE: 1997-05-23
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OR APPLICATION NUMBER: 60/057,761
OR PELLING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/047,595
OR FILING DATE: 1997-05-23
OR APPLICATION NUMBER: 60/047,599
OR FILING DATE: 1997-05-23
OR APPLICATION NUMBER: 60/047,588
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,593
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,614
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,501
FILING DATE: 1997-05-23
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                                        1 CXXYGNSPKGFAY 13
                                                                                Similarity
7; Conserv
                                                                                  Conservative
                                                                                                    53.8%;
                                                                                μ
,
                                                                                                    Score 44;
Pred. No.
                                                                                  Mismatches
                                                                                                    DB 12; Length 365; 14;
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RESULT 5
US-09-828-708-3
; Sequence 3, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.

0; Gaps

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APPLICANT: Button, D.

APPLICANT: Schaller, M.

APPLICANT: Schaller, M.

APPLICANT: Schaller, M.

APPLICANT: Schaller, M.

APPLICANT: Schaller, M.

APPLICANT: Schaller, M.

APPLICANT: Suttonatibodies to glucose-6-phosphate isomerase and their participate of invertions and their participation for invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertical invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of invertions of in
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APPLICANT: Schaller, M.

APPLICANT: Schaller, M.

TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici

TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/08844215 Publication No. US20020016445A1 GENERAL INFORMATION:
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Patent No. US20020146753A1
GENERAL INFORMATION:
APPLICANT: Ditzel, H.
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Best Local Similarity
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Best Local (
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PERSSON, MATS AXEL
APPLICANT: ALLANDER, TOBIAS ERIK
TITLE OF INVENTION: HUBAN MONOCLONAL ANTIBODIES SPECIFIC FOR
FITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
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                                                                                                                                          COUNTRY: USA
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Pred. No. 41;
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                 ; Sequence 36, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 32, Application US/10269805
publication No. US20030124129A1
; GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR PILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
SEQ ID NO 32
LENGTH: 108
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Best Local :
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APPLICATION NUMBER: US/08/844,215 FILING DATE: 17-APR-1997 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/635,109 FILING DATE: 19-APR-1996 ATTORNEY/AGENT INFORMATION: 08/635,109 FILING DATE: 19-APR-1996 ATTORNEY/AGENT INFORMATION: 08/635,109 FILING DATE: 19-APR-1996 ATTORNEY/AGENT INFORMATION: 08/635,109 PRICE MCCRACKEN, THOMAS P.
REGISTRATION NUMBER: 38,548 PRESENCE FORCET WINDER: 38,548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (650) 325-7812
TELEPAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
CURRENT APPLICATION NUMBER: US/10/269,805
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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TELECOMMUNICATION INFORMATION: (650) 325-7812
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                                                                                                                                                                                                                                                                                                                                                           Local Similarity 54.5%;
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Local Similarity 54.5%;
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Pred. No. 42;
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Pred. No. 42;
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RESULT 10
US-09-764-903-39
; Sequence 39, Application US/09764903
; Patent No. US20020090674A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ28
; CURRENT APPLICATION NUMBER: US/09/764,903
; CURRENT APPLICATION TOMBER: US/09/764,903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT; ORGANISM: Homo sapiens US-10-269-805-36
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US-09-764-903-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 36
LENGTH: 108
                                                                                                                                                                                                                                                                                                     Sequence 226, Application US/09978295A Patent No. US20020156006A1
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                           APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P
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TYPE: PRT
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es 6; Conserv
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Botstein, David
Desnoyers, Luc
                                      Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
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Gerber, Hanspeter
                                                                                  Godowski, Paul J.
Grimaldi, J. Christopher
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Filvaroff, Ellen
               Napier,
                                     Kljavin,
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James;
                       Sophia S.
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              Mary A.
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Pred. No. 84;
3; Mismatches
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PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-3
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/076454
PRIOR APPLICATION NUMBER: 60/077450
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
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PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR APPLICATION NUMBER: 60/078936
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
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CURRENT FILING DATE: 2001-10-15
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C11
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            OR FILING DATE: 1998-03-31
OR APPLICATION NUMBER: 60/080107
OR APPLICATION NUMBER: 60/080165
OR FILING DATE: 1998-03-31
OR APPLICATION NUMBER: 60/080194
OR APPLICATION NUMBER: 60/080327
OR APPLICATION NUMBER: 60/080327
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OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079689
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079663
OR FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/079923
FILING DATE: 1998-03-30
APPLICATION NUMBER: 60/080105
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FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/079294
FILING DATE: 1998-03-25
APPLICATION NUMBER: 60/079656
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APPLICATION NUMBER: 60/079920
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/080333
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PRIOR FILINO DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-03
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                       APPLICANT:
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OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/084598
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OR APPLICATION NUMBER: 60/084627
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.
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Grimaldi,
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Hillan, Kenneth J
Kljavin, Ivar J.
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                                                                                                                       Paoni,
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                                                                                                                         Nicholas F
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46.2%; Pred. No.
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Patent No.
GENERAL INF
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APPLICANT:
APPLICANT:
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P9630PLC9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT PILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR PILING DATE: 2001-07-30
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Baker Kevin P.
Botstein, David
Bosnoyers, Luc
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J.
Kilavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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Shelton, David L.
Stewart, Timothy A.
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Gerritsen, Mary E.
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Filvaroff, Ellen
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Pred. No. 1.4e+02;
3; Mismatches 4
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PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-10-17
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DR APPLICATION NUMBER: 60/08
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FILING DATE: 1998-04-29
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FILING DATE: 1998-04-29
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wold, Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P26309163
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-07-39
PRIOR FILING DATE: 2001-07-39
PRIOR APPLICATION UNMBER: 60/06250
PRIOR TILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/065311
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US-09-999-822A-226
; Sequence 226, Application US/09999832A
; Publication No. US20020192706A1
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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APPLICATION NUMBER: 60/085697
APPLICATION NUMBER: 60/066364
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Napier, Marv *
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Godowski, Paul
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Botstein, David
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Hillan, Kenneth J
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Pred. No. 1.
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DR FILING DATE: 1997-11-21

DR APPLICATION NUMBER: 60/077450

DR FILING DATE: 1998-03-10

DR PELICATION NUMBER: 60/077632

DR FILING DATE: 1998-03-11

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APPLICATION NUMBER: 60/ FILING DATE: 1998-03-11 APPLICATION NUMBER: 60/ FILING DATE: 1998-03-12

60/077649 3-11 60/077791

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Best Local &
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CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
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RENT FILING DATE: 2001-10-15
OR APPLICATION NUMBER: 09/918585
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Similarity 46.2%;
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Shelton, David L.
Stewart, Timothy A.
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Botstein, David
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Hillan, Kenneth J
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Grimaldi, J. Christopher
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Filvaroff, Ellen
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b. US20030004102A1
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Sophia S.
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Pred. No.
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PRIOR PPLICATION NUMBER: 60/077791
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Query Match 47.5%;
Best Local Similarity 46.2%;
Matches 6; Conservative
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
Score 38; DB 11;
Pred. No. 1.4e+02;
3; Mismatches 4
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Search completed: November Job time: 15.0347 secs 7, 2003, 08:16:55

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                                                                  Matches
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                                                                                               Query Match
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EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL
                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 109 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATA: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                  FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., J
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MO
                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                Local
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                                1 CXXYGNSPKGF 11
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7; Conservative
                                                              Similarity 7; Conserv
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                                                                                                                                                                                                 amino acid
CQQYGNSPYTF 99
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Pack, Peter
Ilag, Vic
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                                                                Conservative
                                                                                                                                                                                                                                                                  (212)596-9090
                                                                                                                                                                                                                                                                                    (212)596-9000
                                                                              48.8%;
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1; Mismatches
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                                                                             Score 39; DB
Pred. No. 19;
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                                                                Mismatches
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                                                                                               DB 4; Length 109;
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RESULT 3

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RESULT 4
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; Patent No. 6538114
; GENERAL INFORMATION:
APPLICANT: Persson, Mate A. A.
APPLICANT: Allander, Tobias E.
APPLICANT: Allander, Tobias E.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-635-109-7
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18,
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                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 327-3400
TELEPAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                         APPLICANT: Scotgen E
APPLICANT: 1014 Hamil
APPLICANT: Menlo Par
APPLICANT: United St
APPLICANT: 1345 Aven
APPLICANT: New York,
APPLICANT: United St
TITLE OF INVENTION:
TITLE OF INVENTION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: MCCTacken, Thomas P
REGISTRATION NUMBER: 38.548
REFERENCE/DOCKET NUMBER: 2300-6146
REFERENCE/DOCKET NUMBER: 2300-6146
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEPHAX: (415) 327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/635,109
FILING DATE: 19-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McCracken, Thomas P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 200 E
STREET: Palo Alto
CITY: Palo Alto
CTATE: California
MCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDENES: single
COMPUTER READABLE FORM:
                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                        STREET: 805 Th
CITY: New York
STATE: New York
                   COUNTRY: U.S.A.
ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
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                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 COQYGSSPRTF 98
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5646253
                                                        New York
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285 Hamilton Avenue, Suite 200
                                                                                             805 Third Avenue
                                                                                                                                                                                                 United States of America
VENTION: RECOMBINANT HUMAN ANTI-LK26
                                                                                                                                                                                                                                        United States of America
1345 Avenue of the Americas
New York, New York 10105
                                                                                                                                                                                                                                                                                                     Menlo Park, California 94025
                                                                                                                                                                                                                                                                                                                       Scotgen Biopharmaceuticals,
1014 Hamilton Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                     Felfe & Lynch
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                                                                                                                                                                                ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.5%; Score 38; DB 4; Length 107; 54.5%; Pred. No. 27;
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US-08-207-996-19
                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFESCT 6.0/ASCII standard
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207,996
FILING DATE: 08-MAR-1994
CILASIFICATION: 530
AUTORNEY/AGENT INFORMATION:
NAME: PASQUALINI, PATTICIA A.
REGISTRATION NUMBER: 100-5363
TELEPHONE: 212-688-9200
TELEPHONE: 212-688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Scotgen
APPLICANT: 1014 Han
APPLICANT: Menlo P:
APPLICANT: United:
APPLICANT: 1345 Ave
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                    TELETAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: United States of America APPLICANT: 1345 Avenue of the Americas APPLICANT: New York, New York 10105
APPLICANT: United States of America TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: RECOMBINANT TITLE OF INVENTION: ANTIBODIES NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 212-688-9200
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                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Pasqualini, Patricia A. REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
FILING DATE: 08-MAR
CLASSIFICATION: 530
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10022
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les 6; Conserv
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5646253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scotgen Biopharmaceuticals,
1014 Hamilton Court
Menlo Park, California 94025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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Patient No. 5646253

GENERAL INFORMATION:
APPLICANT: Scotgen Biopharmaceuticals, I
APPLICANT: 1014 Hamilton Court
APPLICANT: United States of America
APPLICANT: United States of Americas
APPLICANT: New York, New York 10105
APPLICANT: United States of Americas
APPLICANT: New York, New York 10105
APPLICANT: United States of America
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US-08-207-996-20
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                                                                                                                                                        US-08-207-996-20
                                                                                                                                                                                                                                                                                                                            MEDITIM TYPE: 3.5 inch
MEDITIM TYPE: 3.5 inch
COMPTTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Wordberfect 6.0/ASCII standard
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207,996
FILING DATE: 08-MAR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PASQUALINI, PATRICIA A.
REGISTRATION NUMBER: 34,894
REFERBRUCE/DOCKET NUMBER: 1UD-5363
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20,
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                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                             LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                              TELEPHONE: 212-838-3884
TELEPHONE: 212-838-3884
TELEPHONE: 212-838-3884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York
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Local Similarity 46.2%;
es 6; Conservative
                                                                                             Match 47.5%;
Local Similarity 46.2%;
                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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96 CARHGDDPAWFAY 108
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                                    1 CXXYGNSPKGFAY 13
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                                                                          6; Conservative
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1014 Hamilton Court
Menlo Park, California 94025
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                                                                                                                                                                         DNA (genomic)
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                                                                            2; Mismatches
                                                                                             Score 38; DB 1; Length 119;
Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 1;
Pred. No. 30;
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RESULT 7

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PATENT NO. 5646355

PATENT NO. 5646355

GENERAL INFORMATION:

APPLICANY: Scotgen Biopharmaceuticals, Inc.

APPLICANY: 1014 Hamilton Court

APPLICANY: Menlo Park, California 94025

APPLICANY: United States of Americas

APPLICANY: 1345 Avenue of the Americas

APPLICANY: New York, New York 10105

APPLICANY: United States of America

APPLICANY: United States of America
                                                                                                                                                                                                                                                                                                RESULT 8
US-08-207-996-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-207-996-21
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                                                                                                                                                                                                                                                                                Sequence 22,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: PASQUALINI, PATRICIA A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD-5363
TELECOMMUNICATION INFORMATION:
                                TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.0/ASCII standard
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207,996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 TITLE OF INVENTION: ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity tes 6; Conserv
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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                      ADDRESSEE:
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5646253
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E: Felfe & Lynch
805 Third Avenue
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United States of America
1345 Avenue of the Americas
New York, New York 10105
United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27, Application US/08207996 Patent No. 5646253
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: WORDER: PC-DOS/MS-DOS
SOFTWARE: WORDER: PC-DOS/MS-DOS
SOFTWARE: WORDER: US/08/207,996
TOTAL APPLICATION DATA:
APPLICATION NUMBER: US/08/207,996
FILING DATE: 08-MAR-1994
CLASSIFFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PASQUALÍNÍ, PATRÍCÍA A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD-5363
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INFORMATION FOR SEQ ID NO: 22:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD-5363
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MBDIUM TYPE: 3.5 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WOYGDEYFECT 6.0/ASCII standard
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
COMPUTER: IBM PC com
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LENGTH: 119 amino acid
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
COUNTRY: U.S.A.
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FILING DATE: 08-MAR-1994
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                            United States of America
1345 Avenue of the Americas
New York, New York 10105
United States of America
VUNITION: RECOMBINANT HUMAN ANTI-LK26
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                                                                                                                                                                                                                                                                                                                                                         Felfe & Lynch
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46.2%; Pred. No. 30;
htive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        ANTIBODIES
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Gaps

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             Query Match
Best Local Similarity
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                                                                                           ; TOPOLOGY: unknown; MOLECULE TYPE: protein US-08-760-840A-18
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US-08-760-840A-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18, Application US/08760840A Patent No. 5952484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TRM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WOrdperfect
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/760,840A
FILING DATE: 05-DEC-1996
                                                                                                                                                                                                         TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Paul WALLACE;
APPLICANT: William J. HARRIS;
APPLICANT: Wolfgang J. RETTIG;
APPLICANT: Pilar GARIN-CHESA;
APPLICANT: Lloyd J. OLD
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5952484man D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 95/03094
FILING DATE: 08-MAR-1995
                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: LU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acid
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                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                                                            ENGTH:
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1 CXXYGNSPKGFAY 13
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Similarity 46.2%;
6; Conservative
                                                                                                                                                          amino acids
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805 Third Avenue
                                                                                                                                                                                                                                             212-688-9200
                                                                                                                                           unknown
                                            47.5%;
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                                            Score 38; DB
Pred. No. 30;
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Pred. No.
                              Mismatches
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30;
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RESULT 12
US-08-760-840A-20
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US-08-760-840A-19
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                                                                                                                             Patent No. 5952484
GENERAL INFORMATION:
                                                                                                                                                  Sequence 20, Application US/08760840A Patent No. 5952484
                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACLDIE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,840A
FILING DATE: 05-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION: 536
CLASSIFICATION: 536
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Paul W
APPLICANT: Paul WALLACE;
APPLICANT: William J. HARRIS;
APPLICANT: Wolfgang J. RETTIG;
APPLICANT: Holigang J. RETTIG;
APPLICANT: Lloyd J. OLD
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: OUT NEW YORK THEE NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: William J. HARRIS,
APPLICANT: Wolfgang J. RETTIG,
APPLICANT: Pilar GARIN-CHESA,
                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hanson, No. 5952484man REGISTRATION NUMBER: 30,946 REFERENCE/DOCKET NUMBER: LJU TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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APPLICANT: Pilar GARIN-C
APPLICANT: Lloyd J. OLD
                                                                                                                                                                                                                                                                                                                        47.5%;
Local Similarity 46.2%;
es 6; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: unknown TOPOLOGY: unknown
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                                                                                                                                                                                                                                                         96 CARHGDDPAWFAY 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 amino acids
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Pred. No. 30;
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STPEANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21, Application US/08760840A Patent No. 5952484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                            STREET: 805 Third Avenue CITY: New York
                                                                                                                                                                                                                                                                                                APPLICANT: Paul WALLACE;
APPLICANT: William J. HARRIS;
APPLICANT: Wolfgang J. RETTIG;
APPLICANT: Pilar GARIN-CHESA;
APPLICANT: Lloyd J. OLD
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5952484man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 53
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown
MOLECULE TYPE: protein
SOPTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,840A
FILING DATE: 05-DEC-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US.
FILING DATE: 05-DEC-19
                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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FILING DATE: 08-MAR-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Wordperfect
                                                                                                                                                                    COUNTRY: U
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Local Similarity 46.2%;
es 6; Conservative
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                                      CLASSIFICATION DATA:

PRIOR APPLICATION NUMBER: PCT/US 95/03094

FILING DATE: 08-MAR-1995

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION: 536

ATTORNEY/AGENT INFORMATION: 0946

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5363.1 D.

TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION FOR 586-9200

TRLEFAX: 212-688-9200

TRLEFAX: 212-688-9200

TRLEFAX: 114-388-3884

INFORMATION FOR 580 ID NO: 22:
SEQUENCE CHARACTERISTICS:

TENCOMUL: 114-388-3864
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INFORMATION FOR SEQ ID NO: 21:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                 SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,840A
FILING DATE: 05-DEC-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
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LENGTH: 119 amino acid
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REFERENCE/DOCKET NUMBER: LU
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
FILING DATE: 08-MAR-
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MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lloyd J. OLD
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
NUMBER OF SEQUENCES: 31
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SOFTWARE: Wordberfort
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TYPE: amino STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
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                                    LENGTH:
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               amino acid
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Y: U.S.A.
                                119 amino acids
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805 Third Avenue
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Wolfgang J. RETTIG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paul WALLACE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pilar GARIN-CHESA;
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Sequence 28, Application US/08760840A
Patent No. 5952484
GENERAL INFORMATION:
APPLICANT: Paul WALLACE;
APPLICANT: William J. HARRIS;
APPLICANT: William J. HARRIS;
APPLICANT: William J. RETTIG;
APPLICANT: William J. RETTIG;
APPLICANT: Pilar GARIN-CHESA;
APPLICANT: Lloyd J. OLD
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSED: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
CONTRY: New York
COMPUTER: BO5 Third Avenue
STATE: New York
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: Wordperfect
CURRENT APPLICATION NUMBER: US/08/760,840A
FILING DATE: 05-DEC-1996
CLASSIFICATION DATA:
APPLICATION UMBER: PCT/US 95/03094
FILING DATE: 08-MAR-1995
CLASSIFICATION: 536
ATTORNEY/ REGENT INFORMATION:
Search completed: November 7, 2003, 07:30:11 Job time: 2.3498 secs
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TELEPAX: 212-836-3884
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS;
LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                 Matches
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Best Local Similarity 46.2%;
Matches 6; Conservative
                                                                                                                                                                                                                                                           STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: HAISON, NO. 5952484man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                         y Match 47.5%; Score 38; DB 2;
Local Similarity 46.2%; Pred. No. 30;
hes 6; Conservative 2; Mismatches
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                                                                          CARHGDDPAWFAY 108
                                                                                                                                                                                                                                                                                                         unknown
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                                                                                                                                                         5; Indels
                                                                                                                                                                                              Length 119;
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                                                                                                                                                    0;
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November 7, 2003, 07:21:18; Search time 2.0721 Seconds (without alignments) 742.581 Million cell updates/sec
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Title: Perfect score: Sequence: US-09-661-9928-106 82 1 FRNRGMTALLKVSSCD 16

Run on:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR\_76:\* pir2:\* pir3:\* pir4:\* pirl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	۵٥	7	თ	ហ	4	ω	N	ս	İ	Result No.
37	37	37	37.5	37.5	38	38	38	38.5	38.5	39	39	39	39	39	39	39	39	40	40	40	41	41	42	44	70	70	76	82	1 1	Score
45.1	45.1	45.1		45.7	٠	46.3	•		47.0	47.6	47.6	47.6	47.6	47.6	47.6	47.6		48.8	•		50.0	0	۲	53.7	•	85.4	92.7	100.0		Query
151	129	58	376	172	485	485	300	467	455	1208	1099	1058	558	512	505	160	157	573	536	76	1120	873	220	275	2133	869	2319	2351	1 (	Length
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E71547	F82515	AB2880	T42673	B75368	AE3244	T03426	T21149	D97402	AD2620	T34469	A59311	D82654	T19269	AB2865	A97642	T44703	A87117	B96639	B81319	A97957	T14275	B86471	\$44966	E83412	T42763	A25945	A47004	EZHU		Ħ
hypothetical prote	₩.		hypothetical prote	hypotherical prote	sucrose phosphoryl	ä	سر		qmi] 1	hypotherical prote				hypothetical prote	sugar transporter	lipopolysaccharide	probable phosphopa	protein T1F9.16 (i	N-acylneuraminate				lmbR protein - Str	2			н	lation fact		Description

44	4 4 . W N I	4 4 6	38	37	36	35	4	<b>ω</b>	32 2	31	30
9 B	ა ა . ი ი ი	36. 36. 5	37	37	37	37	37	37	37	37	37
43.9	43.9	43.9	45.1	45.1	<b>\$</b> 5.1	45.1	45.1	45.1	45.1	45.1	45.1
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SS8344 F90779	169156 A60279	A34498 S42609 S01033	860138	T29064	G98327	AF2955	H72208	T33760	T48291	T25948	A45989
Shiga-like toxin I Shiga toxin 2 subu	shiga-like toxin i shiga-like toxin i	glycoprotein antig shiga-like toxin I shiga-like toxin I	sex factor aggrega		hypothetical 91.8K	GGDEF family prote	conserved hypothet	sphingosine-1-phos	hypothetical prote	hypothetical prote	peroxisome assembl

# ALIGNMENTS

ernate	lation
names:	lation factor VIII p
antihemophilic	VIII precursor
ernate namee: antihemophilic factor A; coagulation factor VIIIc;	[validated] - human
factor VI	
IIc:	

procoagulant com

C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence revision 28-Aug-1985 #text change 08-Dec-2000
C;Accession: IS4318; A00525; T58059; A23584; A26174; A42348; A43986; S63527; S66445; F
R;Gitschier, J.; Wood, W.I.
Hum. Mol. Genet. 1, 199-200, 1992
A;Title: Sequence of the exon-containing regions of the human factor VIII gene.
A;Reference number: I54318; MUID:93265012; PMID:1303178
A;Accession: I54318

A;Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA

A;Residues: 1-1921,'8',1923-2351 <RES>
A;Cross-references: GB:M88648; NID:gl82381; PIDN:AAA52420.1; PID:gl82383
R;Wood, W.I.; Capon, D.U.; Simonsen, C.C.; Eaton, D.L.; Gitschier, J.; Keyt, B.; Seebu Nature 312, 330-337, 1984
Nature 312, 330-337, 1984
A;Title: Expression of active human factor VIII from recombinant DNA clones.
A;Reference number: A00525; MUID:85061548; PMID:6438526
A;Accession: A00525

R;Toole, J.J.; Knopf, J.L.; Wozney, J.M.; Sultzman, L.A.; Buecker, J.L.; Pis, D.N.; Hewick, R.M.
Nature 312, 342-347, 1984
A;Title: Molecular cloning of a cDNA encoding human antihaemophilic factor.
A;Reference number: I58059; MUID:85061550; PMID:6438528
A;Accession: I58059 A;Molecule type: mRMA
A;Residues: 1-2351 <MCO>
A;Cross-references: EMBL:X01165; EMBL:X01166; EMBL:X01179
A;Cross-references: EMBL:X01165; EMBL:X01166; EMBL:X01179
B;Toole, J.J.; Knopf, J.L.; Wozney, J.M.; Sultzman, U.A.; Buecker, J.L.; Pittman, D.D.
B, D.N.; Hewick, R.M.

A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ

A;Residues: 174,'V',76-1259,'E',1261-2351 <RE2>
A;Cross-references: GB:K01740; NID:g182802; PIDN:AAA52484.1; PID:g182803
R;Truett, M.A.; Blachet, R.; Burke, R.L.; Caput, D.; Chu, C.; Dina, D.; Hartog, K.;
B.; Randolph, A.; Urdea, M.S.; Valenzuela, P.; Dahl, H.H.; Favalaro, J.; Hansen, J.
DNA 4, 333-349, 1985

A;Title: Characterization of the polypeptide composition of human factor VIII:C and A;Reference number: A23584; MUID:86081164; PMID:3935400 A;Accession: A23584

A; Molecule type: mRNA
A; Residues: 1-2351 <TRU>
A; Residues: 1-2351 <TRU>
A; Cross-references: GB: M14113; NID: g182817; PIDN: AAA52485.1; PID: g182818
R; Eaton, D; Rodriguez, H; Vehar, G.A.
Biochemistry 25, 505-512, 1986

A; Title: Proteolytic processing of human factor VIII. Correlation of specific cleavage

A;Reference number: A26174; MUID:86159740; PMID:3082357 A;Accession: A26174

A;Molecule type: protein A;Residues: 20-36;392-399,'X',401-402;1668-1678;1709-1722,'D',1723-1725;1741-1755 <BA1 R;Pittman, D.D.; Wang, J.H.; Kaufman, R.J.

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Protein Sci. 4, 740-746, 1995

A; Title: Locations of disulfide bonds and free Cysteines in the heavy and light chains A; Reference number: A56216; MUID:95338127; PMID:7613471

A; Contents: annotation; disulfide bonds

A; Note: 329-Cys, 711-Cys, and 2019-Cys were shown to have free sulfhydryls

R; Kjalke, M.; Hedding, A.; Talbo, G; Persson, E.; Thomsen, J.; Ezban, M.

Bur. J. Biochem. 234, 773-779, 1995

A; Title: Amino acid residues 721-729 are required for full factor VIII activity.

A; Reference number: S63527; MUID:96163459; PMID:8575434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 733-752;753-759 <XJA>
R;Lind, P.; Larsson, K.; Spira, J.; Sydow-Baeckman, M.; Almstedt, A.; Gray, E.; Sandberg Eur. J. Biochem. 232, 19-27, 1995
A;Title: Novel forms of B-domain-deleted recombinant factor VIII molecules. Construction A;Reference number: S66445; MUID:96048024; PMID:7556150
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A;Title: Characterization of the human factor VIII gene. A;Reference number: A56196; MUID:85061547; PMID:6438525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: Xq28-Xq28
A;Introns: 48/2; 89/1; 130/1; 201/1; 224/1; 263/1; 337/1; 424/2; 481/3; 513/1; 584/3; C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A/Status: preliminary
A;Molecule type: protein
A;Residues: 1668-1685 <LIN>
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A;Meeidues: 'X',517-523;1853-1860,'X',1862-1864,'X',1866 <FAY>
A;Reeidues: 'X',517-523;1853-1860,'X',1862-1864,'X',1866 <FAY>
R;Leyte, A.; van Schijndel, H.B.; Niehrs, C.; Huttner, W.B.; Verbeet, M.P.; Mertens,
J. Biol. Chem. 266, 740-746, 1991
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A;Title: Intersubunit fluorescence energy transfer in human factor VIII
A;Reference number: A43986, MUID:89340500; PMID:2503509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 266, 740-746, 1991
A;Title: Sulfation of Tyr(1680) of human blood coagulation factor VIII is essential for A;Reference number: A56109; MOUD:91093266; PMID:1898735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 20-36;356-371;392-408;582-594;1668-1669,'X',1671;1672-1692;1693-1708;1709-1
A;Experimental source: recombinant material from Chinese hamster ovary cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry 31, 3315-3325, 1992
A,Title: Identification and functional importance of tyrosine sulfate residues within re
A,Reference number: A42348; MUID:92207952; PMID:1554716
                                                                                                                                                                                                                                                                                F;1668-2351/Product: coagulation factor VIIIa light chain #status experimental <ACL>F;1709-2038/Domain: A3 <DA3>
                                                                                                                                                                                                                                                                                                                                                                                                                   F;402-730/Domain: ferroxidase repeat homology <FO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Description: acts as a cofactor, with calcium and phospholipid, for the factor IXa pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: GDB:F8C
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R;Gitschier, J.; Mood, W.I.; Goralka, T.M.; Wion, K.L.; Chen, E.Y.; Eaton, D.H.; Vehar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h, Note: sequence extracted from NCBI backbone and corrected to correspond with the publ
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7,1716-2038/Domain: ferroxidase repeat homology <FO3>
7,2039-2191/Domain: C1 <DC1>
7,2039-22191/Domain: C1 <DC1>
7,2039-27.88/Domain: discoidin I amino-terminal homology <DN1>
7,2192-2351/Domain: C2 <DC2>
7,2192-2351/Domain: discoidin I amino-terminal homology <DN2>
7,2192-2345/Domain: discoidin I amino-terminal homology <DN2>
7,60,258,601,776,803,847,919,962,982,1020,1024,1074,1085,1204,1274,1278,1301,1319,1403,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Regwords: acute phase; blood coagulation; duplication; glycoprotein; hemophilia A; ;1-19/Domain: signal sequence #status predicted <SIG-;20-2351/Product: coagulation factor VIII #status experimental <MAT-;20-740/Product: coagulation factor VIII #beavy chain #status experimental <ACH-;20-740/Product: coagulation factor VIIIa heavy chain #status experimental <ACH-;20-356/Domain: Al <DA1-;20-356/Domain: Al <DA1-;20-356/Domain: ferroxidase repeat homology <FO1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Pathway: blood coagulation
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A; Rolecule type: mRNA
A; Rolecule type: mRNA
A; Residues: 1-2319 < ELD>
A; Cross-references: GB:L05573; NID:g192456; PIDN:AAA37385.1; PID:g192457
A; Cross-references: GB:L05573; NID:g192456; PIDN:AAA37385.1; PID:g192457
C; Superfamily: coagulation factor VIII; discoidin I amino-terminal homology; ferroxid
F;1-19/Domain: signal sequence #status predicted <SIG>
F;3-349/Domain: ferroxidase repeat homology <FO2>
F;402-730/Domain: ferroxidase repeat homology <FO2>
F;402-730/Domain: ferroxidase repeat homology <FO3>
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                                                                                                                                                                                                                                                                              R;Toole, J.J.; Pittman, D.D.; Orr, E.C.; Murtha, P.; Wasley, L.C.; Kaufman, R.J. Proc. Natl. Acad. Sci. U.S.A. 83, 5939-5942, 1986
A;Title: A large region ([approx]95 kDa) for human factor VIII is dispensable for in A;Reference number: A25945; MUID:86287369; PMID:3016730
                                                                                                                                                                                                                                                                                                                                                                                                                                 coagulation factor VIII - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Datc: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: A47004
R;Elder, B.; Lakich, D.; Gitschier, J.
Genomics 16, 374-379, 1993
A;Title: Sequence of the murine factor VIII cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1667-1668/Cleavage site: Arg-Glu (unidentified proteinase) #status experimental F;1708-1709/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status experime F;1740-1741/Cleavage site: Arg-Ala (coagulation factor Xa) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;1686-2006/Domain: ferroxidase repeat homology <FO3>
F;2007-2156/Domain: discoidin I amino-terminal homology <DN1>
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                                                                                                                    C; Superfamily: coagulation factor VIII; discoidin I amino-terminal homology; ferroxid
                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-869 < TOO>
                                                                                                                                                                                                                A;Status: nucleic
                                                                                                                                                                                                                                                      A;Accession: A25945
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Matches
                                                             Query Match
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                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FRNRGMTALLKVSSCD 16
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                           Similarity
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                                                                                                                                                                                                                acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 82; DB 1; 1
100.0%; Pred. No. 1.3e-06;
tive 0; Mismatches 0;
                           85.4%; Score 70; I
0
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Pred. No. 1.7e-0
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                             DB 2;
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                           ,7e-05;
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                                                          Length 869;
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Indels
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2 RNRGMTALLKVSSCD 16

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lmbR protein - Streptomyces lincolnensis
C;Species: Streptomyces lincolnensis
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Oct-1999
C;Accession: $69825; $44966
R;Peschke, U.; Schmidt, H.; Zhang, H.Z.; Piepersberg, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.Cry, S.; Olson, M.V.
Nature 406, 959-964, 2000
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A; Residues: 1-2133 <LOL>
A; Cross-references: EMBL:049517; NID:g1511633; PID:g1511634; PIDN:AAB06705.1
A; Cross-references: EMBL:049517; NID:g1511633; PID:g1511634; PIDN:AAB06705.1
C; Superfamily: coagulation factor VIII; discoidin I amino-terminal homology; ferro C; Keywords: acute phase; blood coagulation; duplication; glycoprotein; hemophilia.
C; Keywords: acute phase; blood coagulation; duplication of SIG>
F;1-19/Domain: signal sequence #status predicted <MAT>
F;20-2133/Product: coagulation factor VIII #status predicted <MAT>
F;23-349/Domain: ferroxidase repeat homology <FOXI>
F;402-730/Domain: ferroxidase repeat homology <FOXI>
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A;Reference number: Z22269
A;Accession: T42763
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
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C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jun-2000
C;Accession: T42763
                                                                                                                                                                                                                                                                                             片
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: streptomycin 6-kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Reseidues: 1-275 <STO>
A;Cross-references: GB:AE004612; GB:AE004091; NID:g9947846; PIDN:AAG05247.1; GSPDB:GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: E83412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: B83412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 streptomycin 3^{\prime\prime}-phosphotransferase PA1858 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa
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Best Local S
Matches 14
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                       8
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RiTheologis, R.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, I ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A.;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A.;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallor Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                 myosin-like protein myl - common sunflower
N;Alternate names: ATM1 homolog protein myl; unconventional myosin
C;Species: Helianthus annuus (common sunflower)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 08-Sep-2000
C;Accession: T14275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A:Residues: 1-873 <STO>
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A; Start codon: GTG
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A;Title: Molecular characterization of the lincomycin-production gene cluster of Strep A;Reference number: S69805; MUID:96020646; PMID:8577249
A;Accession: S69825
                   A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 1
C; Superfamily: Arabidopsis thaliana hypothetical protein F26C24.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB;AE005172; NID:g11386301; PIDN:AAG35092.1; GSPDB:GN00141 C;Genetics:
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                                                                                   A;Reference number: Z17957
A;Accession: T14275
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                                                                                                                                             A; Description: Functional
                                                                                                                                                                          submitted to the EMBL Data Library, March 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein T32G9.38 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
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A;Residues: 1-1120
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Matches
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Best Local :
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9; Conservat
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<VUG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%;
                                                                                                                                             analysis of an unconventional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
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Pred. No.
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Pred. No. 25;
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C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C;Accession: A97957
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B. e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, Y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: A97957
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                                                                                                                                                                                          A;Gene: neuA
C;Keywords:
                                                                                                                                                                                                                                                   A;MOLEGULE type: DNA
A;Residues: 1-536 <PAR>
A;Residues: 1-536 <PAR>
A;Cross-references: GB:AL139077; GB:AL111168; NID:96968444; PIDN:CAB73398.1; PID:9696857
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                               A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp. A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: B81319
                                                                                                                                                                                                                                                                                                                                                                                                                         R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; (C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Nature 403, 665-668, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-acylneuraminate cytidylyltransferase (EC 2.7.7.43) Cj1143 [imported] - Car C;Species: Campylobacter jejuni C;Date: 31-Mar-2000 #text_change 03-Jun-2002
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A97957
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A;Molecule type: DNA
A;Residues: 1-76 <KUR>
A;Cross-references: GB
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C;Superfamily: myosin heavy chain 95F; myosin motor domain homology
F;120-782/Domain: myosin motor domain homology </Myo>
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C;Genetics:
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Best Local S
Matches 7
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Best Local S
Matches 7
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Best Local
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7; Conserva
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                           FKNENSNALISVVECD 449
                                                                 FRNRGMTALLKVSSCD 16
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                                                                                                            Conservative
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                                                                                                                              Score 40;
Pred. No.
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Pred. No. 3.4;
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Pred. No. 31;
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                                                                                                            Mismatches
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lipopolysaccharide core biosynthesis protein [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
                                                                              T44703
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protein T1F9.16 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B96639
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alone
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, t.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A;Authors: Hunter, J.L.; Jin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall
Rizzo, M.; Rooney, T.; Rowley, D.; Sakanno, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakanno, H.
Rizzo, M.; Rooney, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallor
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: B96639
                                                                                                                                                                        A;Gene: coaD
C;Superfamily: lipopolysaccharide core biosynthesis protein kdtB
                                                                                                                                                                                                                                                                                      Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.;
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: A87117
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-157 <8T0>
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A87117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Cole, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroeam, M.A.; Rutherford, K.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable phosphopantetheine adenylyltransferase [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001 C;Accession: A87117
                                                                                                                                                                                                                                                             A;Cross-references: GB:AL450380; NID:g13093433; PIDN:CAC30616.1; GSPDB:GN00147
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A; Residues: 1-573 <STO>
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Best Local (
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                                           2 RNRGMTALLK 11
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                                                                                         Similarity 7; Conserv
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7; Conserv
                                                                                            Conservative
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84
                                                                                                                   47.6%;
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Pred. No.
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-512 <KUR>
A;Cross-references: GB;AE008688; PIDN:AAL43336.1; PID:g17740829; GSPDB;GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
                                                                                                                                                                  A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AB2865
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A97642
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A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tun A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: A97642
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C;Genetics:
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A; Residues: 1-505 < KUR>
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R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, May 1998
A;Reference number: 222830

A;Accession: T44703
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Local Similarity 60.0%;
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VARIANT HEMA CYS-1708.
MEDLINE=89274393; PubMed=2499363;
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"Sulfation of Tyr1680 of human blood
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  (arginine-372-->histidine).";
                                                                                                                                                                                                                                                                                                                                                              internal heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                /ARIANT HEMA CYS-391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90105723; PubMed=2104766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT HEMA CYS-1708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Direct characterization of factor VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT HEMA HIS-391.
MEDLINE=89264602; PubMed=2498882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              resulting in moderately severe Blood 74:2688-2691(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thrombin cleavage site in Blood 74:1612-1617(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE=90001543; PubMed=2506948;
Shima M., Ware J., Yoshioka A., Fukui H., Fulcher C.A.;
Shima M., Ware J., Yoshioka A., Fukui H., Fulcher C.A.;
"An arginine to cysteine amino acid substitution at a critical
"An arginine to cysteine amino acid substitution at a critical
"Thrombin cleavage site in a dysfunctional factor VIII molecule.";
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  denaturing gradient gel electrophoresis ns in the factor VIII gene.";
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M., Hoyer L.W.;
                                                                                                                                                                                                                          Wong C., Kochhan
H., Antonarakis S.
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1. 75:73-77(1990)
                                                                                                                                                                                                                                                                    -1699 AND CYS-1708.
PubMed=2105906;
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a missense mutation
in cleavage site.";
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Best Local &
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Mus musculus (Mouse).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ro
                                                                                                                                                                                                                                                                                                                                                                                                               MSSP, P00451; 1CFG.
MSD; MSI:88383; F8.
IntexPro; IPR001117; Cu-oxidase.
IntexPro; IPR000421; FA58_C.
Pfam; P700394; Cu-oxidase; 3.
Pfam; P700754; F5 F8 type C; 2.
SMART; SM00231; FA58C; 2.
                                                                                                                                                                                                               Signal;
SIGNAL
CHAIN
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PROSITE; PS0022; FA58C 3; 2.

PROSITE; PS00079; MULTICOPPER OXIDASE1; 3.

PROSITE; PS00079; MULTICOPPER OXIDASE1; 3.
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Q06194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-C57BL/6 X CBA; TISSUE-Liver;

MEDLINE-9330511; PubMed-8314577;

Elder B., Lakich D., Gitschier J.;

Elder B., Lakich D., Gitschier J.;

"Sequence of the murine factor VIII cDNA.";

"Sequence of the murine factor VIII cDNA.";

Genomics 16:374-379(1993).

-i- FUNCTION: FACTOR VIII, ALONG WITH CALCIUM AND PHOSPHOLIPID, ACT6

AS A COFACTOR FOR FACTOR IXA WHEN IT CONVERTS FACTOR X TO THE

ACTIVATED FORM, FACTOR XA.

-i- SUBCELLULAR LOCATION: Extracellular.

-i- TISSUE SPECIFICITY: FOUND IN MOST TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Coagulation factor VIII precursor (Procoagulant F8 OR CF8 OR F8C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Contains 3 F5/8 type A domains. SIMILARITY: Contains 2 F5/8 type C domains. SIMILARITY: STRONG, TO COAGULATION FACTOR V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; L05573; AAA37385.1; -. A47004; A47004.
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Rodentia;
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B.
F5/8 TYPE A 3.
PLASTOCYANIN-LIKE
                                                                      F5/8 TYPE A 2.
PLASTOCYANIN-LIKE
PLASTOCYANIN-LIKE
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PLASTOCYANIN-LIKE
PLASTOCYANIN-LIKE
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COAGULATION FACTOR
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Pred. No. 3.5e-07;
; Mismatches 0;
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RESULT 3

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AC P12263; Q95243;

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DT 01-NOV-1997 (Rel. 3

DT 15-SEP-2003 (Rel. 4
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SEQUENCE FROM N.A.
Healey J.F., Lubin
                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                            Coagulation factor
F8 OR CF8.
Sus scrofa (Pig).
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MOD RES
                                    NCBI_TaxID=9823;
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                                                                                      12, Created)
    35, Last sequence update)
    42, Last annotation update)
or VIII precursor (Procoagula
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  I.M., Lollar
                                                   Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
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93.8%;
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SULFATION (BY SIMILARITY).
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InterPro; IPR001117; Cu-oxidase.
InterPro; IPR000421; FA58 C.
Pfam; PF00394; Cu-oxidase; 3.
Pfam; PF00394; FC-oxidase; 3.
Pfam; PF00754; F5 F8 type-C; 2.
SMART; SM00231; FA58C; 2.
PROSITE; PS01285; FA58C 2; 2.
PROSITE; PS01285; FA58C 2; 2.
PROSITE; PS01029; MULTICOPPER_OXIDASE1; 3.
Blood coagulation; Repeat; Plasma; Acute p
Signal; Glycoprotein; Sulfation.
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PIR; A25945; A25945.
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MEDLINE=86287369;
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Kaufman R.J.;
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          PubMed=7510693;
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MEDLINE=2238257; PubMed=12477932;

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A StrausDerg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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B Brownstein M.J., Usdin T.B., Toshiyuki J., Malek J.A., Gunaratne P.H.,

A Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Q99N23;
15-SEP-2003
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
C57BL/6; TISSUE=Kidney;
chimmin L.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hewett-Emmett D., Shimmin L.C.; "Characterization and evolution of two new members of the alpha-carbonic anhydrase gene family in mouse: Carl3 and Carl5."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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nydrase XV precursor (EC 4.2.1.1)
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Matches 8
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A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 ful
r human and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
--- FUNCTION: Reversible hydration of carbon dioxide (By
--- CATALYTIC ACTIVITY: H(2)CO(3) = CO2ATON: Zinc (By similarity).
--- SUBCELULAR LOCATION: Secreted (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF231122; AAK16671.1; -.
EMBL; EC019975; AAH19975.1; -.
HSSP; Q64444; ZZM
MGD; MGI:1931324; Car15.
InterPro; IPR001148; Euk COanhd.
Pfam; PF00194; Carb_anhydrase; 1
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MEDLINE=21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
                                                                                                                                                                                                                       Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                     pyrophosphorylase).
COAD OR KDTB OR ML1663 OR
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 42, Last annotation update)
Phosphopantetheine adenylyltransferase (EC 2.7.7.3)
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30-MAY-2000
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SIGNAL
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                                                                                                                                                                                                                                                                                                                 phosphate adenylyltransferase) (PPAT)
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PS00162; EUK_CO2_ANH
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InterPro; IPR004821; Cyt tran rel.
InterPro; IPR004820; CytIdylyIrransf.
InterPro; IPR001980; LPS biosynth.
Pfam; PF01467; CTP transf 2; 1.
PRINTS; PR01020; LPSBIOSNTHSS.
TIGRPAMS; TIGR01510; coab prev kdtB; 1.
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01-FEB-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3'-dephospho-CoA.

-i- PATHWAY: Coenzyme A (CoA) biosynthesis; fourth step.
-i- SUBUNT: Homohexamer (By similarity).
-i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-i- SIMILARITY: Belongs to the bacterial coaD family.
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Nature 409:1007-1011(2001).
-!- FUNCTION: Reversibly transfers an adenylyl
                                           MEDLINE-95047244; PubMed-7958772;
Brown L.D., Dennehy W.E., Rawlings D.E.
"The F1 genes of the F1F0 ATP synthase
Thiobacillus ferrooxidans complement Es
                                                                                                                                                                                                                                                                                             Thiobacillus
                                                                                                                                                                                                                                                                                                                                    ATP synthase
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                                                                                                                                                STRAIN-ATCC
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Acidithiobacillaceae; Aci
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TIGRPAMs; TIGR00125; cyt_tran_rel; 1.
Transferase; Nucleotidyltransferase;
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HSSP; P23875; 1B6T.
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EMBL; AL583923;
                                                                                                                                                                    SEQUENCE FROM N.A.
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CATALYNIC ACTIVITY: ATP + pantetheine 4'-phosphate =
Microbiol.
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.. 31, Last sequence upda
l. 41, Last annotation up
--- chain (EC 3.6.3.14).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
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                                                                                                                                                                                                                                          ria; Gammaproteobacteria; Acidithiobacillales; Acidithiobacillus.
  122:19-26(1994).
                                              complement Escherichia
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Pred. No. 3.
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se from the acidophilic bacterium
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[ J.R.,
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RESULT 7
PEX2_CRIC
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents
SEQUENCE FROM N.A.
MEDLINE-94309666; PubMed=8035823;
Tsukamoto T., Shimozawa N., Fujik
                                                                 Thieringer R., Raetz C.R.H.;
"peroxisome-deficient Chinese hamster ovary cells with
mutations in peroxisome assembly factor-1.";
J. Biol. Chem. 268:12631-12636(1993).
                                                                                                                                                                                                          Cricetulus griseus (Chinese hamster)
Bukaryota; Metazoa; Chordata; Crania
Mammalia; Eutheria; Rodentia; Sciuro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pfam; PF00006; ATP-synt_ab; 1.
pfam; PF00306; ATP-synt_ab_C; 1.
pfam; PF02874; ATP-synt_ab_N; 1.
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NP BIND 170 177 1

ACT SITE 374 374 8

SEQUENCE 514 AA; 55600 MW;
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ATP synthesis; CF(1); ATP-binding; H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR004100; ATPase_a/bN.
InterPro; IPR000790; ATPase_aC.
InterPro; IPR005594; ATPsynthF1_alpha.
                                                                                                                          MEDLINE=93286102; PubMed=7685346;
                                                                                                                                         TISSUE=Ovary;
                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                NCBI_TaxID=10029;
                                                                                                                                                                                                   Cricetulus.
                                                                                                                                                                                                                                                          PXMP3 OR PEX2 OR PAF1 OR PMP35.
                                                                                                                                                                                                                                                                        protein
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TIGRFAMs; TIGR00962; atpā; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAS THREE MAIN SUBUNITS: A, B AND C. SIMILARITY: Belongs to the ATPase alpha/beta chains family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT.

CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate
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GRADIENT ACROSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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7; Conserv
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JNITS: ALPHA(3), BETA(3), GAN
THREE MAIN SUBUNITS: A, B AN
                                                                                                                                                                                                                                                                                                                                                                                                                                      FRDRGMNALI
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IPR000194; ATPase_a/bcentre.
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          Shimozawa N., Fujiki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                      259
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70.0%;
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BY SIMILARTTY
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Pred. No.
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Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y SIMILARITY.
8349B6BC651BCB6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                        n update)
(Peroxin-2) (Peroxisomal membrane
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19;
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RESULT 8
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Peroxisome assembly factor 1: nonsense mutation in a peroxisome-
deficient Chinese hamster ovary cell mutant and deletion analysis
Mol. Cell. Biol. 14:5458-5465(1994).
FUNCTION: SOMEMHAT IMPLICATED IN THE BIOGENESIS OF PEROXISOME:
-:- SUBCELLULAR LOCATION: Integral membrane protein. Peroxisomal.
-:- SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p52191; Q9J187;
01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
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PROSITE; PS00518; ZF RING; 1; 1.
PROSITE; PS50089; ZF RING; 2; 1.
Transemembrane; Peroxisome; Zinc.
TRANSNEM 139 158 BY
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InterPro; IPRO01841; Znf_ring.
Pfam; PF04757; Pexz_Pex12; 1.
Pfam; PF00097; zf_C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Mammalia, Eutheria, Rodentia, NCBI TaxID=10116;
                   MEDIINE=20287495; PubMed=10764726;
Tucker S.J., Imbrici P., Salvatore L., D'Adamo M.C.,
"pH dependence of the inwardly rectifying potassium
and localization in renal tubular epithelia.";
J. Biol. Chem. 275:16404-16407(2000).
                                                                                                                                                                                                                                                                                   STRAIN=Sprague-Dawley;
MEDLINE=95179470; PubMe
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PIR; A45989; A45989.
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                                                                                                                                  SEQUENCE FROM N.A.
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Adelman J.P.
                                                                                                                                                                              Recept.
                                                                                                                                                                                                        'Cloning and expression of a family :hannels.";
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FUNCTION: INWARD RECTIFIER K+ CHANNELS ARE CHARACTERIZED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123
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194
243
246
304 AA;
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212
283
246
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                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
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BY SIMILARITY.
BY SIMILARITY.
RING-TYPE.
C->Y: LOSS OF E
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84EC5FA613C148BF CRC64;
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ص
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                                                                   channel,
                                                                                       Pessia M.;
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                                                                                                                                            BM86 BOOMI
P20736;
01-FEB-1991
01-FEB-1991
01-NOV-1997
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                                                                                       01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation (Protective Bulder)
Glycoprotein antigen BM86 precursor (Protective Boophilus microplus (Cattle tick).
Eukaryota, Metazoa, Arthropoda, Chelicerata, Ara Barasitiformes; Ixodida; Ixodidae; Boophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF249676; AAF74265.1; -.
InterPro; IPR001838; K+channel_IR.
InterPro; IPR001622; K+channel_pore.
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EMBL; AF249676; AAF74265.1
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PRINTS; PR01320; KIRCHANNEL.
Rand K.N., Moo
Willadsen P.,
           MEDLINE=90099323;
Rand K.N., Moore T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potassium
                                                  SEQUENCE
                                                                          NCBI_TaxID=6941;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: SEEMS TO FORM HETERODIMER WITH KIR4.1/KCNJ10 OR KIR2.1/KCNJ2.

SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: IN THE BRAIN, TESTIS, LIVER, SPLEEN, KII SIEMAXILLARY GLAND, AND ADRENALS.
SIMILARITY: BELONGS TO THE INWARD RECTIFIER-TYPE K+ CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GREATER TENDANCY TO ALLOW POTASSIUM TO PLOW INTO THE CELL RATHER THAN OUT OF IT. THEIR VOLTAGE DEPENDANCE IS REGULATED BY THE CONCENTRATION OF EXTERCELLULAR POTASSIUM; AS EXTERNAL & IS RAISED, THE VOLTAGE RANGE OF THE CHANNEL OPENING SHIFTS TO MORE POSITIVE VOLTAGES. THE INWARD RECTIFICATION IS MAINLY DUE TO THE BLOCKAGE OF OUTWARD CURRENT BY INTERNAL MAGNESIUM, KCNUI6 MAY BE INVOLVED IN THE REGULATION OF FLUID AND PH BALANCE (BY
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7; Conserv
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 Cobon G.S.;
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Pred. No. 24;
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ROLE IN THE CONTROL OF POLYAMINE-MEDIATED CHANNEL GATING AND IN THE BLOCKING BY INTRACELLULAR MAGNESIUM (BY SIMILARITY).

RGSCTSDTNTRRRSFSAVAMVSSCENPEETSLSPQDECKEV
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M1 (POTENTIAL).
H5 (PORE-FORMING) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Willadsen P., Riding G.A., McKenna R.V., Kemp Milelsen J.W., Lahnstein J., Cobon G.S., Gough. "Immunologic control of a parasitic arthropod. protective antigen from Boophilus microplus.", J. Immunol. 143:1346-1351 (1989).
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PROSITE; PS00022; EGF_1; FALSE_NEG.

PROSITE; PS01186; EGF_2; FALSE_NEG.
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SIGNAL
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MEDLINE=89309823;
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IPR006210; IEGF.
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N.
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HYDROPHOBIC, REMOVED DURING
(BY SIMILARITY).
EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
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EGF-LIKE 5.
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01-MAR-1989 (Rel. 1
01-MAR-1989 (Rel. 1
28-FEB-2003 (Rel. 4
SHIGA-11ke toxin II
                                                                                                        DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                Schmidt H., Scheef J., Janetzki-Mittmann C., Datz M., Karch H.;
Schmidt H., Scheef J., Janetzki-Mittmann C., Datz M., Karch H.;
"An ilex trnA gene is located close to the Shiga toxin II operon
enterohemorrhagic Escherichia coli 0157 and non-0157 strains.";
FEMS Microbiol, Leett. 149:39-44 (1997).
-i- FUNCTION: THE B SUBUNIT IS RESPONSIBLE FOR BINDING THE TOXIN
SPECIFIC RECEPTORS ON THE TARGET CELL SURFACE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A., O'Brien A.D., Holmes R.K., Newland J.W.;

Jackson M.P., Neill R.J., O'Brien A.D., Holmes R.K., Newland J.W.;

"Nucleotide sequence analysis and comparison of the structural genes

for Shiga-like toxin I and Shiga-like toxin II encoded by

bacteriophages from Escherichia coli 933.";

FEMS Microbiol. Lett. 44:109-114(1987).
                                                                                                                                                                                                                           EMBL; X07865; CAA30715.1; -.
EMBL; X10775; CAA71748.1; -.
PIR; S01033; S01033.
                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBUNIT: THE SHIGA-LIKE TOXINS CONTAIN A SINGLE A MULTIPLE COPIES OF A B SUBUNIT.
-1- SIMILARITY: BELONGS TO THE SLT BETA FAMILY.
                                                                                                                                                                                                                                                                                 entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT:
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Viruses; dsDNA viruses,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                    Conservative
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. 10, Last sequence update)
. 41, Last annotation update)
II subunit B precursor (Verotoxin
                                                                                                                                                                   F beta; 1.
SLT_beta; 1.
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                                                                                                        9874 MW;
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                                                                Score 36;
Pred. No.
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Pred. No. 4
                                                                                                     POTENTIAL.
SHIGA-LIKE TOXIN II SUBUNIT
BY SIMILARITY.
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                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
40% ribosomal protein 515-6.
RPS15F OR ATSG63070 OR MDC12.3.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                  ARATH
R15F_ARATH
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GO; GO:0018024; F:histone-lysine N-methyltransferase activity; IDA.
GO; GO:0016571; P:histone methylation; IDA.
Pfam; PF05205; Cps15; 1.
Hypothetical protein.
SEQUENCE 142 AA; 16429 MW; 12E73F0C3DD225D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X70529; CAA49922.1; -. EMBL; Z36127; CAA85221.1; -. FIR; S32960; S32960.
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entitles requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
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Hypothetical 16.4 F
YBR258C OR YBR1726.
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01-OCT-1994
"Structural analysis of Arabidopsis thaliana (
Sequence features of the regions of 1,191,918 physically assigned Pl clones.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                   Nakamura Y.,
Tabata S.;
                                                                                                      STRAIN=cv.
                                                                                                                                                                                                                                                                                                                                     Q9FMI6;
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                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                       NCBI_TaxID=3702;
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                                                                                    MEDLINE=98162728;
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complete sequence of a 19,482 bp segment located
of chromosome II from Saccharomyces cerevisiae.";
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41,
                                                                 PubMed=9501997;
S., Kaneko T.,
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edons; core eudicots; Rosid
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HSSP; P80381; 1QXF.
InterFro; IPR002222; Ribosomal S19.
InterPro; IPR005713; S15_euk_arch.
Pfan; PF00203; Ribosomal S19; 1.
PRINTS; PR00975; RIBOSOMALS19.
ProDom; PD001012; Ribosomal_S19; 1.
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APSZ AERPE STANDAL,

30-MAY-2000 (Rel. 39, Created)

30-MAY-2000 (Rel. 39, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

16-OCT-2001 (Rel. 40, Last annotation update)
                    MEDLINE=99310339, PubMed=10382966;
Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosug
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
                                                                                                                                                                                                                                                                      Nomura N., Sako Y., Uchida A., "Molecular characterization and postsplicing fate of three introns within the single rRNA operon of the hyperthermophilic archaeon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aeropyrum pernix.
Archaea; Crenarchaeota; Thermo
Desulfurococcaceae; Aeropyrum.
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TIGREAMS; TIGRO1025; rps6 arch; 1.
PROSITE; PS00323; RIBOSOMAL_519; 1.
Ribosomal protein; Multigene family.
SEQUENCE 160 AA; 18576 MW; A85F03A34DA37649 CRC64;
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                                                                                                                                         STRAIN=K1;
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                                                                                                                                                                                                                                                  Aeropyrum
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Plant Physiol. 127:398-415(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE S19P FAMILY
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RESULT 14
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Best Local
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"Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
                                                                                                                                                                                    EMBL; X87611; CAA60934.1;
EMBL; Z49512; CAA89536.1;
PIR; S55200; S55200.
SGD; S0003773; YJR012C.
                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequer
01-OCT-1996 (Rel. 34, Last annota
Hypothetical 23.2 kDa protein in
YJR012C OR J1440 OR YJR83.25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its the EMPL propriet institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
                                                                                                     Hypothetical protein;
TRANSMEM 17 3
SEQUENCE 207 AA; 2
                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=S288c / FY1679; de Haan M., Smits P.H.M., Grivell L.A.; Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro, IPR001982; Endonuc_LAG/HNH.

Pfam; PP0961; LAGLIDADG 1; 1.

Ffam; Pr0961; LAGLIDADG 1; 1.

Hydrolase; Nuclease; Endonuclease; Intron homing; Complete proteome.

Hydrolase; Nuclease; Endonuclease; Intron homing; Complete proteome.

KSYSLSSLNKKSKRKRSLEBILKIIPCDKAVEPPGER -->
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EMBL; AP000062; BAA80926.1; -.
PIR; A72580; A72580.
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Porein; Transmembrane.
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                                                  1; Length 207;
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<u>ب</u>
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Matches : 8; Conserv
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HSSP; Q16828; 1MKP.
InterPro; IPR001340; DS_phosphatase.
InterPro; IPR001763; Rhodanese-like.
InterPro; IPR001763; Rhodanese-like.
InterPro; IPR00137; TYR_phosphatase.
Pfam; PF00782; DSPc; 1.
Pfam; PF00781; Rhodanese; 1.
SMART; SM00195; DSPc; 1.
SMART; SM00450; RHOD, 1.
SMART; SM00450; RHOD, 1.
SMART; SM00450; RHOD, 1.
PROSITE; PS00164; TYR_PHOSPHATASE_1; 1.
PROSITE; PS00164; TYR_PHOSPHATASE_2, 1.
PROSITE; PS00056; TYR_PHOSPHATASE_2, 1.
PROSITE; PS00056; TYR_PHOSPHATASE_DDAL; 1.
PROSITE; PS00056; TYR_PHOSPHATASE_DDAL; 1.
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Oncogene 19:3537-3545 (2000).
Oncogene 19:3537-3545 (2000).
IPPOSENTATION: RECULATES MITOGENIC SIGNAL TRANSDUCTION BY
DEPHOSPHORYLATING BOTH THR AND TYR RESIDUES ON MAP KINASES
BERK, AND ERK2 (BY SIMILARITY).
IPPOSENTE ACTIVITY: PROTECTION PROPERTY (1):00 - protein
TYPOSINE + phosphate.

TYPOSINE + phosphate.

TYPOSINE ACTIVITY: A phosphoprotein + H(2)O - a protein +
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=White leghorn;
MEDLINE=20379359; PubMed=10918612;
Fu S.-L., Waha A., Vogt P.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DUS4_CHICK STANDARD; PRT; 375 AA.

(99PW71);
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Dual specificity protein hosphatase 4 (EC 3.1.3.48) (EC 3.1.3.16)
(Mitogen-activated protein kinase phosphatase-2) (MAP kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DUSP4 OR MKP2.
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GMTALLKVSS 14
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375 AA;
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178
                                                           Conservative
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                                                                                                                                                                           41052 MW;
                                                    43.9%; Score 36; DB 1; Length 375;
80.0%; Pred. No. 33;
tive 1; Mismatches 1; Indels
                                                                                                                                                                       PROTEIN-TYROSINE PHOSPHATASE.
BY SIMILARITY.
; 179290D0C2BEEEF1 CRC64;
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                                                       Gaps
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202 GITALLNVSS
 211
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Search completed: November 7, Job time: 3.15354 secs 2003, 07:28:11

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Result
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Maximum DB seq length: 2000000000
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Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                 Score
       protein search, using sw model
                                                                                                                                                                                                                                                                                                SPTREMBL_23:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_fungal:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_vortebrate:*
12: sp_virus:*
13: sp_vertebrate:
14: sp_unclassifit
15: sp_archeap:*
17: sp_archeap:*
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Match
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Gapop 10.0 , Gapext 0.5
     830525 seqs, 258052604 residues
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82
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O62730 canis famil
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Q86310 homo sapien
Q80938 mus musculu
Q54372 streptomyce
Q933W7 campylobact
Q933W2 campylobact
Q94387 campylobact
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Q96488 campylobact
Q96488 corynebacte
Q86482 orynebacte
Q86482 scrabidopsis
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005176 agrobacteri	9 ara		Q8pb87 xanthomonas			Q8vg81 mus musculu		Q8cup6 oceanobacil	kluyveromyc	arabidopsi	arabidopsi	μ.		a		Q944i3 arabidopsis		Q9hla8 thermoplasm	4 str	homo	pollo	homo	5	helianthus				Q9s916 arabidopsis

## ALIGNMENTS

D Q	Quer Best Mato	A D D R R P P P P P P P P P P P P P P P P	RESULT 062730
1 FRNRGMTALLKVSSCD 16             710 FRNRGMTALLKVSSCN 725	Query Match 93.9%; Score 77; DB 6; Length 2343; Best Local Similarity 93.8%; Pred. No. 3e-05; Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	O62730 PRELIMINARY; PRT; 2343 AA.  O62730; O1-AUG-1998 (TIEMBLrel. O7, Created) O1-AUG-1998 (TIEMBLrel. O7, Last sequence update) O1-AUG-1998 (TIEMBLrel. O7, Last sequence update) Pactor VIII. Canis familiaris (Dog). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. [1] — ROM N.A. TISSUB-Ridney, and Spleen; Gordy P.W., Bowen R.A.; "Characterization of the camine factor VIII cDNA."; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases!- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS. EMBL; AF049489; AAC05384.1; HSSP; P00451; 1CGG. InterPro; IPR001117; Cu-oxidase. InterPro; IPR001117; Cu-oxidase. InterPro; IPR00121; FA58 C. Pfam; PF00394; Cu-oxidase; 3 Pfam; PF00394; Cu-oxidase; 3 Pfam; PF00394; F5-58 TyPe-C; 2. PROSITE; PS01286; FA58C 2; 2. PROSITE; PS01286; FA58C 2; 2. PROSITE; PS01286; FA58C 2; 2. PROSITE; PS01286; FA58C 2; 2. PROSITE; PS01286; FA58C 2; 2. PROSITE; PS01286; FA58C 2; 2. PROSITE; PS01286; FA58C 3; 2. PROSITE; PS01286; FA58C 3; 2. PROSITE; PS01286; FA58C 3; 2. PROSITE; PS01286; FA58C 3; 2. PROSITE; PS01286; FA58C 3; 2. PROSITE; PS01286; FA58C 3; 2. PROSITE; PS01286; FA58C 3; 2. PROSITE; PS01286; FA58C 3; 2. PROSITE; PS01286; FA58C 3; 2. PROSITE; PS01286; FA58C 3; 2. PROSITE; PS01286; FA58C 3; 2. PROSITE; PS01286; FA58C 3; 2. PROSITE; PS01286; FA58C 3; 2. PROSITE; PS01286; FA58C 3; 2. PROSITE; PS01286; FA58C 3; 2. PROSITE; PS01286; FA58C 3; 2. PROSITE; PS01286; FA58C 3; 2. PROSITE; PS01286; FA58C 3; 2. PROSITE; PS01286; FA58C 3; 2. PROSITE; PS01286; PA58C 3; 2. PROSITE PROSITE; PA58C 3; 2. PROSITE PROSITES	10.7 1 3.0

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018806
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Best Local S
Matches 15
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MEDLINE=20437337; PubMed=10984043;

Stover C.K., Pham K.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folentino E., Westbrock-Wadman S., Lim R.M.,

Brody L.L., Coulter S.N., Hong G.K.-S., Wu Z., Paulsen I.T.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

Opportunistic pathogen.",

Nature 406:959-964(2000)
                 EMBL; AE004612; AAG05247.1; -.
InterPro; IPR006748; APH_6_hur;
Pfam; PF04655; APH_6_hur; I.
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01-MAR-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The canine factor VIII cDNA and 5' flanking sequence."; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
EMBL; AF016334; AAB87412.1; -.
HSSP; P00451; 1CFG.
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InterPro; IPR000421; FA58 C.
Pfam; PF00394; Cu-oxidase; 3.
Pfam; PF00754; F5 F8 type C; 2.
SMART; SM00231; FA58C; 2.
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Canis familiaris (Dog).
Canis familiaris (Dog).
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PS01286; PA58C 2; 2.
PS00079; MULTITOPPER OXIDASE1;
2343 AA; 265829 MW; A054FAI
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Canis.
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Pfam; PR00069; pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS000107; PROTEIN KINASE ATP; 1
PROSITE; PS50011; PROTEIN KINASE DOM; 1
PROSITE; PS50011; PROTEIN KINASE DOM; 1
ATP-binding; Kinase; Transferase.
SEQUENCE 265 AA; 30817 MW; 65AB271A
receptor genes.";
Submitted (UTL-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AB065782; BAC06002.1; -.
InterPro; IRR000276; GPCR_Rhodpsn.
                                                                                         SEQUENCE FROM N.A.
Suwa M., Sato T., Okouchi l
Sutsumi S., Aburatani H.,
"Genome-wide discovery and
                                                                                                                                                                                                                                                              GBNGLO;
01-0CT-2002 (TrEMBLrel. 22, Created
01-0CT-2002 (TrEMBLrel. 22, Last se
01-MAR-2003 (TrEMBLrel. 23, Last an
Seven transmembrane helix receptor.
                                                                                                                                                                                                           Bukaryota; Metazoa;
Mammalia; Eutheria;
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HSSP; P24941; 1BUH.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Catarrhini;
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Q54372;
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01-MAR-2003 (TERMBLrel. 20, Last sequence update)
01-MAR-2003 (TERMBLrel. 23, Last annotation update)
Olfactory receptor MOR174-1.
Mus musculus (Mouse).
Bukaryota: Marsacci
MEDIINE=96020646; PubMed=8577249;
Peschke U., Schmidt H., Zhang H.Z., Piepersberg W.;
"Molecular characterization of the lincomycin-production gene cluster
                                                                                                                                                                                                                Streptomycineae; Streptomycetaceae; NCBI_TaxID=1915;
                                                                                                                                                                                                                                                                     Streptomyces lincolnensis.
Bacteria; Actinobacteridae; Actinomycetales;
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SEQUENCE
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EMBL; AY073244; AAL60907.1; -
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; pP00001; 7tm 1; 1.
PRINTS; PR00237; GFCRRHODOPSN.
PROSITE; PS00237; GFROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     LmbR protein.
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"The olfactory receptor genulat. Neurosci. 0:0-0(2002).
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PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Sciurognathi; Muridae; Murinae; Mus.
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Q93MP7;
01-DEC-2001 (TEMBLEC 1 1
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Q933W2;
Q1-DEC-2001
Q1-DEC-2001
Q1-MAR-2003
Guerry P., Szymanski C.M., Prender Pattarini D.L., Moran A.P.; "Phase Variation of Campylobacter affects Virulence.";
                                                                                                                                                                              Campylobacter jejuni.
Bacteria; Proteobacteria;
Campylobacteraceae; Campy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gilbert M., Michilewicz J., Karwaski M.-F., Cunningham A., Wakarchuk W.W., Wakarchuk W.W., "The genetic basis for the variation in the lipo-oligosaccharide the mucosal pathogen, Campylobacter jejuni: Biosynthesis of sialy ganglioside mimics in the core oligosaccharide."; Submitted (UIL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                    STRAIN=81-176;
                                                                                                                                                                                                                                                                     CMP-NeuNAc synthetase
                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                      NCBI_TaxID=197;
                                                                                                                                                                                                                                                     NEUA1.
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InterPro; IPR003329; Cytidylyl trans.
Pfam; PF02348; CTP_transf_3; 1.
SEQUENCE 221 AA; 24915 MW; CC7F77
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Mol. Microbiol. 16:1137-1156(1995).

EMBL; X79146; CAAS5755.1; -.

InterPro; IPR001585; Transaldolase.

Pfam; PP00923; Transaldolase; 1.

PROSITE; P801054; TRANSALDOLASE 1; 1.

SEQUENCE 220 AA; 23491 MW; 59158145A16A4EF7 CRC64;
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NCBI_TaxID=197;
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Bacteria, Proteobacteria,
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synthetase (CMP-NeuSAc synthetase).
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64.3%;
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                                                               Prendergast M.M.,
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Pred. No. 1
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No. 11;
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                                                               Hickey T.E.,
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X MEDIINE-20127862; PubMed-10660542;

XA Gilbert M., Brisson J.-R., Karwaski M.-F., Michniewicz J.,

Cunningham A.-M., Wu Y., Young N.M., Wakarchuk W.W.;

"Biosynthesis of ganglioside mimics in Campylobacter jejuni OH4384;

If identification of the glycosyltransferase genes, enzymatic synthesis

of model compounds, and characterization of nanomole amounts by 600-

MHZ 1H and 13C NMR analysis.";

MHZ 1H and 13C NMR analysis.";

MHZ 1H and 13C NMR analysis.";

EMBL; AF167344; AAF34146.1;

REMBL; AF130984; AAF34146.1;

REMBL; AF130984; AAF31774.1;

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Matches 7
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Best Local :
               Q9FOM6;
01-MAR-2001 (TEMBLICE1. 1
01-MAR-2001 (TEMBLICE1. 2
01-MAR-2003 (TEMBLICE1. 2
CMP-sialic acid synthetas
 CMP-sialic acid
Campylobacter je
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Submitted (UUL-2001) to the EMBL/GenBank/DDBU databases.

ENBL; AF305571; AAL09372.1; -.
EMBL; AF401528; AAL05994.1; -.
EMBL; AF401528; AAL06008.1; -.
EMBL; AF401529; AAL06008.1; -.
InterPro; IPB003229; Cytidylyl trans.
Pfam; PF02348; CTP transf_3; 1.
SEQUENCE 221 AA; 25002 MW; 3358AB8A6B4493AE CRC64;
                                                                                                Q9F0M6
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Q9K387;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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STRAIN=ATCC 43456, and &
Gilbert M., Michniewicz
Wakarchuk W.W.;
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7; Conserva
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d synthetase.
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43.8%;
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musculus (Mouse).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ro
NCBI TaxID=10090;
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Gilbert M., Michniewicz J., Wakarchuk W
"The LOS biosynthesis locus of Campylob;
Submitted (DEC-1999) to the EMBL/GenBani
EMBL; AF215659; AAG41982.1;
InterPro; IPR003329; Cytidylyl trans.
Pfam; PF02348; CTP transf 3; 1.
SEQUENCE 221 AA; 25015 MW; CA321E85
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Q938X3;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
                                                                               Q99N23 PKBHLIFEL 17, Created)
Q99N23;
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation anhydrase
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STRAIN-ATCC 43460;
Gilbert M., Michniewicz J.,
Wakarchuk W.W.;
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Bacteria; Proteobacteria;
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NCBI_TaxID=197;
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NCBI_TaxID=197;
[1]
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Pfam; PF02348; CTP_transf_3; 1.
SEQUENCE 221 AA; 25014 MW; FC3A3E
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Campylobacteraceae, Campylobacter.
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Rodentia;
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43.8%;
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Campylobacter jejuni: Bio
the core oligosaccharide.
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Pred. No. 11;
3; Mismatches
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of Campylobacter :
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                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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SEQUENCE FROM N.A.
STRAIN=A3(2) / M15;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins !
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., O'Neil S
Pariandream M.A., Rutherford K., Rutter S.,
Rutter S.,
Raylor
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STRAIN-A3(2);

MEDLINE-97000351; PubMed-8843436;

Redenbach M., Kieser H.M., Denapaite D., Bichner A
Kinashi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic a
the 8 Mb Streptomyces coelicolor A3(2) chromosome.
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9KYI4;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Riboflavin-specific deaminase.
RIBD OR SCO2688 OR SCC6IA.09.
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Bentley S.D., Parkhill .
Submitted (MAY-2000) to
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Submitted (MAY-2000)
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SEQUENCE
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STRAIN=C57BL; TISSUE-Kidney;
Hewett-Emmett D., Shimmin L.C.;
"Characterization and evolution of two new members of the alphacarbonic anhydrase gene family in mouse: Carl3 and Carl5.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (DEC-2001) to the
EMBL; AF231122; AAK16671.1;
EMBL; BC01975; AAH19975.1;
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EMBL/GenBank,
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"The entire genomic sequence of Corynebacterium efficiens Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005219; BAC18374.1; -.
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SEQUENCE
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STRAIN=YS-314 / AJ 12310 / DSM 44549 / JC
KAWARABAYASI Y., Yamazaki J., Hino Y., Ki
Ikeo K., Suzuki M., Mashima J., Itoh T.,
Usuda Y., Sugimoto S.;
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Corynebacterineae; Corynebacteriaceae;
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Pfam; PF01872; RibD_C; 1.
TIGREAMS; TIGR00326; cubact_ribD; 1.
TIGREAMS; TIGR00227; ribD_Cterm; 1.
PROSITE; PS00903; CYT_DCMP_DEAMINASES;
COMPLETE PROTEOME.
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Nature 417:141-147(2002)
EMBL; AL939113; CAB92254
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InterPro; IPR004794; Eubact_ribD
InterPro; IPR002734; RibD_C.
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136
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537 AA;
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Pred. No. 43;
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Kikuchi H.,
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Maximum Match 100%
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seg length: 2000000000
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Gapop 10.0 , Gapext 0.5
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Match Length
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82
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195.799 Million cell updates/sec
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'(cgn2_6/ptodata/2)pubpaa/PCT_NEW_PUB.pep:*
'(cgn2_6/ptodata/2)pubpaa/US06_PUBCOMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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           US-10-006-091-1
US-10-047-257-1
US-10-025-900-1
US-10-095-718-2
US-09-957-641-2
US-10-131-510A-2
US-10-133-907-4
US-10-133-927-4
US-10-133-927-4
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## ALIGNMENTS

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APPLICANT: Yee, Helena
ITITLE OF INVENTION: Expression System for Factor VIII
FILE REFERENCE: MSB-7255.1
CURRENT APPLICATION NUMBER: US/10/006,091
CURRENT FILING DATE: 2001-12-06
J. NUMBER OF Seq ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SSQ ID NO 1
LENGTH: 1438
TYPE: PRT
CRGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10006091
Publication No. US20020102730A1
GENERAL INFORMATION:
APPLICANT: Cho, Myung-Sam
APPLICANT: Chan, Sham-Yuen
APPLICANT: Kelsey, William
APPLICANT: Yee, Helena
                                                       RESULT 2
US-10-047-257-1
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US-10-006-091-1
Sequence 1, Application US/10047257 Publication No. US20020115152A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 16; Conserva
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Sequence 2, Application US/10095718
Publication No. US20020131956A1
GENERAL INFORMATION:
APPLICANT: Walsh, Christopher
APPLICANT: Chao, Hengjun
APPLICANT: Chao, Hengjun
APPLICANT: Lynch, Carmel
APPLICANT: Stepan, Tony
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US-10-095-718-2
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; OTHER INFORMATION: human factor VIII sequence
US-10-225-900-1
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US-10-225-900-1
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
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TITLE OF INVENTION: Expression System for Factor VIII
FILE REFERENCE: MSB-7255.2
CURRENT APPLICATION UNMERS: US/10/047,257
CURRENT FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
TENTOTU. 1438
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Best Local
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CURRENT FILING DATE: 2002-08-22
PRIOR APPLICATION NUMBER: US/09/209,916
PRIOR FILING DATE: 1998-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Expression System for Factor VIII FILE REFERENCE: MSB-7255
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                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: human factor VIII sequence
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TYPE: PRT
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Kelsey, William
Yee, Helena
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Chan, Sham-Yuen
Kelsey, William
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; Sequence 2, Application US/10131510A
Publication No. US2003016536A1
; GENERAL INFORMATION:
APPLICANT: Lollar, John S
: TITLE OF INVENTION: Modified Factor VIII
: FILE REFERENCE: 75-95J
: CURRENT APPLICATION NUMBER: US/10/131,510A
: CURRENT FILING DATE: 2002-07-10
: PRIOR FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: U.S. 09/037,601

RESULT 6 US-10-131-510A-2

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CURRENT APPLICATION NUMBER: US/10/095,718
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 09/689,430
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/158,780
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1471
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                                                                                                                                                  ; TYPE: PRT; ORGANISM: Homo sapiens US-09-957-641-2
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                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 2332
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09957641
Publication No. US20020182670A1
GENERAL INFORMATION:
APPLICANT: Emory University
TITLE OF INVENTION: MODIFIED FACTOR VIII
FILE REFERENCE: 75-00
                                                                              Matches
                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/957,641 CURRENT FILING DATE: 2001-09-16 PRIOR APPLICATION NUMBER: US 60/234047 PRIOR FILING DATE: 2000-09-19 PRIOR APPLICATION NUMBER: US 60/236460 PRIOR FILING DATE: 2000-09-29
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TITLE OF INVENTION: Adeno-Associated Virus Vectors Encoding Factor VIII and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 35052/204375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens B-domain deleted factor VIII
                                                                          Local Similarity es 16; Conserv
  697
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                      1 FRNRGMTALLKVSSCD 16
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FRURGMTALLKVSSCD 712
                                                                      100.0%; Score 82; DB 10; ilarity 100.0%; Pred. No. 8.2e-06; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 4.9
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/US97/11155
PRIOR FILING DATE: 1997-06-26
PRIOR PPLICATION NUMBER: PCT/US94/13200
PRIOR PPLICATION NUMBER: U.S. 08/212,133
PRIOR APPLICATION NUMBER: U.S. 08/212,133
PRIOR FILING DATE: 1994-03-11
PRIOR PPLICATION NUMBER: U.S. 07/864,004
PRIOR PILING DATE: 1992-04-07
NUMBER OF SEQ ID NOS: 40
SOFTWAKE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10187319
Publication No. US20030068785A1
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PRIOR APPLICATION NUMBER: U.S. 08/670,707
PRIOR FILING DATE: 1996-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Lollar, John S.
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 40
                                                                   TELEFAX: 303/499-8089
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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APPLICATION NUMBER: US 09/523,656
FILING DATE: 2000-03-10
APPLICATION NUMBER: US 09/037,601
FILING DATE: 1998-03-10
APPLICATION NUMBER: WO PCT/US97/11155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Greenlee, Lorance L.
REGISTRATION NUMBER: 27,894
REFERENCE/DOCKET NUMBER: 75
                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 08/670,707
FILING DATE: 1996-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/187,319 FILING DATE: 27-Aug-2002 CLASSIFICATION: <Unknown>
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STATE: Colorado
                         LENGTH: 2332 amino acids
TYPE: amino acid
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STRANDEDNESS: single
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                                                                                                                                           TELEPHONE: 303/499-8080
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; LENGTH: 2351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-829-4
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US-10-132-829-4
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US-10-133-907-4
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                                                                                             Sequence 4, Application US/10132829
Publication No. US20030044982A1
GENERAL INFORMATION:
APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
TITLE OF INVENTION: With vesicle vector
TITLE OF INVENTION: With vesicle vector
TITLE REFERENCE: 6627-PA179
CURRENT APPLICATION NUMBER: US/10/132,829
CURRENT APPLICATION UNMBER: 001-04-25
PRIOR APPLICATION UNMBER: 60/286,314
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 5
SOUTHARR: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
TITLE OF INVENTION: With vesicle vector
TITLE OF INVENTION: With vesicle vector
TITLE REFERENCE: 6627-PA1170
CURRENT APPLICATION NUMBER: US/10/133,907
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 60/286,314
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 5
SOPTWARE: PatentIn version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/10133907
Publication No. US20030195223A1
GENERAL INFORMATION:
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                                                                                   SEQ ID NO 4
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Best Local Similarity
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TYPE: PRT
ORGANISM: Homo sapiens
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                            716 FRNRGMTALLKVSSCD 731
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Walsh, Christopher

APPLICANT: Walsh, Christopher

APPLICANT: Burstein, Haim

APPLICANT: Lynch, Carmel

APPLICANT: Lynch, Carmel

APPLICANT: Munson, Keith

TITLE OF INVENTION: Adeno-Associated Virus Vectors Encoding Factor VIII and

TITLE OF INVENTION: Adeno-Associated Virus Vectors Encoding Factor VIII and

TITLE OF INVENTION: Methods of Using the Same

FILE REFERENCE: 35052/204375

CURRENT APPLICATION NUMBER: US/10/095,718

CURRENT FILING DATE: 2002-03-12

PRIOR APPLICATION NUMBER: 09/689,430

PRIOR APPLICATION NUMBER: 09/689,430

PRIOR FILING DATE: 1099-10-12

PRIOR FILING DATE: 1099-10-12

NUMBER: OF SEQ ID NOS: 5

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; ORGANISM: Homo sapiens
US-10-172-712-27
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US-10-172-712-27
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Query Match
Best Local Similarity 93...
Thes 15; Conservative
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SEQ ID NO 27
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Publication No. US20030125232A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/10095718
Publication No. US20020131956A1
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APPLICANT: PELLEQUER, JEAN-LUC
TITLE OF INVENTION: STABILIZED PROTEINS WITH ENGINBERED DISULFIDE BONDS
FILE REFERENCE: 4198-4001US1
CURRENT APPLICATION NUMBER: US/10/172,712
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: 60/298,578
PRIOR APPLICATION NUMBER: 60/298,578
PRIOR PLING DATE: 2001-06-14
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GRIFFIN, JOHN H. APPLICANT: GALE, ANDREW J.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: canine B-domain deleted factor VIII
                                                                                                                                                                                                                                                                                                                                                  BNGTH: 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
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Local Similarity 100.0%;
hes 16; Conservative 0
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                                                         93.9%; Score 77; DB 14; Length 1431;
93.8%; Pred. No. 3.9e-05;
tive 1; Mismatches 0; Indels
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CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: U.S. 09/315,179
PRIOR FILING DATE: 1999-05-20
PRIOR PELICATION NUMBER: U.S. 09/037,601
PRIOR PELICATION NUMBER: U.S. 08/670,707
PRIOR PELICATION NUMBER: U.S. 08/670,707
PRIOR PELICATION NUMBER: PCT/US97/11155
PRIOR APPLICATION NUMBER: PCT/US97/11155
PRIOR PILING DATE: 1997-06-26
PRIOR PELICATION NUMBER: PCT/US94/13200
PRIOR PILING DATE: 1994-11-15
PRIOR APPLICATION NUMBER: U.S. 08/212,133
PRIOR PILING DATE: 1994-03-11
PRIOR APPLICATION NUMBER: U.S. 07/864,004
PRIOR PILING DATE: 1994-03-11
PRIOR APPLICATION NUMBER: U.S. 07/864,004
PRIOR PILING DATE: 1994-03-11
PRIOR APPLICATION NUMBER: U.S. 07/864,004
PRIOR FILING DATE: 1992-04-07
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US-10-131-510A-6
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US-10-187-319-6
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Publication No. US20030166536A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 2319
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TITLE OF INVENTION: Modified Factor VIII
FILE REFERENCE: 75-95J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Lollar, John S.
APPLICANT: Lollar, John S.
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSES: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 92.7%; Score 76; DB 12; Local Similarity 93.8%; Pred. No. 0.0001;
                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: FLOODY disk

COMPUTER: 1BM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

REPLICATION MUMBER: US/10/187,319

FILING DATE: 27-Aug-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/523,656
FILING DATE: 2000-03-10
APPLICATION NUMBER: US 09/037,601
FILING DATE: 1998-03-10
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CURRENT APPLICATION NUMBER: US/10/131,510A
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US. 09/315,179
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
PRIOR PILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: U.S. 09/037,601
PRIOR PILING DATE: 1998-03-10
PRIOR PILING DATE: 1996-06-26
PRIOR PILING DATE: 1997-06-26
PRIOR PILING DATE: 1997-06-26
PRIOR FILING DATE: 1997-06-36
PRIOR FILING DATE: 1994-03-11
PRIOR APPLICATION NUMBER: PCT/US97/11155
PRIOR PILING DATE: 1994-11-15
PRIOR APPLICATION NUMBER: U.S. 08/212,133
PRIOR PILING DATE: 1994-03-11
PRIOR PILING DATE: 1992-04-07
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTIN VEX. 2.0
SOFTWARE: PATENTIN VEX. 2.0
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                      RESULT 15
US-10-187-319-4
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                                                                                                                                                                         Matches
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Best Local :
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TITLE OF INVENTION: Modified Factor VIII
FILE REFERENCE: 75-95J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-131-510A-4
                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Sus scrofa
                                                                                                                                                                                              Local
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                                                                                                 326 RNRGMTALLKVYSCD 340
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                                                                                                                                    2 RNRGMTALLKVSSCD 16
                                                                                                                                                                                              Similarity
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TITLE: Sequence of the Murine Factor VIII cDNA
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REGISTRATION NUMBER: 27,894
REFERENCE/DOCKET NUMBER: 75-95K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: WO PCT/US97/11155
FILING DATE: 1997-06-26
APPLICATION NUMBER: US 08/670,707
FILING DATE: 1996-06-26
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93.3%;
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                                                                                                                                                                                              Score 70; 1
Pred. No. 0
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0.0001;
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Search completed: November 7, 2003, 08:16:56 Job time: 15.0347 secs
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                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/670,707
FILING DATE: 1996-06-26
ATTORNEY/AGENT INFORMATION:
NAME: Greenlee, Lorance L.
REGISTRATION NUMBER: 27,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                          IOCATION: 1..368
OTHER INFORMATION: /note= "Predicted amino acid
Other of porcine factor VIII A2 domain, defined as residues
bequence of porcine factor VIII, amino acids 373-740. Residues
homologous to human factor VIII, amino acids 373-740. Residue
1-4 are from known porcine amino acid sequence."

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
                                                                                            326 RNRGMTALLKVYSCD 340
                                                                                                                                                                                         14;
                                                                                                                         2 RNRGMTALLKVSSCD 16
                                                                                                                                                                                                                Similarity
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FILING DATE: 27-Aug-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 368 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 303/499-8080
TELEFAX: 303/499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 09/523,656
FILING DATE: 2000-03-10
APPLICATION NUMBER: US 09/037,601
FILING DATE: 1998-03-10
APPLICATION NUMBER: WO PCT/US97/11155
FILING DATE: 1997-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boulder
STATE: Colorado
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE TYPE: spleen
                                                                                                                                                                                         Conservative
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                                                                                                                                                                                      85.4%; Score 70; DB 15; Length 368; 93.3%; Pred. No. 0.00016; tive 0; Mismatches 1; Indels
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Result
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Maximum Match 100%
Listing first 45 s
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein - protein search, using sw model
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         pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 2000000000
         November 7, 2003, 07:21:18 ; Search time 2.3498 Seconds (without alignments) 288.098 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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      \begin{array}{c} 1144 \\ 123 \\ 223 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 \\ 233 
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US-08-882-083-2

US-08-588-107-2

US-09-243-539-2

US-09-224-867-4

US-09-224-867-4

US-08-212-133A-8

US-08-474-503-6

US-08-6770-707A-6

US-09-037-601-6

US-09-315-179-6
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US-08-683-83-83-39-3
US-08-684-0048-4
US-08-251-937A-4
US-08-251-937A-2
US-08-276-594A-2
US-08-277-077A-2
US-08-670-707A-2
US-09-037-601-2
US-09-037-601-2
US-09-523-656-2
PCT-US94-13200-2
US-08-121-202-2
US-08-121-202-2
US-08-121-202-2
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RESULT 2 US-08-683-839B-3 ; Sequence 3, Application US/08683839B ; Patent No. 5744326 ; Patent No. 5744326 ; Patent No. 5744326 ; APPLICANT: 111, Charles . R. et al. TITLE OF INVENTION: Use of Viral Cis-Acting Post-Transcriptional ; TITLE OF INVENTION: Regulatory Sequences To Increase Expression of ; TITLE OF INVENTION: Intronless Genes Containing Near-Consensus Splice Site NUMBER OF SEQUENCES: 18 ; CORRESPONDENCE ADDRESS: } ADDRESSEE: LAHIVE & COCKFTELD STREET: 60 State Street, suite 510 CITY: Boston STATE: Massachusetts COUNTRY: USA ZIP: 02109-1875	Query Match 100.0%; Score 82; DB 4; Length 1438; Best Local Similarity 100.0%; Pred. No. 1.4e-06; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 16; Conservative 16 Or 1 FRNRGWTALLKVSSCD 16	RESULT 1 US-09-209-916-1 US-09-209-916-1 Requence 1, Application US/09209916 Patent No. 6358703 GENERAL INFORMATION: APPLICANT: Chan, Sham-Yuen APPLICANT: Chan, Sham-Yuen APPLICANT: Kelsey, William APPLICANT: Kelsey, William APPLICANT: We, Helena TITLS OF INVENTION: Expression System for Factor VIII FILE REFERENCE: MSB-7256 CURRENT APPLICATION NUMBER: US/09/209,916 CURRENT FILING DATE: 1998-12-10 NUMBER OF SEQ ID NOS: 2 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1 LENGTH: 1438 TYPE: PRT ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: human factor VIII sequence	28 76 92.7 2319 4 US-09-523-656-28 Sequence 28, Appli 29 76 92.7 2319 5 PCT-US94-13200-6 Sequence 6, Appli 30 70 85.4 367 1 US-07-864-004B-2 Sequence 2, Appli 31 70 85.4 367 1 US-08-251-937A-2 Sequence 2, Appli 32 70 85.4 368 1 US-08-212-133A-6 Sequence 2, Appli 34 70 85.4 368 1 US-08-212-133A-6 Sequence 4, Appli 36 70 85.4 368 2 US-08-670-707A-4 Sequence 4, Appli 36 70 85.4 368 3 US-09-037-601-4 Sequence 4, Appli 39 70 85.4 368 3 US-09-315-179-4 Sequence 4, Appli 39 70 85.4 368 5 PCT-US94-13200-4 Sequence 4, Appli 40 70 85.4 561 1 US-08-212-237A-6 Sequence 4, Appli 40 70 85.4 868 1 US-09-531-656-4 Sequence 4, Appli 41 70 85.4 868 1 US-08-121-202-4 Sequence 6, Appli 41 70 85.4 868 1 US-08-212-337A-6 Sequence 6, Appli 41 70 85.4 868 1 US-08-251-937A-6 Sequence 6, Appli 59 70 85.4 868 1 US-08-251-337A-6 Sequence 6, Appli 59 70 85.4 868 1 US-08-251-337A-6 Sequence 6, Appli 59 70 85.4 1090 5 PCT-US93-03275-6 Sequence 6, Appli 59 70 85.4 1443 2 US-08-670-707A-39 Sequence 3, Appli 59 70 85.4 1443 2 US-08-670-707A-39 Sequence 3, Appli 59 70 85.4 1443 2 US-08-670-707A-39 Sequence 3, Appli 69 70 70 85.4 1443 2 US-08-670-707A-39 Sequence 3, Appli 69 70 70 85.4 1443 2 US-08-670-707A-39 Sequence 3, Appli 69 70 70 85.4 1443 2 US-08-670-707A-39 Sequence 3, Appli 69 70 70 70 70 70 70 70 70 70 70 70 70 70
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Patent No. 5364771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                              TELEFAX: 404-815-6555 INFORMATION FOR SEQ ID NO: 4:
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INFORMATION FOR SEQ ID NO: 3:
                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EMU106
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6508
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/07/864,004B
FILING DATE: 07 APRIL 1992
CLASSIFICATION: 435
                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lollar, John S.
APPLICANT: Runge, Marschall S.
TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: (617)227-7400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1100
CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Remillard, Jane E. REGISTRATION NUMBER: 38,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/683,839B
FILING DATE: 11-MARCH-1996
                                     ENGTH:
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                                   2332 amino acids
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US-08-251-937A-4
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     Best Local Similarity Matches 16; Conserv
                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application Patent No. 5583209
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                            FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: Liver cDNA sequence
                                                                                                                                                                                                                                                                                  TELEFAX: 404-815-6555
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1100
CITY: Atlanta
STATE: Georgia
STATE: US
                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Pratt, John S.
REGISTRATION NUMBER: 29,476
REPERENCE/DOCKET NUMBER: EM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                    HYPOTHETICAL: NO
                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2332 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 07-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lollar, John S.
APPLICANT: Runge, Marschall S.
TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: Liver cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 31-MAY CLASSIFICATION: 435
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 30309
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Similarity 100.0%; Pred. No.
16; Conservative 0; Mismatch
                                                                                                                                                                                                                                  amino acid
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100.0%; Score 82; DB 1; I ilarity 100.0%; Pred. No. 2.5e-06; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1100 Peachtree Street
                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-1994
                                                                                                                                                                                                                  single
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                                Length 2332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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RESULT 6
US-08-276-594A-2
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                                                                         Patent No.
                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 404-572-6555
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2332 amino aci
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                 APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: 104-572-6508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,7
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 30303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lollar, John S.
APPLICANT: Runge, Marschall S.
TITLE OF INVENTION: Hybrid Hur
                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                ORGANISM: HO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Atlanta
STATE: Georgia
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 07-APF
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/2
FILING DATE: March 11, 1994
                                                                                                                                                                                                                                          Local
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    Application US/08276594A
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                                                            INFORMATION:
                                                                                                                                                                                                                            16;
                                                                                                                                                                                            1 FRNRGMTALLKVSSCD 16
                                                                                                                                                                                                                                          Similarity
                                                                                                                                                             FRNRGMTALLKVSSCD 712
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                                                                                                                                                                                                                                                                                                                                ; NO
YPE: N-terminal
YONEMURA, Hiroshi
TAJIMA, Yoshitaka
SUGAWARA, Keishin
MASUDA, Kenichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                2332 amino acids
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E: Liver cDNA sequence
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Pred. No. 2.5e-06;
                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                     Length 2332;
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                                                                                                                                                                                                                              PATENT NO. 574446

PATENT NO. 574446

GENERAL INFORMATION:
APPLICANT: Emory University
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
V41794FFICK & Cody
                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08474503 Patent No. 5744446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/950,191
FILING DATE: 24-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 243262/1991
FILING DATE: 24-SEP-1991
ATTORNEY/AGENT INFORMATION:
                        ZIP: 30309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 74129/195/AOPA TELECOMMUNICATION INFORMATION: TELEPHONE: (302)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 18-JUL-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                  STATE:
                                                                                                                                                                                               STREET: 1100
CITY: Atlanta
 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 3000 K STREET: Washington
                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: WEGNER, Harold C. REGISTRATION NUMBER: 25,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                                           COUNTRY:
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3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                1100 Peachtree Street, Suite 2800
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07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 82; DB 1; 100.0%; Pred. No. 2.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROCESS FOR PREPARING HUMAN COAGULATION FACTOR VIII PROTEIN COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Release #1.0, Version
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               US/08/474,503
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FRAGMENT TYPE: N-terminal
CRIGINAL SOURCE:
CRGANISM: Homo sapien
TISSUE TYPE: Liver cDNA sequence
US-08-474-503-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
FILING DATE: 15-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,133
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,004
FILING DATE: 07-APR-1992
APPLICATION NUMBER: US 07/864,004
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Greenlee, Lorance L.
REGISTRATION NUMBER: 27,894
REFERENCE/DOCKET NUMBER: 75-95F
TELECOMMUNICATION INFORMATION:
TELEPANE: 303/499-8089
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PStentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: YES
ANTI-SENSE: NO
ANTI-STRUCT TYPE: N-terminal
                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US94/13200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: EMITELECOMMUNICATION INFORMATION: TELEPHONE: 404-815-6500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pratt, John S.
REGISTRATION NUMBER: 29,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Soulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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LENGTH: 2332 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Colorado
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Pred. No. 2.5e-06;
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US-09-037-601-2
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; TISSUE TYPE: Liver
US-08-670-707A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
                                                                                                                                                                                                                                                                APPLICATION UNMERR: US/09/037,601
FILING DATE: 26-JUN-1996
CLASSIFICATION: 26-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US94/13200
FILING DATE: 15-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,133
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA: US 08/212,133
PRIOR APPLICATION NUMBER: US 07/864,004
FILING DATE: 07-APR-1992
AFTORNEY/AGENT INFORMATION:
NAME: PENDER US 07/864,004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 618037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 16; Conservative 0
                                                                                                                                                   TELEFAX: 303/499-8089
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Lollar
                                MOLECULE TYPE: pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2332 amino acids
                                                                                                                                                                                                 NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 75-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 80303
COMPUTER READABLE FORM:
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2332 amino acids
                 HYPOTHETICAL:
ANTI-SENSE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL:
ANTI-SENSE: 1
 RAGMENT TYPE:
                                                              STRANDEDNESS: single TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boulder
STATE: Colorad
                                                                                                                                                                                 TELEPHONE:
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                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NO
YPE: N-terminal
                                                                                                                                                                 303/499-8089
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not relevant
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N-terminal
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Pred. No. 2.5e-06;
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; ORGANISM: Home
; TISSUE TYPE:
US-09-037-601-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-315-179-2
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US-09-315-179-2
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SEQ ID NO 2
LENGTH: 2332
                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09523656 Patent No. 6458563
                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Patent No. 6376463
GENERAL INFORMATION:
                                                                                                          CURRENT APPLICATION NUMBER: US/09/523,656
CURRENT FILING DATE: 2000-03-10
EARLIER APPLICATION NUMBER: 09/037,601
EARLIER FILING DATE: 1998-03-10
EARLIER APPLICATION NUMBER: 08/670,707
EARLIER FILING DATE: 1996-06-26
                                                                                                                                                                                                                                                                                                                                            -09-523-656-2
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Best Local Similarity
                                                                        SOFTWARE: PatentIn Ver.
                                                                                          NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                      APPLICANT: LOllar S., John
TITLE OF INVENTION: MODIFIED FACTOR VIII
FILE REFERENCE: 75-951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER APPLICATION NUMBER: PCT/US94/13200 EARLIER FILING DATE: 1994-11-15 EARLIER PEPLICATION NUMBER: U.S. 08/212,133 EARLIER FILING DATE: 1994-03-11 EARLIER FILING DATE: 1994-03-11 EARLIER APPLICATION NUMBER: U.S. 07/864,004 EARLIER FILING DATE: 1992-04-07 NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: U.S. 09/037,601
EARLIER FILING DATE: 1998-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/315,179
CURRENT FILING DATE: 1999-05-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lollar, John S
TITLE OF INVENTION: Modified Factor VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 75-95H
ORGANISM: Homo sapiens
                   LENGTH: 2332
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: U.S. 08/670,707
EARLIER FILING DATE: 1996-06-26
EARLIER APPLICATION NUMBER: PCT/US97/11155
EARLIER FILING DATE: 1997-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                     697
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Pred. No. 2.5e-06;
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; TISSUE TYPE: Liver cDNA sequence
PCT-US93-03275-4
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                                                                Matches
                                                                              Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application PC/TUS9303275
GENERAL INFORMATION:
APPLICANT: Lollar John S.
APPLICANT: Runge, Marschall S.
TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 16; Conserv
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-BOS #1.0,
                                                                                                                                                                             PRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 07/864004
                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: EM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA;
APPLICATION NUMBER: PCT/US93/032:
FILING DATE: 19930407
                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Kilpatrick & Cody
                                                                                                                                                                                                                                                              TYPE: AMINO ACID STRANDEDNESS: sir TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Atlanta
STATE: Georgi
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697 FRNRGMTALLKVSSCD
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                             1 FRNRGMTALLKVSSCD 16
                                                                l Similarity
16; Conserv
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                                                                Conservative
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                                                                                                                                                                                                                                                                              single
                                                         100.0%; *-
                                                                              100.0%; Score 82;
100.0%; Pred. No.
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712
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                                                            Mismatches
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                                                                          2.5e-06;
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RESULT 13 PCT-US94-13200-2

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Sequence 2, Application PC/TUS9413200 GENERAL INFORMATION:

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RESULT 14
US-08-121-202-2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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APPLICANT: Pittma:
APPLICANT: Rehemt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2334
TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
MOLECULE TYPE: pro'
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 2:
                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                   APPLICANT: Kaufman, Randal J.
TITLE OF INVENTION: CHIMERIC PROCOAGULANT PROTEINS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: Liver cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION MAMBER: PCT/US94/13200
FILING DATE: 15-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Emory Univer
TITLE OF INVENTION: Hyl
NUMBER OF SEQUENCES: 1:
CORRESPONDENCE APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
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LENGTH: 2332 amino aci
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                               APPLICANT:
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                        COUNTRY:
                                                                                                                                          CITY: Cambridge
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CITY: Atlanta
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Rehemtulla, Alnawaz
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linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 82; DB 5; ilarity 100.0%; Pred. No. 2.5e-06; Conservative 0; Mismatches 0;
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US-08-366-851A-2
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US-08-366-851A-2
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SEQUENCE CHARACTERISTICS:
LENGTH: 2351 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                TELEFAX: (619) 452-2616
INFORMATION FOR SEQ ID NO:
                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 9300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 452-1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IEM FC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
OPERATING SYSTEM: FC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hsu, David Chi-Tang
APPLICANT: Chang, Steven
TITLE OF INVENTION: Retroviral Delivery of Full Length Factor VIII
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: GI 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1210 X8574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Meinert, M. C.
REGISTRATION NUMBER: 31,544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,202
FILING DATE: 14-SEP-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
                               TOPOLOGY:
                                                                                                                                                                                                                                          APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 514
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         TYPE: protein
                                          amino acid
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11055 Roselle Street
                                                               2351 amino acids
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De Polo, Nicolas J.
Hsu, David Chi-Tang
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